



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 120754

TO: Ginny Portner
Location: REM/3B02/3C18
Art Unit: 1645
Friday, April 30, 2004

Case Serial Number: 08/487032

From: Deirdre Arnold
Location: Biotech-Chem Library
REM 1A64
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** Supervised by David Schreiber*

Search Notes

Thank you for using STIC services.

PATENT COOPERATION TREATY

From the INTERNATIONAL SEARCHING AUTHORITY

To: ELIZABETH A. HANLEY
LAHIVE & COCKFIELD
60 STATE STREET
BOSTON, MASSACHUSETTS 02109
UNITED STATES OF AMERICA

PCT

NOTIFICATION OF TRANSMITTAL OF THE INTERNATIONAL SEARCH REPORT OR THE DECLARATION

(PCT Rule 44.1)

ENTERED DOCKETED

June 7, 1997 - Amend After Search

Date of Mailing
(day/month/year) **07 APR 1997**

Applicant's or agent's file reference
GTN-001CPPC

FOR FURTHER ACTION See paragraphs 1 and 4 below

International application No.
PCT/US96/18542

International filing date
(day/month/year)
15 NOVEMBER 1996

Applicant
ASTRA AKTIEBOLAG

1. ☒ The applicant is hereby notified that the international search report has been established and is transmitted herewith.
Filing of amendments and statement under Article 19:
 The applicant is entitled, if he so wishes, to amend the claims of the international application (see Rule 46):
When? The time limit for filing such amendments is normally 2 months from the date of transmittal of the international search report; however, for more details, see the notes on the accompanying sheet.
Where? Directly to the International Bureau of WIPO
 34, chemin des Colombettes
 1211 Geneva 20, Switzerland
 Facsimile No.: (41-22) 740.14.35
For more detailed instructions, see the notes on the accompanying sheet.
2. ☐ The applicant is hereby notified that no international search report will be established and that the declaration under Article 17(2)(a) to that effect is transmitted herewith.
3. ☐ With regard to the protest against payment of (an) additional fee(s) under Rule 40.2, the applicant is notified that:
 - ☐ the protest together with the decision thereon has been transmitted to the International Bureau together with the applicant's request to forward the texts of both the protest and the decision thereon to the designated Offices.
 - ☐ no decision has been made yet on the protest; the applicant will be notified as soon as a decision is made.
4. **Further action(s):** The applicant is reminded of the following:
 - Shortly after 18 months from the priority date, the international application will be published by the International Bureau. If the applicant wishes to avoid or postpone publication, a notice of withdrawal of the international application, or of the priority claim, must reach the International Bureau as provided in rules 90 bis 1 and 90 bis 3, respectively, before the completion of the technical preparations for international publication.
 - Within 19 months from the priority date, a demand for international preliminary examination must be filed if the applicant wishes to postpone the entry into the national phase until 30 months from the priority date (in some Offices even later).
 - Within 20 months from the priority date, the applicant must perform the prescribed acts for entry into the national phase before all designated Offices which have not been elected in the demand or in a later election within 19 months from the priority date or could not be elected because they are not bound by Chapter II.

Name and mailing address of the ISA/US
Commissioner of Patents and Trademarks
Box PCT
Washington, D.C. 20231
Facsimile No. (703) 305-3230

Authorized officer

KENNETH R. HORLICK

Telephone No. (703) 308-0196

APR 11 1997

PATENT COOPERATION TREATY

PCT

INTERNATIONAL SEARCH REPORT

(PCT Article 18 and Rules 43 and 44)

| | | |
|--|---|--|
| Applicant's or agent's file reference GTN-001CPPC | FOR FURTHER ACTION see Notification of Transmittal of International Search Report (Form PCT/ISA/220) as well as, where applicable, item 5 below. | |
| International application No. PCT/US96/18542 | International filing date (<i>day/month/year</i>) 15 NOVEMBER 1996 | (Earliest) Priority Date (<i>day/month/year</i>) 17 NOVEMBER 1995 |
| Applicant ASTRA AKTIEBOLAG | | |

This international search report has been prepared by this International Searching Authority and is transmitted to the applicant according to Article 18. A copy is being transmitted to the International Bureau.

This international search report consists of a total of 3 sheets.

☒ It is also accompanied by a copy of each prior art document cited in this report.

1. ☐ Certain claims were found unsearchable (See Box I).

2. ☒ Unity of invention is lacking (See Box II).

3. ☒ The international application contains disclosure of a nucleotide and/or amino acid sequence listing and the international search was carried out on the basis of the sequence listing

☒ filed with the international application.

☐ furnished by the applicant separately from the international application,

☐ but not accompanied by a statement to the effect that it did not include matter going beyond the disclosure in the international application as filed.

☐ transcribed by this Authority.

4. With regard to the title, ☒ the text is approved as submitted by the applicant.

☐ the text has been established by this Authority to read as follows:

5. With regard to the abstract,

☒ the text is approved as submitted by the applicant.

☐ the text has been established, according to Rule 38.2(b), by this Authority as it appears in Box III. The applicant may, within one month from the date of mailing of this international search report, submit comments to this Authority.

6. The figure of the drawings to be published with the abstract is:

Figure No. _____

☐ as suggested by the applicant.

☐ because the applicant failed to suggest a figure.

☐ because this figure better characterizes the invention.

☒ None of the figures.

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US96/18542

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:
1-7 regarding SEQ ID NO: 9, 46, 59, 69, 83, 97, 98, 101, 109, and 114

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
☐ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US96/18542

A. CLASSIFICATION OF SUBJECT MATTER

IPC(6) :C07H 21/04

US CL :536/23.7

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 536/23.7

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

APS, MEDLINE, BIOSIS, CA, DERWENT

search terms: H. pylori, vaccine, gene, protein

C. DOCUMENTS CONSIDERED TO BE RELEVANT

| Category* | Citation of document, with indication, where appropriate, of the relevant passages | Relevant to claim No. |
|-----------|--|-----------------------|
| A | US 5,403,924 A (COVER et al.) 04 April 1995. | 1-7 |
| A | US 5,434,253 A (THOMPSON et al.) 18 July 1995. | 1-7 |
| A, P | US 5,527,678 A (BLASER et al.) 18 June 1996. | 1-7 |

☐

Further documents are listed in the continuation of Box C.

☐

See patent family annex.

| | |
|---|--|
| * Special categories of cited documents: | *T* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention |
| *A* document defining the general state of the art which is not considered to be of particular relevance | *X* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone |
| *E* earlier document published on or after the international filing date | *Y* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art |
| *L* document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified) | *G* document member of the same patent family |
| *O* document referring to an oral disclosure, use, exhibition or other means | |
| *P* document published prior to the international filing date but later than the priority date claimed | |

Date of the actual completion of the international search

13 MARCH 1997

Date of mailing of the international search report

07 APR 1997

Name and mailing address of the ISA/US
Commissioner of Patents and Trademarks
Box PCT
Washington, D.C. 20231

Facsimile No. (703) 305-3230

Authorized officer

KENNETH R. HORLICK

Telephone No. (703) 308-0196

Restructor
4/98

BIOTECHNOLOGY DATA SCREEN

SN 08/487,032 INVNTR SMITH, DOUGLAS GAU 1802 DT-IN-LOC 01/13/98

LOCN 1819 GROUP ART UNIT 1819

STATUS: 030 DOCKETED NEW CASE - AVAILABLE FOR EXAMINATION

TITLE: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO HELICOBACTER PYLORI
FOR DIAGNOSTICS AND THERAPEUTICS

ENT-CD DATE DEFINITION

CRFF 03/25/97 ERROR (S) IN CRF CORRECTED BY STIC

CRFN 02/23/96 CRF DOES NOT MATCH APPLICATION SPECIFICATION / APPLICANT

END OF DISPLAY

- SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1547 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: circular

Figure 559
 (pages 1 - 407)

- (ii) MOLECULE TYPE: DNA (genomic)
 (iii) HYPOTHETICAL: NO
 (iv) ANTI-SENSE: NO
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori
 (xi) SEQUENCE DESCRIPTION:

| | |
|--|------|
| ATGTGTTCTC AGGAAATTTT ATCAAGCTTG CAAACCATTA TTGCCGAACA ATTTTCTATA | 60 |
| AATATCATCA CTCAGCTTGC TAATAAACTC ACACAAGTTA AAAATCTAAA TTTTTTTGAG | 120 |
| AATAAGACC ATACTATCAA GCTTAACACT ATCCATAACG GACTGCACAT CCGCCCCCTA | 180 |
| AATTATGTCA GTAATCTTTT TTTCAATCTA CAACGCATTA TAGGGCTTAT CAGTCTGTTT | 240 |
| GGGATATTAT TTTCCATTAG TATTTATCTA CCCTTTATAA TGATTTTGTG AACAGTGCCT | 300 |
| TGTATTCTCA TTTCCAACCA TATAGCAAAA AAACATAGTG CTTCCATAGA TAAACTTCAA | 360 |
| GACCAAAAAG AAAGCATGCA AAATTACTTA TACTCTGGAC TAGATAACCA AAAGAACAAG | 420 |
| GACAACCTAT TATTTAACTT CATGCTAAAT TTTCACCATA AATTTATTGA AACAAAAGAA | 480 |
| TTGTATCTCA ATAATTTTGT GAAAGTAGCC CAAAAAACT TAATATTTAC CATATATGCT | 540 |
| GATGTTTTAA TCACCACTCT AAGTATTGCA CTATTTTTTC TAATGGTTTT TATTATCCTT | 600 |
| TCAAAATTAA TTGGTGTGGG AGCAATTGCT GGGTATATCC AAGCATTTAG CTCTACCCAA | 660 |
| CAACAACCTAC AAGATTTATC ATTTTATGGA AAGTGGTTTT TTGCTATCAA TAAATACTTT | 720 |
| GAAAATTATT TCTGTATTTT AGATTACAAA ATACCGAAAC CAGAAACACA AATCAAATTA | 780 |
| GAAGAAAAAA TCCATAGCAT TACATTTGAA AATATTAGTT TCTCTTATCC TAATTCAAAA | 840 |
| CTTATTTTTG AAAACTTTAA TCTCTCTTTA CACTCTAATA AAATTTATGC ATTAGTCGGC | 900 |
| AAGAATGCTA GCGGAAAAAG CACGCTGATT AATTTATTAT TAGGTTTTTA TACCCCAAAT | 960 |
| TCAGGTCAAA TTATCATTA TAACAAATAC CCATTACAAG ACTTGGAACCT AAATAGCTAC | 1020 |
| CATCAACAAA TGAGTGCCAT ATTTCAAGAT TTTTCTCTTT ATGCTGGGTA TAGCATTGAT | 1080 |
| GATAATCTTT TTATGCAAAA CAATATCACT AAAGAGCAAT TGAAGCAAAA AAGAGAAATA | 1140 |
| CTAAAATCTT TTGATGAGAA TTTTCAAAAT TGTCTTAATG ATTGCAACAA CACACTATTT | 1200 |
| GGAGCGCAAT ATAATGGGGT AGATTTTTCT TTAGGTCAAA AGCAACGCAT AGCTACCATG | 1260 |

| | | | | | | |
|------------|------------|------------|------------|------------|------------|------|
| AGAGCCTTTT | TAAAACCAAG | TAATTGCATT | GTTTTAGATG | AGCCAAGCAG | CGCCATCGAT | 1320 |
| CCCATTATGG | AAAAAGAGTT | TTTAGATTTT | ATTTTAAAA | AATCGCAATC | TAAGATGGCT | 1380 |
| TTAATTATTA | CACACCGCAT | GAATAGTGTC | AAGCAAGCTA | ATGAAATTAT | CGTGTTAGAT | 1440 |
| CAAGGCAAAC | TAATAGAACA | GGGCAACTTT | GAAACCCTTA | TGAAAAACA | GGGATTATTT | 1500 |
| TGCGAATTGT | TTTTGAAACA | ACAATAC | | | | 1527 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGGAGCGCA AGACGCTCCA GAGCATTTTA TGTTTAATAA AAAAAGAAAT GATGAGACCA | 60 |
| AAAGGTATTC TAATGAATTG TTGCAGGSCT TGGAAACACC AGGTTCTTAA GCAAAGCACG | 120 |
| ACAGGTTTAG TGGTGTGAG CATTATCTCT TCTACAGCCC CCTTTATTGG TTTGTTTGGG | 180 |
| ACGGTAGTTG AAATTTTAGA AGCGTTTAAC AATTGGGCG CGTTAGGTCA AGCTTCTTTT | 240 |
| EGAGTGATCG CACCCATTAT TTCTAAGGCG CTTATCGCCA CCGCTGCAGG GATTTTAGCA | 300 |
| GCCATTCCAG CCTATTCTTT TTAATTGATC TTAAAGCGCA AGGTGTATGA TTTATCGGTT | 360 |
| TATGTGCAGA TGCAAGTGGA TATTTTGTCT TCTAAAAA | 399 |

(2) INFORMATION FOR SEQ ID NO:1038312_f3_3.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 474 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGCATGAAC GCATTGAAAG AGGTATTRGA AATAATGAAT GTAAAGAAAT TTTTGGCAAT | 60 |
| GAACTCAAAC AAAGAAAGAC AAAATTGATT GAAGACATAG AACGGCGGTT CAAAGAATGC | 120 |
| GAGGAACAAT TCCGTGGAAG TGTAGGAAAA AATATTGAAC AACTTGAAGA AAGAGTTAAA | 180 |
| GATTCTCTAG CGATTATAAA ACGCATCAAT AACCTTGGTC TTAATCCTAA TTCTAATTTT | 240 |
| AATATGGATA GCGGCATTGA TACAATAGGC TTATTTAGTT CAATAGGAGG TTTGGTGTTG | 300 |
| CTTCTATTGA CGCCTGTAGT AGGTGAGTTT GCGTTAATTG CAGGAGTGGG TTTAGCATT | 360 |
| GTGGGGGTAG GTAAATCAAT ATGGAGTTTT TTTGATTCAG ATTATAAAAA ATCCCAACAA | 420 |
| AGAAAAGAAG TGGATAAGAA TTTACATCAA ATTTGCGAAA AATTGTGCAG GATG | 474 |

(2) INFORMATION FOR SEQ ID NO:10407625_f2_11.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 336 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGCCTGGCG TGTATCAAAT GAGTATAGAG CCTCTTTTAA AAGAATGCGA AGAATTAGTG | 60 |
| GGTTTAGGCA TAAAAGCCGT TTTATTGTTT GGCATTCCTA AACATAAGGA CGCTACAGGA | 120 |
| AGCCATGCGT TAAATAAGGA TCACATTGTC GCAAAAGCTA CGAGAGAAAT TAAAAACGA | 180 |
| TTTAAGGATT TGATCGTTAT AGCGGATTG TGTTTTTCG AATACACCGA CCATGGGCAT | 240 |
| TGCGGGATTT TAGAAAACGC TTCTGTGTCT AACGATAAAA CGCTAAAGAT TTTAAATCTT | 300 |
| CAAGGGCTTA TTTTGCTGAA AGCGGTGTGG ATATTC | 336 |

(2) INFORMATION FOR SEQ ID NO:104792_f1_1.nt:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 195 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: FLAGELLAR HOOK-ASSOCIATED PROTEIN 1 HAP1

| | |
|---|-----|
| GTGGAAAACA ACAAGAGTTT AAAGCATGCG AATGAGTTAA GGGATAAGCG AGATGAATTA | 60 |
| GAGTTTCATT TCGGAGAGCT TTTCGGGGGG AATGTTTTTA AAAGCAGCAT TAAAACCCAT | 120 |
| TCGCTCACAG ATAAAGACTC AGCGGACTTT GATGAGAGCT ATAACCTTAA TATCGGGCAT | 180 |
| GGGYTCAATA TSATA | 195 |

(2) INFORMATION FOR SEQ ID NO:10580417_c2_23.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1857 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|--|------|
| GTGTTTGTGG CAAGCAAACA AGCTGACGAA CAAAAAAGC TAGTTATAGA GCAAGAGGTT | 60 |
| CAAAAGCGGC AGTTTCAAAA AATAGAAGAA CTTAAAGCAG ACATGCAAAA GGGTGTCAAT | 120 |
| CCCTTTTTTTA AAGTCTTGTT TGATGGGGGG AATAGGTTGT TTGGTTTCCC TGAAACTTTT | 180 |
| ATTTATTCTT CTATATTTAT ATTGTTTGTA ACAATTGTAT TATCTGTTAT TCTTTTTCAA | 240 |
| GCCTATGAAC CTGTTTTGAT TGTAGCGATT GTTATTGTGC TTGTAGCTCT TGGATTCAAG | 300 |
| AAAGATTACA GGCTTTATCA AAGAATGGAG CGAGCGATGA AATTTAAAAA ACCTTTTTTTG | 360 |
| TTTAAGGGCG TGAAAAACAA AGCGTTCATG AGCATTTTTTt CcATGAAGCC TAGTAAAGAA | 420 |
| ATGGCTAATG ACATCCACTT AAATCCAAAC AGAGAAGACA GGCTTGTGAG CGCTGCAAAC | 480 |
| TCCTATCTAG CGAATAACTA TGAATGTTTT TTAGATGATG GGGTGATCCT TACTAACAAC | 540 |
| TATTCTCTTT TAGGCACAAT CAAATTGGGG GGCATTGATT TTTTAACCAC TTCCAAAAAA | 600 |
| GATCTCATAG AGTTACACGC TTCTATTTAT AGCGTTTTTA GGAATTTTGT TACCCCTGAA | 660 |
| TTCAAATTTT ATTTTCACAC TGTTAAAAAG AAAATCGTTA TTGATGAAAC CAATAGGGAT | 720 |
| TATGGTCTTA TTTTTTCTAA TGATTTTCATG CGAGCCTATA ATGAGAAGCA AAAGAGAGAA | 780 |
| AGTTTTTATG ATATTAGTTT TTATCTCACC ATAGAGCAAG ATTTATTAGA CACTCTCAAT | 840 |
| GAACCCGTTA TGAATAAAAA GCATTTTGCA GACAATAATT TTGAAGAGTT TCAAAGGATT | 900 |
| ATTAGAGCCA AGCTTGAAAA CTTCAAAGAT AGGATAGAGC TCATAGAAGA GCTACTGAGT | 960 |
| AAATACCACC CCACTAGATT AAAAGAATAC ACTAAAGATG GCATTATTTA CTCCAAACAA | 1020 |
| TGCGAATTTT ACAATTTTCT TGTGGGAATG AATGAAGCCC CTTTTATTTG CAACAGAAAA | 1080 |
| GACTTGTATC TCAAGGAAAA AATGCATGGT GGGGTGAAAG AAGTTTATTT TGCCAATAAG | 1140 |
| CATGGAAAAA TCTTAAATGA CGATTTGAGT GAAAAATATT TTAGCGCTAT TGAGATCAGT | 1200 |
| GAATACGCCC CTAAATCACA GAGCGATTTG TTTGATAAAA TCAACGCTCT AGACAGCGAA | 1260 |

| | | | | | | |
|-------------|------------|------------|------------|------------|-------------|------|
| TTTATCTTTA | TGCATGCTTA | TTCGCCTAAA | AACTCACAAG | TTTTAAAGGA | CAAAC TAGCT | 1320 |
| TTCACCTCTA | GAAGGATTAT | TATTAGTGGA | GGCTCCAAAG | AGCAAGGCAT | GACTTTGGGT | 1380 |
| TGCTTGAGCG | AATTAGTGGG | TAATGGTGAT | ATTACGCTAG | GCAGTTATGG | TAATTCTTTA | 1440 |
| GTGCTGTTTG | CTGATAGCTT | TGAAAAAATG | AAACAAAGCG | TTAAGGAATG | CGTCTCTAGT | 1500 |
| CTTAACGCTA | AAGGTTTTTT | AGCCAACGCA | GCGACTTTCT | CTATGGAAAA | TTACTTTTTT | 1560 |
| GCCAAACATT | GCTCTTTTAT | CACGCTTCCT | TTTATTTTTG | ATGTAACTTC | TAACAATTTT | 1620 |
| GCTGATTTCa | TAGCGATGAG | AGCGATGAGT | TTTGATGGCA | AAGAAGACAA | TAACGCTTGG | 1680 |
| GGCAATAGCG | TGATGACGTT | AAAAAGCGAG | ATCAATTCGC | CTTTTTATTT | GAACTTCCAC | 1740 |
| ATGCCCCACTg | ATTTTGGTTC | AGCTTCAGCA | gGaCACACTT | TGATACTTGG | CTCAACCGGT | 1800 |
| TCAGGTAAGa | ACAGTGTTTA | TGTCCATGAC | TCTAAACGCT | ATGGGGCAAT | TTGCCTA | 1857 |

(2) INFORMATION FOR SEQ ID NO:10664078_c2_14.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| GTGAAAACAT CGTGTTTGGT TACAATAGGG AGGATCCGGG GCGTTTTTAT CATTAAGGCG | 60 |
| CAGTTGTTGC TTCGTGAGGG AGGTTTTATG AATTTTACCG CTTATAACAC GAAGACGCCA | 120 |
| GGGCATTTGC ATTTGTATGT GCATAAGGGG CATACGGAAT TAGGCGAGGG TGAAAGGCTG | 180 |
| ATTAAAACTT TATCCATGAA ATTAGCGCAA GGGTTGCCTA AAGAATGGAG GGTTTTCCCT | 240 |
| AGCAATGAAT GGCCTAAGGA ATTTAATATT TTAGCTTTAC CTTATGAAGT GTTTGCAAAA | 300 |
| GAGCGCGGGA GCTCTTGGGC GAAGCATTTA | 330 |

(2) INFORMATION FOR SEQ ID NO:10675632_f2_3.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: H+-transporting ATP synthase alpha chain homolog

| | |
|---|-----|
| GTGGCTAAAG ACATCATCAG CGAGTCTCAA AACCTTTGCG CAAGAAAATT CCGCCGTTTG | 60 |
| TATGCGTTAT TGAAAGAAAA TGAAATGCTC ATTCGCATCG GATCTTATCA AATGGGGAAC | 120 |
| GATAAAGAGC TTGATGAAGC GATTAAGAAA AAGGCTCTAA TGGAGCAATT TTTAGTGCAA | 180 |
| GATGAAAACG CTTTACYAGC CTTT | 204 |

(2) INFORMATION FOR SEQ ID NO:10677187_c1_9.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1338 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|--|------|
| ATGAAATCAC GCCCAATCCT CGCACAAGCT TACGCGCTCC AAATGATGGT CAAACAGATC | 60 |
| GCTTTTTTTAG AAACCATTTT AGTGGAAAAC GAGCAAGACG CTTTGATTTT GGAAAATTCT | 120 |
| TTGATCAAGC AGCTCAAGCC TAAATACAAC ATTCTTTTAA GAGACGATAA AACTTACCCT | 180 |
| TATATTTACA TGGATTTTTC TATTGATTTT CCTATCCCTT TAATCACACG AAAAATCTTA | 240 |
| AAACAGCCTG GCGTTAAATA TTTTGGCCCT TTTACGAGCG GGGCTAAGGA TATTTTGGAC | 300 |
| AGCTTGTATG AATTGCTCCC TTTGGTTCAA AAGAAAAATT GCATCAAGGA TAAAAAGGCA | 360 |
| TGCATGTTTT ATCAAATAGA GCGTTGTAAA GCCCCATGCG AGGATAAAAT CACTAAAGAA | 420 |
| GAATATTTAA AAATCGCTAA AGAATGTTTA GAAATGATTG AAAATAAAGA CAGGCTCATC | 480 |
| AAAGAGCTTG AATTGAAAAT GGAGCGCCTT TCTAGTAACT TCGTTTTTGA AGAAGCCTTA | 540 |
| ATTTATAGGG ATAGGATTGC AAAAATCCAA AAAATCGCCC CTTTCACTTG CATGGATTTA | 600 |
| GCCAAACTCT ACGATTTGGA TATTTTGTCT TTTTATGGTG GGAACAACAA GGCGGTGTTA | 660 |
| GTGAAAATGT TCATGCGTGG GGGTAAAATC ATTTCTTCAG CGTTTGAAAA AATCCACTCT | 720 |
| CTCAACGGGT TTGACACTGA TGAAGCGATG AAACAAGCCA TTATCAATCA TTACCAATCG | 780 |
| CATTTGCCTT TGATGCCTGA ACAAATCTTA TTGAGCGCTT GTTCTAATGA AACGCTTAAA | 840 |
| GAATTGCAAG AGTTTATCTC TCACCAATAT TCTAAAAAAA TCGCTCTTAG CATTCCTAAA | 900 |
| AAGGGTGATA AGCTCGCTTT AATAGAAATC GCTATGAAAA ACGCTCAAGA GATTTTTAGC | 960 |
| CAAGAAAAAA CCTCTAATGA AGATCGGATC TTAGAAGAAG CGCGATCGCT CTTCAATTTA | 1020 |
| GAGTGCGTGC CTTATAGGGT AGAAATCTTT GACACAAGCC ACCATTCAAA CAGCCAATGC | 1080 |
| GTGGGGGGAA TGGTCGTGTA TGAAAACAAT GCATTTCAAA AAGACTCTTA TCGGCGCTAC | 1140 |
| CATCTAAAAG GCTCTAACGA ATATGATCAA ATGAGCGAAT TGCTCACCAG AAGGGCTTTA | 1200 |
| GACTTTGCTA AAGAGCCACC GCCTAATTTG TGGGTGATAG ATGGAGGGAG GGCGCAATTA | 1260 |

AACATCGCTT TAGAAATTTT AAAAAGCAGC GGGAGTTTGT TAGAAGTGAT CGCTATTTCT 1320

AAAGAAAAAA GGGGATTC 1338

(2) INFORMATION FOR SEQ ID NO:1071890_f3_3.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| GTGAGTTTGG GGGCGTTTCA GGGGTATTAT GGAGGGCTAG TGGATTTAGT GGGGCAAAGG | 60 |
| TTGAGCGAAA TTTGGAGCGC GATCCCCATG CTTTTTTTAC TCATTGTGAT TTCTAGCGCG | 120 |
| TTCAATTCTA ATTTTGGAT CATCTTGTTT TTAGTCTTGC TCTTTAGCTG GATGGGGCTT | 180 |
| TCTCAAGTCG TGCGCACGGA GTTTTTAAAA GCAAGGAATA TGGACTACAC CAAAGCCGCT | 240 |
| AGAGCGTTGG GG | 252 |

(2) INFORMATION FOR SEQ ID NO:10723412_f2_2.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: hypothetical abc transporter in bcr 5' region

```
ATGAGTGAAG CCTATTTTTT ACACCATAAA AACGCTTCTC AAGTGTCTCT TAATGAACAA      60
GTTTTAAACG TTATGAAACA AGTTCAATTG GATGAAAATT TTTGGAATGT TTCTCTTATG      120
```

(2) INFORMATION FOR SEQ ID NO:10737627_f3_10.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 900 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| GTGATCCTGA TATTTATCAT CGTGGTGGAA GATCAGAAAG GCATTTTCCC TATCGCAGCG | 60 |
| TCAAAAAGAA AAAGCCAAAG CTCTGTGATC ATTGAAGACG TGTGCTTCAG CAAAGAGGAT | 120 |
| TTTGTAGAAG GGGCAAAAGC GATTGAGGGG CTTTAAAAA AACATGGCTT TAAGGATAAT | 180 |
| GGCATTATTT TTGGGCATGC GTTAAGCGGG AATTGCACT TTGTCGTTAC GCCGATTCTA | 240 |
| GAAAATGAAG CTGAAAGAAA AGCGTTTGAA AATTAGTTT CTGAGATGTT TTTAATGGTG | 300 |
| AGCAAAAGCT CTGGCTCTAT TAAAGCCGAA CATGGCACAG GCAGGATGGT AGCCCCTTTT | 360 |
| GTGGAAATGG AGTGGGGAGA AAAAGCTTAT AAGATCCACA AACAAATCAA GGAATTGTTT | 420 |
| GATCCTAATG GCCTTTTAAA CCCTGATGTG ATCATCACAA ACGATAAAGA AATCCACACT | 480 |
| AAAAATTTAA AGAGCATTTA CCCTATTGAA GAGCATTTGG ACATGTGCAT GGAATGTGGG | 540 |
| TTTTGTGAAA GGATCTGCCC CAGTAAAGAT TTATCCTTAA CGCCACGACA ACGCATCGTC | 600 |
| ATCCACAGAG AGGTAGAGCG TTTGAAAGAA AGGGTAAGTC ATGGTCATGA TGAAGATCAG | 660 |
| GTTTTACTAG ATGAGCTTTT AAAAGAGTCT GAATACTTAG CGCATGCCAC TTGCGCGGTG | 720 |
| TGCCATATGT GTTCCACTTT ATGCCCTTTA GGGATTGATA CCGGGAGYAT CGCTTTAAAT | 780 |
| CATTATCAAA AAAACCCTAA AGGCGAAAAG ATCGCTTCAA AGATTCTTAA ATCACATGCA | 840 |
| AACGACCACA AGCGTGGCTC GTTTTTCTTT AAAARGCGCT TTCGTGGTTT CAAAAACTCA | 900 |

(2) INFORMATION FOR SEQ ID NO:10742963_c1_8.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 642 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|--|-----|
| ATGAAAGAAA AAAACTTTTG GCCTTTAGGA ATCATGAGCG TGCTTATTTT TGGGCTTGGG | 60 |
| ATCGTG GTGT TTTTAGTGGT GTTTGCCCTA AAAAATTCGC CTAAAAATGA TTTAGTGTAT | 120 |
| TTCAAGGGTC ATAACGAAGT GGATTTAAAC TTTAACGCCA TGCTTAAAAC TTATGAAAAC | 180 |
| TTTAAATCCA ATTATCGTTT TTCAGTGGGT TTAAAGCCTC TTACCGAAAG CCCTAAAACC | 240 |
| CCCATTTTGC CCTATTTTTC TAAAGGCACG CATGGGGATA AAAAAATCCA AGAAAACCTT | 300 |
| TTAAACAACG CTTTGATTTT AGAAAAGTCC AACACGCTTT ATGCACAATT GCAACCGCTC | 360 |
| AAACCCGCTT TAGATTCGCC AAATATTCAA GTGTATTTAG CGTTCTATCC CAGCCAATCC | 420 |
| CAGCCCAGAT TATTAGGAAC GCTTGATTGT AAAAACGCAT GCGAACCTTT AAAATTTGAT | 480 |
| TTGTTAGAGG GCGATAAAGT GGGGCGCTAT AAGATCCTTT TTAAATTTGT TTTTAAAAAT | 540 |
| AAAGAAGAAT TGATTTTGGA GCAACTGCTT TTTTAAAGTA GCATGGCTTG TATGGGTATA | 600 |
| TCAATTTTAA AAAACGCTAA AGCATTTTTT AAATACAAAA TA | 642 |

(2) INFORMATION FOR SEQ ID NO:10745275_f3_8.nt:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 411 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGCCCATTA AAGGCTCTTT TTTAGCCAGA AACCGCCTGG TGATCGCTTT AACCGATGCG | 60 |
| GTGATTATCC CCAAGCGGA TTTAAAAAGC GGCTCTATGA GCAGTGCGAG ATTAGCCCAG | 120 |
| AAATACCAAA AACCTTGTT TGTTTTACCC CAACGCCTGA ATGAGAGCGA CGGCACTAAT | 180 |
| GAGCTTTTAG AAAAAGGGCA GGCTCAAGGG ATATTTAATA TTCAAATTT TATAAACACC | 240 |
| CTTTTAAAAG ATTACCATTT AAAAGAAATG CCTGAAATGA AAGATGAATT TTTAGAATAT | 300 |
| TGCGCGAAAA ACCCTAGCTA TGAAGAAGCG TATCTCAAAT TTGGGGATAA GCTTTTAGAA | 360 |
| TACGAGCTGT TGGGTAAGAT TAAGCGCATC AATCATCTCG TGGTGTTAGC A | 411 |

(2) INFORMATION FOR SEQ ID NO:11132778_f1_4.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 816 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: ATP-BINDING PROTEIN ABC

| | |
|---|-----|
| ATGGTAGTAG AATTAAAAA CATTGAAAAG ATTTATGAAA ACGGGTTTCA TGCTCTAAAA | 60 |
| GGCGTGAATT TGGAATTGAA AAAAGGCGAT ATTTTGGGCG TGATAGGCTA TTCAGGGGCG | 120 |
| GGGAAATCCA CGCTCATTCG CTTGATCAAT TGTTTAGAGC GCCCCAGTTC TGGCGAAGTT | 180 |
| TTAGTCAATG GGGTCAATCT GTTAAACTTA AAGCCTAAAG AATTGCAAAA AGCGCGCCAA | 240 |
| AAAATAGGCA TGATTTTCCA GCATTTCAAT TTATTGAGCG CTAAAAACGT GTTTGAAAAC | 300 |
| GTCGCTTTCG CTCTAGAAAT CGCCCGATGG GAAAAAACTA AGATTAAATC AAGGGTGCAT | 360 |
| GAATTGTTGG AATTAGTGGG GTTAGAAGAT AAAGTGCATT TTTATCCTAA ACAGCTCAGC | 420 |
| GGCGGGCAAA AACAACGAGT GGCGATCGCT AGGAGTTTAG CGAATTGCCC TAATTTGTTG | 480 |
| CTTTGCGATG AAGCCACATC CGCTTTGGAT TCTAAAACCA CGCATTCTAT TTTAACGCTT | 540 |
| CTAAGCGGCA TTCAAAAAAA GTTTGATTTG AGCATCGTTT TCATCACACA CCAGATTGAA | 600 |
| GTGGTTAAAG AATTGTGCAA TCAAATGTGT GTGATCAGCA GCGGCGAAAT CGTAGAAAGA | 660 |
| GGCTCGGTGG AAGAAATTTT TGCTAACCTT AAACATGCTG TTACTAAAGA ATTGCTTGGC | 720 |
| ATCAAAAACG AACATGCGGA TCAAAAATCG CAAGACATTT ATCGCATCGT GTTTTTAGGG | 780 |
| GAGCATTTAG ACGAGCCGAT CATTTCTAAW TTTTGW | 816 |

(2) INFORMATION FOR SEQ ID NO:114505_c1_12.nt:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 318 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | |
|--|-----|
| ATGGGGGCTT TGATAGCCAT GTTTTTTTTA ATGCTCATTA AAAAGACTAT CGCTTATAAA | 60 |
| GAAGATAAAA AGAGCGCGGC TTAAAGGTC GTGCCTTATT TGGTGGCGTT GATGAGCTTA | 120 |
| GCCTTTAGCT GGTATTTGAT CGTGAAGGTT TAAAACGCC TCTATGCGGT GAGTTT TGAA | 180 |
| ATCCAGCTCG CTTGCGGTTG TGTCCTTGCG CTTT TGATT TTATCCTTTT TAAAAGATTT | 240 |
| GTGTTAAAAA AAGCCCCGCA ATTAGAAAAT AGCCACGAAA GCGTCAATGA GCTTTT TAAT | 300 |
| GTCCCTTTGA TTTT TGCC | 318 |

(2) INFORMATION FOR SEQ ID NO:116018_c3_29.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGATTAAAA GAATTGCTTG TATTTTAAGC TTGAGCGCGA GTTTAGCGTT AGCTGGCGAA | 60 |
| GTGAATGGGT TTTTCATGGG TCGGGGTTAT CAACAAGGTC GTTATGGCCC TTATAACAGC | 120 |
| AATTACTCTG ATTGGCGTCA TGGCAATGAC CTTTATGGTT TGAATTTCAA ATTAGGTTTT | 180 |
| GTAGGCTTTG CCAATAAATG GTTTGGGGCT AGGGTGTATG GCTTTTTAGA TTGGTTTAAC | 240 |
| ACTTCAGGGA CTGAACACAC CAAAACCAAT TTGCTCACCT ATGGCGGCGG TGGCGATTTG | 300 |
| ATTGTCAATC TCATTCCTTT GGATAAATTC GCTCTAGGTC TCATTGGTGG CGTTCAATTA | 360 |
| GCCGGAAACA CTTGGATGTT CCCTTATGAT GTCAATCAAA CCAGATTCCA GTTCTTATGG | 420 |
| AATTTAGGCG GAAGAATGCG TGTTGGGGAT RCAGTGCGTT TGAAGCGGGC G | 471 |

(2) INFORMATION FOR SEQ ID NO:1171928_f3_10.nt:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 834 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGTATCGCC ATGTGTTGAA AGATTTCTCC CTAGATTTTA GCAAAGAAAG CGTTCAAGAG | 60 |
| CTGTTTAACC AGCTGGCTAA AGACACTTTT TTATTGCTTT TGCCTGTTTT AATCATTTTA | 120 |
| ATGGTGGTGG CGTTTTTGTC TAATGTCTTG CAATTTGGCT GGCTCTTTGC CCCTAAAGTC | 180 |
| ATTGAGCCTA AATTTTCTAA AATCAACCCT ATCAATGGCG TCAAAAACCT TTTTCTTTTA | 240 |
| AAAAAGATCC TTGATGGGAG TTTGATCACT TTAAAAGTTT TTTTAGCTTT TTTTCTGGGG | 300 |
| TTTTTCATCT TTTCTTATT TTTAGGGGAA TTAAACCATG CGGCTCTTTT GAATTTGCAA | 360 |
| GGCCAGTTGT TGTGGTTTAA AAGCAAGGCG TTATGGCTCA TTTCTTCGCT TTTATTTTTA | 420 |
| TTTTTTGTCT TGGCTTTTGT GGATTTAATC ATCAAACGCC GCCAATACAC TAACTCTTTA | 480 |
| AAAATGACTA AACAAGAAGT TAAGGACGAA TACAAACAGC AAGAAGGAAA CCCAGAAATC | 540 |
| AAAGCCAAAA TCCGCCAGAT GATGGTAAAA AACGCCACGA ATAAATGAT GCAAGAAATC | 600 |
| CCCAAATCCA ATGTCGTGGT GACTAACCTT ACCCATTATG CCGTCGCTCT CAAATTTGAT | 660 |
| GAAGAACACC CTGTGCCTGT GGTAGTGGCT AAAGGCACGG ATTATTTAGC CATTAGGATT | 720 |
| AAGGGTATCG CCAGAGAGCA TGACATAGAA ATTATAGAAA ATAAAACGCT CGCTAGAGAG | 780 |
| CTTTATAGAG ACGTGAAATT GAACGCCACC ATACCAGAAG AATTGTTTGA GCGG | 834 |

(2) INFORMATION FOR SEQ ID NO:11719687_f3_4.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGAATACAA GSCCCTTAAT CGCTACGCTT TTGCAAGCGC CTTTGCATGT TTTAGGGATT | 60 |
| AGAGAGCCAG TTTCTTTTCA GCCTTTTAC CCCAAAACAG AAAAGCCTAA TCGCCCTCAA | 120 |
| AAGTTCGCGC ATGTTTCTAG CATGCCCAGT TTGGAATTTT TAGAAAAATT GGTGATCCGC | 180 |
| TACCTTTTAG AAGACAGAAG CCTATTGGAT TTAGCGGTGG GTTATATCCA TAGTGGGGTA | 240 |
| TTCTTGCATA AAAACAAGA ATTTGACGCT TTATGTCAAG AAAAATTGGA CGACCCTAAA | 300 |
| TTAGTTGCGT TATTATTAGA TGCGAATTTA CCCCTAAAAA AAGGGGGTTT TGAAAAGGAA | 360 |

(2) INFORMATION FOR SEQ ID NO:1179838_c3_44.nt:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 678 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGGGGCAGG CATTTTTAA AAAAATTGTT GGCTGTTTCT GTCTTGGTTA TTTATTTTAA | 60 |
| TCTAGCGCAA TAGAAGCAGT AGCACTTGAC ATTAAGAATT TTAATCGTGG TAGGGTGAAA | 120 |
| GTGGTGAATA AGAAGATTGC TTATTTGGGA GATGAAAAAC CTATTACGAT TTGGACTTCA | 180 |
| TTAGACAATG TTACCGTGAT CCAACTTGAA AAAGATGAAA CTATTTCTTA CATCACAACA | 240 |
| GGTTTCAATA AAGGTTGGAG TATTGTGCCT AATTCTAATC ATATATTCAT TCAACCTAAA | 300 |
| TCGGTAAAAA GTAATCTCAT GTTTGAAAAA GAAGCAGTGA ATTTTGCCCT AATGACAAGA | 360 |
| GATTACCAAG AATTTTAA GACAAAAAA CTTATCGTAG ATGCGCCTGA CCCTAAAGAA | 420 |
| TTAGAAGAAC AAAAAAAGC TCTAGAAAAA GAAAAAGAAG CTAAAGAACA GGCGCAAAAG | 480 |
| GCACAAAAAG ATAAAAGAGA AAAAAGAAAG GAGGAGCGTG CAAAAAATAG AGCCAATTTA | 540 |
| GAAAATCTCA CTAACGCTAT GAGTAACCCA CAAAATTTGA GCAATAACAA AAATCTTAGC | 600 |
| GAATTGATCA AGCAACAGAG AGAAAATGAA TTAGACCAA TGGAACGAAC TAGAGGACAT | 660 |
| GCAAGAGCAG GCTCAAGC | 678 |

(2) INFORMATION FOR SEQ ID NO:11876471_f2_2.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGAATACAG AAATTTTAAC CATCATGTTA GTTGTCTCCG TGCTTATGGG ATTGGTAGGC | 60 |
| TTAATAGCGT TTTTATGGGG GGTAAAGC GGTCAGTTTG ACGATGAAA ACGCATGCTT | 120 |
| GAAAGCGTGT TGTATGACGC GCGAGCGACT | 150 |

(2) INFORMATION FOR SEQ ID NO:1204418_c3_5.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 390 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGTTTGTAG CGGCCGGGCT TGGGGCTTAT GCGATCGCGC TTTTCCACCT CTTTACGCAT | 60 |
| GCGTTCTTCA AATCCCTCCT TTTCTTAGGC TCAGGCAATG TCATGCATGC GATGGAAGAC | 120 |
| AATCTGGATA TTACTAAAAT GGGCGCTTTA TACAAGCCTA TGAGGATCAC AGCTGTCTTT | 180 |
| ATGATTATAG GGTCAGTGGC TTTGTGTGGG ATCTACCCCT TTGCGGGCTA TTTCTCCAAA | 240 |
| GACAAGATTT TAGAGGTCGC CTTTGGGATG CACCACCACA TTTTATGGTT TGTTCTTTTG | 300 |
| ATTGGGGCGA TCTTTACCGC TTTTATAGC TTCAGACTCA TCATGCTGGT GTTTTTTGCA | 360 |
| CCCAAACAAC ATGAAATCAA CCACCCCCCA | 390 |

(2) INFORMATION FOR SEQ ID NO:1206675_c1_17.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 549 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | |
|--|-----|
| ATGTTTATAT CTTCTTCTTA CACGCTGAGT TTTGTATGGC TTTTTTTAAT TTTCTTTTTT | 60 |
| TTCAAAAATA AGCCATTGGG TTTGAGGTTT TCGCTCTCTT TGATAAGCGT GATTTTAAGC | 120 |
| AATATCGCTT TGAAAGACTC CCTATCGCTC AATGAATTTT TAAGCAGTTT TACAGCCCCC | 180 |
| TTAAGCCCCT TTAGCTGTCT TTTGATCCTT GCTTATGCAA GCTTTTCTTG CCATATACTC | 240 |
| AAAAAGCCCC CTTTAGAAAC CTTGCAATCT TATAGCGTCA TGCTGTTTTT CAATCTGTTG | 300 |
| CTTTTGACAG ATATTTTAGG GTTTTTGCCT TTTTCAATCT ACCATCATTT CATGGCTTCT | 360 |
| CTGATTTTTTA GCGCGCTTTT TTGCAGCAGT TTGTTTTTGA GTAGCCCCTT ATTAGGCGTG | 420 |
| ATCGCTTTAG TGGCTTTATC CAGTTCGCTT TTGATGCGTT CTAATTTTCA AATCTTAGAT | 480 |
| TCTTTATTGG ATTTCCCATT ATTTCTTTTT GTCTTTTTTA AGACTTTATA TCTTGCTAAA | 540 |
| AAAAGGTTA | 549 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 705 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|--|-----|
| ATGCGCCTAG ATTACGCCCT ATTCAACCAG CATTTAGCAA ATAGCAGAGA AAAAGCTAAA | 60 |
| GCGTTGGTTT TAAAAAACA GGTTTTAGTC AATAAAATGG TGGTTTCTAA ACCCTCTTTT | 120 |
| ATCGTTAAAG AGGGCGATCA AATTGAACTC ATCGCTCCCA ATCTATTCGT TAGCAGGGCT | 180 |
| GGGGAAAAAT TAGGGGCTTT TTTAGAAGAT CATTTTATAG ATTTTAAAGA AAAGGTGTGTT | 240 |
| TTAGATGTGG GAGCGAGTAA GGGAGGCTTT AGTCAAGTGG CTCTTTTAAA AGGGGCTAAA | 300 |
| AAGGTGCTTT GCGTGGATGT GGGGAAAATG CAATTAGATG AAAGTTTGAA AAACGACCAA | 360 |
| CGCATAGAAT GTTACGAAGA ATGCGATATT AGAGGGTTTA AAACGCCAGA AAAAATTGAT | 420 |
| TTAGCACTTT GTGATGTGAG CTTTATTTCT TTATATTGTA TTTTAGAAGC GATTTTGCCT | 480 |
| TTAAGCGGTG AATTTTTAAC GCTTTTCAAA CCGCAATTG AAGTGGGCAG AACAATAAAA | 540 |
| CGCAATAAAA AGGGGGTGGT GATGGATAAA GAAGCCATTT TGAACGCTTT AGAAAACTTT | 600 |
| AAAAACCATT TAAAAACAAA GGATTTTCAA ATCTTAACGA TCCAAGAAAG CTTAGTGAAA | 660 |
| GGGAAAAACG GGAATGTTGA ATTTTTTATC CATTTCAAGC GAGCC | 705 |

(2) INFORMATION FOR SEQ ID NO:12520952_c1_9.nt:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 264 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGAGCCTAC CACCGGTTTG CATTTTGAAA GATGTGAATC ACCTTTTACA AGTCTTRCAT | 60 |
| TCTTTGGTGG CGTTAGGCAA TTCCATGCTA GTGATTGAGC ATAATTTAGA CATCATCAAA | 120 |
| AACGCTGACT ACATTATAGA CATGGGGCCT GATGGGGGGG ATAAGGGCGG GAAAGTCATT | 180 |
| GCGAGCGGCA CGCCTTTAGA AGTGGCGCAA AATTGCGAAA AAACCCAAAG CTATACGGGA | 240 |
| AAATTTTtag CTTTGGAATT GAAA | 264 |

(2) INFORMATION FOR SEQ ID NO:1256885_f3_4.nt:

29

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 444 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|--|-----|
| ATGCAAAATC GATCGCATGA AATACAAGGC GTATCACACA TTAAGAATAA TTATAAATTT | 60 |
| TTCACCAAAG AGCTTGACAA TTATATCAGC AAAGGGTATC GCATTGAAGA GATTTATGGC | 120 |
| GCGTTTTTGT GGCTCAAAAT CGTAGCCATA GGTTTAGAGT TGGGCGAAGA CGATCCGCAA | 180 |
| GTGGTGTTTG AGAGCATCAA CGCTACAGGC GTGCAATTAA AAGGGCTGGA TCTCATCCGC | 240 |
| AACTATTTGA TGATGGGGGA AAATYCTGAC AACCAGAATC GTCTTTATAA TACTTATTGG | 300 |
| GTGCCTTTAG AAAATTGGCT TGGTGAAAAG GATTTGAATG ATTTTCATCAA AACCTATTTG | 360 |
| AGAATCTATT TTGAGGATAG AGTTACAAGA GGGAGAGCGC GAAGTGTATT ACGCGCTAAA | 420 |
| AGCCCACCAC AGAGACAATT TCCC | 444 |

(2) INFORMATION FOR SEQ ID NO:12617677_f3_5.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGGATACCA TAAAAAGCAT TCCATAAGA ACTTTTATTT TACTCTATAA AAGCTCACCA | 60 |
| AAATGTGTTG TGTTGGCATC AATTACAGTG CTATTTGTCG GCATTCTTYC ATCTCTGAAT | 120 |
| ATTCTTGTTA TGATAAAATT GATTGATATT GTGGTGAATC TATTACAAAA GCATACGCAT | 180 |
| TTTGAATACA GCTTGCTGTT ACCAACTTTA CTACTATGGG GAGCCTTGCT GTTTTAAACG | 240 |
| CATGTGTTCT CAGGAAATTT TATCAAGCTT GCAAACCATT ATTGCCGAAC AATTTTCTAT | 300 |
| AAATATCATC ACTCAGCTTG C | 321 |

(2) INFORMATION FOR SEQ ID NO:12694087_f1_2.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 408 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|--|-----|
| ATGATCTTTT ACACCACCAT TAAAGAGCCT TTAAAAAACC TCCAATACCG CTATGCGCAA | 60 |
| TTTTTTGGCA AGATCAAGCC TTGTTTCGTTT TTAGAGTCTC TAAAATCATG CTTTTTTCAA | 120 |
| ACCTATTCTT TTTCTTTAAC GCGAAAACAA GATTTCAAAT CGCATTGCG CCATTTCATT | 180 |
| GACAGCGCCC ATTCCAACGC CTTAGTGGGT AATTGTATC GAGCGTTATT CATAGGGGAT | 240 |
| AGCTTGAATA AAGACTTAAG AGACAGGGCT AACGCGCTAG GGATCAACCA CTTACTGGCC | 300 |
| ATTAGCGGGT TTCATTTAGG GATTTTGAGC GCGAGCGTGT ATTTTCTTTT CTCTCTTTTT | 360 |
| TATACCCCCT TACAAAAACG CTATTTCCCT TACAGGAACG CTTTTTWA | 408 |

(2) INFORMATION FOR SEQ ID NO:12698442_f3_9.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGAATAAAC CATTTTTAAT CTTACTCATA GCCCTAATTG CCTTTAGCGG CTGTAACATG | 60 |
| AGAAAATACT TCAAACCCGC TAAACACCAA ATTAAAGCGA AGCGTATTTC CCTAACCATT | 120 |
| TGCAAGAAAG CATCGTTTCG TCTAATCGTT ATGGAGCCAT TT | 162 |

(2) INFORMATION FOR SEQ ID NO:12897656_f1_1.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGGCGGCTT GGAACACTTT AGTAGAAAAA ATCATCGCTC CTAAACACAA GGTCAAAT | 60 |
| GGTTTTGTGG GCAAGTATTT AAGCTTAAAA GAATCTTATA AATCCTTGAT TGAAGCCCTA | 120 |
| ATCCATGCGG GGGCGCATCT GGATACGCAA GTCAATATTG AATGGCTGGA TAGCGAGAAT | 180 |
| TTTAATGAAA AGACTGATTT AGAGGGCGTT GATGCGATTT TAGTGCCGGG GGGCTTTGGA | 240 |
| GAAAGGGGGA TTGAGGGCAA AATTTGCGCC ATTCAAAGGG CTAGGTTAGA AAAACTCCCC | 300 |
| TTTTTAGGGA TTTGTTTGGG CATGCAATTA GCGATCGTTG AATTTGTGCG CAAATGTTTT | 360 |
| AGGCTTGAAA GGGGC | 375 |

(2) INFORMATION FOR SEQ ID NO:12969218_f1_4.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 747 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGACTAAAG CGTTTGTGCC TTTAAGTTTG TTAGTGAGCG CGATTTTATT AGCGTTTTCG | 60 |
| CTCATCTTAA TCCCCACTTC TAAGAGCGCT TATTACGGGT TTTTGCGTCA AAAAAAAGAC | 120 |
| AAGATTGACA TTAACATCAG AGCGGGTGAA TTCGGGCAAA AATTAGGCGA TTGGCTCGTG | 180 |
| TATGTGGATA AGACTGAAAA CAATTCCTAT GATAATTTGG TGCTTTTTTTC TAATAAAAGT | 240 |
| CTCTCTCAAG AAAGCTTTAT TTTGGCTCAA AAAGGCAATA TCAACAATCA AAACGGCGTG | 300 |
| TTTGAATTGA ATTTGTATAA CGGGCATGCG TATTTCACTC AAGGCGATAA AATGCGTAAG | 360 |
| GTTGATTTTG AAGAATTGCA TTTGCGCAAC AAGCTCAAGT CTTTCAATTC TAATGATGCG | 420 |
| GCTTATTTGC AAGGCACGGA TTATTTGGGT TATTGGAAAA AAGCCTTTGG TAAAAACGCT | 480 |
| AATAAAAATC AAAAACGCCG TTTTCTCAA GCGATCTTAG TTTCCTTGTT CCCTTTAGCG | 540 |
| AGCGTGTTTT TAATCCCCTT ATTTGGCATC GCCAACCCGC GATTCAAAAC GAATTGGAGT | 600 |
| TATTTCTYAWG TCCTTGGAGC GGTGTTGGGTW TATTTTTTAA TGGTGCATGT GATTTCTACG | 660 |
| GATTTGTTTT TGATGACCTT TTTCTTCCCC TTTATTTGGG CGTTTATTTT TTATTTATTG | 720 |
| TTTAGAAAAT TCATTTTAAA GCGTTAT | 747 |

(2) INFORMATION FOR SEQ ID NO:13178562_c3_14.nt:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 258 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | |
|--|-----|
| ATGAGTAAGA GCGCGATTTT TGTTCTTTCT GGCTTTTCTAG CGTTCTTGCT CTATGCTTTG | 60 |
| TTATTATATG GTTTGTTGTT AGAAAGGCAT AATAAAGAAG CAGAGAAAAT CCTTTTAGAT | 120 |
| TTAAATAAAA AGGACGAACA AGCCATTGAC TTGAATTTAG AAGATCTGCC AAGCGAGAAA | 180 |
| AAGAATGAAA AAATTRA AAAA AGTAACGGAA AAACAGGACG ATTTTTTTAGA GCCTAAAAGA | 240 |
| AGAACCCTAAA GAGGAGCC | 258 |

(2) INFORMATION FOR SEQ ID NO:1364378_c1_6.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| GTGATGGCTC AATCCTTGCT TGTTCATGCC TTTTTTGCCG CCTTGCTCGC CCTAGCCTTT | 60 |
| ATGATCAATC TTTACACCCT TTTTAAAGAA AAGAATTTCA TCCAATTGAA CCGGAAAATC | 120 |
| TATCTTGTCA TGCCAGCGAT TTATATTCTT TTAAGCATCG CTCTTTTGAG TGGGGTTTTT | 180 |
| ATTTGGGCGA TGCAACAATT TGAATTTTCT TTTAGCGCTG TTGTCATGCT TTTGGGGTTG | 240 |
| TTGTTGATGC TCATTGCAGA AATCAAACGC CATAAAAGCG TGAAATTCGC TATCACTAAA | 300 |
| AAAGAAAGGA TGAAAGCCTA TATCAAAAAA GCTAAAATCC TGTATTTTTT AGAAACGATT | 360 |
| CTTATCATCG TGTTAATGGG CATT | 384 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| GTGCGTAATG TGGTTTTATT CATTTTAACA GCGATCTTTT TAGCGTTCAT GCTTTTAGTG | 60 |
| AGTTATTGCA TGCCCCATTA TAGCGTGGCT GTCATTAGCG GGGTGGAAGT CAAAAGAATG | 120 |
| AATGAAAATG AAAACACGCC CAATAATAAG GAAGTAAAAA CCCTTGCTAG AGATGTCTAT | 180 |
| TTTGTGCAAA CTTACGACCC TAAGGATCAA AAAAGCGTGA CCGTCTATCG TAACGAAGAC | 240 |
| ACGCGCTTTG GCTTCCCTTT TTATTTTAAG TTAAATTCGG CTGATATTTT AGCTCTCGCC | 300 |
| AAAGTT | 306 |

(2) INFORMATION FOR SEQ ID NO:1367157_f2_2.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|--|-----|
| ATGTTTAAAA AAATCATTTT TTTGTGCGTT TTTTGTAGATG GGGGATTTGT CATTCCACCC | 60 |
| CTTGAAGCCA TGCCTATTTT GCGCAATAAA ACCCCCAAAA AAAATTACCA AGAAGCCCAT | 120 |
| GAAAAGCTCT ATAGAAGCAT CATTAACCGC CAAAASSTCA CGCGTAAAAA AAGCGGGTGG | 180 |
| TATTTTTTTAG GGGGGGTTGG CGCTGTAGAA GCCATTAAGG ACTATCAAGG CAAGGAAATG | 240 |
| AAAGATTGGA TGCCACGCTC AATT | 264 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| GTGCATTTTA CGTGTATCTT TCTAACCCTA TTAAAATGGA TTTTGCCAGC CAAAAACAAG | 60 |
| CAGGCGTGCA AAAAGGCCAC CAACCAGATC CATTCAAGGY YTGCAAAACA TCCAGCAAAA | 120 |
| TATCCCCCCT CAAGTATTAA CCCCTCAATC CAAGCGGGTA TACAAGGGGT GATGCAAGGT | 180 |
| TTTGGGGCTT TGAGCAGCAY YTTAGAAGYC CCCYTATTTG TTTTYAAGC AAAATGTGGG | 240 |
| TGGATTGGGG GCTTTGAGCA TTATTTATCC CCTTTATATG GGTGGGGCAA GATTCACGAT | 300 |
| GGTGCGCATT GCGATTTGAT GCAAAAAGAC GCCAATGGAA GGGGTATCGG CTTGGAAAAA | 360 |
| GGTCTTCCAC CTTTCAAGGG GCTG | 384 |

(2) INFORMATION FOR SEQ ID NO:1370202_c3_6.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGCAGAAGT TTTTCTCTCG TTTTAGAAGG TGGGCGTTGC CCTTTTATTT TGTGAGCGCT | 60 |
| TTAGCAGCGA TTGATATTGA TGAAGTAACA GAAGCTCAAG CTAATAGCAT TAAATTAAGC | 120 |
| GATCAGTTAG TGAGCCTGAG CGATAAGCTT TTAGAAAAAG CGGTGGATAG GGGGCGCAAT | 180 |
| ACCGATCACT TAAAAGATCT TAACGATTTG CATGAAAAAA TCAAACATTT GCGCTTGATT | 240 |
| TTAGAGCCTA AGCCTAAGGG CAAAGAAGAT AGTCCTAACT TGGGAGGTAA TAAGGATATG | 300 |
| AAAACGGTTG AAATCGGAAG CGGT | 324 |

(2) INFORMATION FOR SEQ ID NO:13704718_f1_1.nt:

41

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| GTGATTTTAG CGTTCGCCTT TGGCATGAGT CTTCTTGGAT TAGCGGGCAT GTTCATTGAT | 60 |
| ATTCCTTTTT TATCCACAGG CGTTCATATC CCTAGAAAAG AGGATATTTT ATGGATTTCT | 120 |
| TTAATAGGGA TTAGCGGGAC TTTAGGGCAG TATTTCTTAA CCTATGCTTA CATGAACGCT | 180 |
| CCTGCTGGGA TCATCGCCCC CATTGAATAC ACCCGCATTG TTTGGGGGCT ATTGTTTGGG | 240 |
| CTGTATTTAG GCGATACATT TTTGGATCTT AAAAGCTCTT TAGGGGTGGC TTTGATCTTA | 300 |
| TGTTTCAGGCT TGCTCATTGC CTTGCCCGCT CTTTTAAAAG AATTAAAAAA AATT | 354 |

(2) INFORMATION FOR SEQ ID NO:13723593_fl_1.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGATCTATT TAGGGAAGAA AAATTTTAAC GCCCTTTTGA AAGGGGCGTA TTTAATGGAT | 60 |
| GAGCATTTTA GAAACGCCCC TTTTGAAAGC AATTTACCCG TTTTAATGGG ATTAATCTGG | 120 |
| CGTGTGGTAT ATCTAACTTT TTTTCCAATC CAAAAAGCCA CT | 162 |

(2) INFORMATION FOR SEQ ID NO:13726562_f1_1.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 864 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|--|-----|
| ATGGCCGCCA AATCCAAAGC GYAAACGCTT AAAGTCTTTT CAAAATTTTT CAGCAATTTT | 60 |
| AAAATCACTA AACTCAAAGA CAACCACGAA GAAGCCCACA AACTTTTTTG AGAAAATAGC | 120 |
| CGTAAAGCCC ATGACACTGA GATCATTTAC TCCACTTTGC AAGTGGTCCC CAGGTATTCA | 180 |
| ATAGAAACCG TGGGCTTTAG TTTGTTGATT TTAGCGGTCT CTTACATCTT ATTCAAATAC | 240 |
| GGCGAAGCTA GAATGGTACT CCCTACCATT TCTATGTATG CCCTAGCGCT TTATCGCATA | 300 |
| CTCCCTTCTG TAACTGGAGT GATCAGCTAT TATAATGAAA TCGCTTACAA CCAGCTTGCA | 360 |
| ACCAATGTTG TTTTAAAG CCTTTCTAAG ACCATCGTTG AAGAGGATTT AGTCCCTTTA | 420 |
| GACTTTAATG AAAAAATCAC TCTCCAAAAC ATTTTCATTCG CTTATAAGTC AAAACACCCG | 480 |
| GTTTTAAAAA ATTTCAACCT CACCATTCAA AAAGGTCAA AAATCGCTCT CATAGGCCAT | 540 |
| AGCGGGTGCG GAAAATCCAC GCTGGCGGAT ATTATTATGG GGCTTACCTA CCCTAAAAGT | 600 |
| GGGGAAATTT TTATTGATAA CACCCTTTTA ACCAGCGAAA ACAGGCGCTC ATGGCGTAAA | 660 |
| AAAATAGGCT ATATCCCCCA AAATATTTAC CTTTTTGATG GCACTGTGGG GGATAATATC | 720 |
| GCTTTTGGA GTGCTATAGA TGAAAAACGC TTGATTAAGG TGTGCAAAT GGCTCATATC | 780 |
| TATGATTTTT TATGCGAGCA TGAGGGCCTT AAAACCCAAG TGGGCGAAGG GGCGCTAAGC | 840 |
| TTAGCGGCGG TCAAAAACAG CGCA | 864 |

(2) INFORMATION FOR SEQ ID NO:1385937_f1_3.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 576 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGCTTGATA TATGGATAGA TATGATAATC TGTATTTTTT ATTTGCTCTT TTTTACGACT | 60 |
| CCTTACATTG TAGGCGATAT TTTGCAATTG AAATTTATCC GTCAAAACT CTGCGAGAAG | 120 |
| CCTGTTTTAC TCCCACAAAA GGATTATGAA GAAGCGGGAA ATTATGCTAT TAGGAAAATG | 180 |
| CAATTATCCA TTATTTCTCA AATTTTAGAT GGGGTGATCT TTGCTGGTTG GGTCTTTTTT | 240 |
| GGTTTGACGC ATTTAGAAGA TCTCACGCAT TATTTAAACC TTCCTGAAAC GCTAGGTTAC | 300 |
| TTGGTGTTTG CCTTGTTGTT TTTAGCGATT CAAAGCGTTT TAGCTTTACC CATTAGCTAC | 360 |
| TATACTACCA TGCATTTGGA TAAGGAATTT GGCTTTTCTA AGGTGAGTTT ATCGTTGTTT | 420 |
| TTTAAGGATT TTTTCAAAGG ATTATTGCTC ACTTTAGGCG TGGGGTTGTT GTTGATTAC | 480 |
| ACTCTCATAA TGATCATTGA ACATGTGGAG CATTGGGAGA TCAGCTCGTT TTTTGTCGTG | 540 |
| TTTGTTTTCA TGATTTTGGC TAATCTTTTT TTACCC | 576 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 504 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|--|-----|
| ATGCTAAAAA AAATATTTTT AACCAACAGC TTAGGGATTT TATGCTCTAG GATTTTTTGGC | 60 |
| TTTTTACGGG ATTTAATGAT GGCCAATATC CTAGGGGCTG GGGTGTATAG CGATATTTTC | 120 |
| TTTGTGGCTT TCAAATTGCC TAATCTATTC AGGCGTATTT TTGCGGAGGG CTCTTTTTCT | 180 |
| CAAAGCTTTT TACCGAGCTT CACACGGAGT TCCATTAAGG GGGGTTTTGC GAGTTTGGTG | 240 |
| GGGCTTATTT TTTGTGGCGT TTTATTCATG TGGTGCTTAT TAGTAGCGCT CAATCCCTTA | 300 |
| TGGCTAACCA AACTCCTAGC TTACGGCTTT GATGAAGAAA CGCTCAAACCT ATGCACCCCT | 360 |
| ATTGTAGCGA TCAATTTTTG GTATCTTTTA TTGGTGTTTA TCACCACTTT TTTAGGCGCG | 420 |
| CTTTTACAAT ACAAACACAG CTTTTTTGCC GCGCTTATGC GCAAGCTTAC TCAATTTATG | 480 |
| CATGATTTTA GCCCTTTTGA TTTC | 504 |

46
(2) INFORMATION FOR SEQ ID NO:1408_c3_19.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 459 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGAATTTAG AAGTGGCTCT AAAGGCGTTT GAAACGCTAT TGCCATGCAA TAAACAAGAA | 60 |
| GTTTTAAAAA ACCTAAAGCC CCTAGATTTA ATCGGCCGTT GCGAGCTTTT AAGCCCTAAC | 120 |
| ATTTTAATAG ATGTGGGGCA TAACCCCAT AGCGCTAAAG CCTTAAAGA AGAAATCAAA | 180 |
| CGCATCTTTA ACGCTCCAAT CGTTTTGATT TATAATTGCT ATCAAGATAA AGACGCTTTT | 240 |
| TTGGTGCTAG AAATTTTAAA GTCTGTGGTT AAAAAGGTTT TGATTTTAGA ATTGCATAAT | 300 |
| EAAAGAATTA TCCAATTAGA AAAACTTAAA GGGATTTTAG AAACTTTAGG GTTAGAACAC | 360 |
| ECCTTGTTTG AAGAACTGAA AGAAAATGAA AATTATTTGG TGTATGGCTC ATTTCTGGTA | 420 |
| ECCAACGCTT TTTATGAACG CTATCCAAAG AAGAGGGAT | 459 |

(2) INFORMATION FOR SEQ ID NO:1411681_f2_1.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|--|-----|
| ATGGCTATCG GGTTCCTGTT AGTGTTTGGG ATTTTACTCA CCCTTTTCTAG CCGTTCTTAT | 60 |
| EGCGTGAGT TTGGGGGCGT TTCAGGGGTA TTATGGAGGG CTAGTGGATT TAGTGGGGCA | 120 |
| AGGTTGAGC GAAATTGGA GCGCGATCCC CATGCTTTTT TTAATCATTG TGATTTC | 177 |

(2) INFORMATION FOR SEQ ID NO:1416312_c1_10.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 666 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGAAGAAAA AAGCAAAAGT CTTTGGGTGT TGTTTTAAAA TGATTCGTTG GTTGTATTTG | 60 |
| GCGGTCTTTT TTTTGTGAG CGTATCAGAC GCTAAAGAAA TCGCTATGCA ACGATTTGAC | 120 |
| AAACAAAACC ATAAGATTTT TGAAATCCTT GCGGATAAAG TGAGCGCCAA AGACAATGTG | 180 |
| ATAACCGCCT CAGGGAATGC GATCCTATTG AATTATGACG TGTATATTCT AGCGGRTAAG | 240 |
| GTGCGTTATG ACACCAAGAC TAAAGAAGCG TTATTAGAAG GCAATATTAA GGTTTATAGG | 300 |
| GGCGAGGGCT TGCTCGTTAA AACCGATTAT GTGAAATTGA GTTTGAACGA AAAATATGAG | 360 |
| ATCATTTTCC CCTTTTATGT CCAAGACAGC GTGAGCGGGA TTTGGGTGAG CGCGGATATT | 420 |
| GCTAGCGGGA AGGATCAAAA ATATAAGATT AAAAACATGA GCGCTTCAGG GTGCAGCATT | 480 |
| GACAACCCCA TTTGGCATGT CAATGCGACT TCAGGCTCAT TTAACATGCA AAAATCGCAT | 540 |
| TTGTCAATGT GGAATCCTAA GATTTATGTC GGCGATATTC CTGTATTGTA TTTGCCCTAT | 600 |
| ATTTTCATGT CCACGAGCAA TAAAGAAGT ACCGGGTTTT TATACCCTGA GTTTGGCACT | 660 |
| TCCMAC | 666 |

(2) INFORMATION FOR SEQ ID NO:14257751_c3_16.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGCTGGATT TTGATTTGGT TCTTTTTGGC GCGACTGGGG ATTTAGCCAT GCGAAAGCTC | 60 |
| TTTGTTTCGC TTTATGAAAT TTATATTTCA TTTATGGTTT TAAAAACGAT TCTAGGATTA | 120 |
| TCGCATCGGG GCGTAAGGAG CTATCCAATG AAGAGTTTT | 159 |

(2) INFORMATION FOR SEQ ID NO:14313885_c3_11.nt:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 327 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: alkylphosphonate uptake genes A through Q

| | |
|---|-----|
| ATGCAAGATT TACCCCATG CCCTAAACGC AACGACGCCT ACACCTACCA TGATGGCACG | 60 |
| CAGTTCGTTT GCTCTAGCTG TTTGTATGAA TGGAATGGAA ATGAAATTAG TAATGAAGAA | 120 |
| TTGATCGTTA AAGATTGCCA TAATAATCTT TTACAAAATG GGGACTCGGT CATTCTCATT | 180 |
| AAAGATTTAA AGGTTAAAGG CTCATCTTTG GTGCTTAAAA AAGGCACTAA AATCAAAAAT | 240 |
| ATCAAGCTTG TCAATAGCGA TCACAATGTG GATTGTAAAG TGGAAGGGCA GAGCTTGTCT | 300 |
| TTAAAATCTG AATTCCTTAA AAAAGCT | 327 |

(2) INFORMATION FOR SEQ ID NO:1431462_c3_9.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: outer membrane 30.2K protein

| | |
|---|-----|
| GTGGATGGGG CTATCATAAC AGGGAATTAT GCCTTGCAAG CAAAACTCAC CGGAGCCTTA | 60 |
| TTTTCAGAAG ATAAGGACTC GCCTTATGCT AATCTTGTAG CCTCTCGTGA GGATAATGCG | 120 |
| CAAGATGAAG CGATAAAAGC GTTGATTGAA GCCTTACAGA GCGAAAAGAC CAGGAAATTC | 180 |
| ATTTTGGATA CCTATAAGGG GGCGATTATC CCGGCTTTT | 219 |

(2) INFORMATION FOR SEQ ID NO:14455461_c2_3.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 711 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| GTGTTYCCA TGCTGGTGTT GGTGTTGAGC GATAATTTTT TAGGGCTTTT CATTGGCTGG | 60 |
| GAAGGGGTGG GGCTATGCTC TTA CTGCTC ATTGGCTTTT GGTATCATAA AAAAAGCGCG | 120 |
| AATAACGCTT CTATTGAAGC CTTTGTGATG AATCGAATCA CGGATTTAGG CATGCTCATG | 180 |
| GGGATTATTT TGATCTTTTG GAATTTTGGC ACCCTCCAGT ATAAAGAAGT CTTTAGCATG | 240 |
| CTCAATAACG CCGATTATTC CATGCTCTTT TACATTAGCG TGTTTCTTTT TATTGGCGCT | 300 |
| ATGGGGAAGA GTGCTCAATT CCCTATGCAC ACATGGTTAG CCAACGCTAT GGAGGGGCCT | 360 |
| ACCCCTGTAT CCGCTCTCAT CCATGCARCG ACGATGGTAA CCGCTGGGGT GTATCTAATC | 420 |
| ATCAGAGCCA ATCCTTTGTA TAGTGCGGTG TTTGAAGTGG GTTATTTTAT CGCATGCTTA | 480 |
| GGAGCGTTTG TGGCTCTTTT TGGAGCGAGC ATGGCTTTAG TCAATAAGGA TTTAAAACGC | 540 |
| ATCGTGGSYT ATTCCACGCT TTCTCAATTA GGGCTATATG TTTGTAGCGG CCGGGCTTGG | 600 |
| GGCTTATGCG ATCGCGCTTT TCCACCTCTT TACGCATGCG TTCTTCAAAT CCCTCCTTTT | 660 |
| CTTAGGCTCA GGCAATGTCA TGCATGCGAT GGAAGACAAT CTGGATATTA C | 711 |

(2) INFORMATION FOR SEQ ID NO:14494077_c1_9.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|--|-----|
| ATGATGATAA CCAAACAATC GTATCAAAGA TTCGCTTTAA TCGGGTTTT TGTGTTTTTCG | 60 |
| CTTTCGGCGT TTATTTTTTAA CACCACGGAG TTTGTCCCTG TTGCACTTCT GTCAGACATT | 120 |
| GCGAAAAGCT TTGAAATGGA GAGCGCAACA GTGGGGCTTA TGATCACTGC TTATGCATGG | 180 |
| GTGGTGTCTC TTGGCTCATT GCCCTTGATG CTGCTTAGCG CTAAAATTGA AAGGAAACGC | 240 |
| TTATTGCTTT TTCTTTTCGC TCTTTTTTATT TTCAGCCATA TCCTTTCGCG T | 291 |

(2) INFORMATION FOR SEQ ID NO:14570443_f3_15.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 840 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGAAACTGA GAGCAAGTGT TTTAATCGGT GTGGCAATTC TGTGCTTAAT TTTAAGTGCG | 60 |
| TGCAGTAACT ATGCGAAAAA AGTGGTGAAA CAAAAGAACC ATGTTTATAC GCCTGTGTAT | 120 |
| AATGAACTGA TAGAGAAGTA TAGTGAGATC CCCTTAAATG ACAAAC TCAAGACACCA | 180 |
| TTCATGGTGC AAGTGAAGTT GCCAAATTAC AAGGACTATT TGTTGGATAA TAAACAAGTT | 240 |
| GTACTAACTT TCAAAC TTGT TCACCATTCT AAAAAGATTA CGCTCATAGG CGATGCCAAT | 300 |
| AAGATCCTCC AATACAAGAA TTA CTTTCCAA GCTAACGGGG CAAGATCTGA CATTGATTTT | 360 |
| TACTTGCAAC CCACTTTGAA TCAAAAGGGT GTGGTGATGA TAGCGAGTAA CTACAATGAT | 420 |
| AATCCCAACA ACAAAGAAAA ACCACAGACC TTTGATGTGT TGCAAGGAAG TCAGCCAATG | 480 |
| CTAGGAGCTA ACACAAAAAA CTTGCATGGC TATGATGTGA GTGGAGCAAA CAACAAGCAA | 540 |
| GTGATCAATG AAGTGGCAAG AGAAAAAGCT CAGCTAGAAA AAATCAATCA GTATTACAAG | 600 |
| ACTCTCTTGC AAGACAAGGA ACAAGAATAT ACCACTAGGA AAAATAACCA ACGAGAAATT | 660 |
| TTAGAAACAT TGAGTAATCG TGCAGGTTAT CAAATGAGGC AGAATGTGAT TAGTTCTGAG | 720 |
| ATTTTAAAGA ATGGCAACTT GAACATGCAA GCCAAAGAAG AAGAAGTTAG GGAGAAGCTA | 780 |
| CAAGAAGAAA GAGAGAATGA ATACTTGCGC AATCAAATCA GAAGTTTGCT CAGTGGTAAG | 840 |

(2) INFORMATION FOR SEQ ID NO:14574201_c3_19.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGTGGTTAG ATCACATCGC TAAAGAGATC AGAAGTTTAG TGGAAAACGA TATTGAAGTG | 60 |
| GGTATTGTGA TTGGTGGAGG CAATATCATT AGGGGGGTTA GCGCGGCTCT AGGGGGGATC | 120 |
| ATTAGGCGCA CCAGTGGGGA TTATATGGGC ATGTTAGCCA CCGTGATTAW GCGG | 174 |

(2) INFORMATION FOR SEQ ID NO:14640637_c2_12.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: variable antigen from Treponema

| | |
|---|-----|
| GTGCATAACT TCCATTGGAA TGTGAAAGGC ACCGATTTTT TCAATGTGCA TAAAGCCACT | 60 |
| GAAGAAATTT ATGAAGGGTT TGCGGACATG TTTGATGATC TCGCTGAAAG GATCGTTCAA | 120 |
| TTAGGACACC ACCCCCTAGT CACTTTATCC GAAGCGATCA AACTCACTCG TGTTAAAGAA | 180 |
| GAAACTAAAA CGAGCTTCCA CTCTAAAGAC ATCTTTAAAG AAATTCTAGA GGACTACAAA | 240 |
| CACCTAGAAA AAGAATTTAA AGAGCTCTCT AACACCGCCG AAAAAGAAGG CGATAAAGTT | 300 |
| ACCGTAACTT ATGCGGACGA TCAATTAGCC AAGTTGCAAA AATCCATTTG GATGCTAGAA | 360 |
| GCCCATTTAG CT | 372 |

(2) INFORMATION FOR SEQ ID NO:14642202_f1_3.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: HYPERSENSITIVITY RESPONSE SECRETION PROTEIN

| | |
|---|-----|
| ATGAATAAAA CCATAAAAGC CGCCGCCCTA GCCTATAACA TGGGGCAAGA TCATGCCCCA | 60 |
| AAAGTGATCG CAAGCGGGGT GGGCGAAGTG GCTAAAAGGA TCATTCAAAA AGCTAAGGAA | 120 |
| TACGATATAG CGCTCTTTTC TAACCCCATG CTGGTGGATT CGCTCTTAAA GGTGGAATTA | 180 |
| GACTGCGCGA TACCTGAAGA ATTGTATGAA AGCGTGGTGC AAGTGTTTTT ATGGCTCAAC | 240 |
| AGCGTGGAAT ATAACGCGCA AATGTCCAAG | 270 |

(2) INFORMATION FOR SEQ ID NO:14645905_c3_14.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 633 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: sensor protein

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| ATGGGGAAAA | TTTCAGCGCA | TTTAGCCCAT | GAAATCAGAA | ACCCCGTAGG | CTCTATCTCT | 60 |
| CTTTTAGCTT | CGGTGTTATT | AAAGCATGCG | AACGAAAAAA | CTAAACCCAT | TGTTGTAGAA | 120 |
| TTGCAAAAAG | CTTTATGGCG | CGTAGAAAGG | ATCATTAAAG | CCACCTTGCT | TTTTTCTAAA | 180 |
| GGCATTCAAG | CCAACCGCAC | CAAGCAAAGT | TTGAAAACGC | TAGAGAGCGA | TCTCAAAGAA | 240 |
| GCCCTAAACT | GCTACACTTA | CTCTAAAGAC | ATTGATTTTC | TTTTTAATTT | TAGCGATGAA | 300 |
| GAAGGGTTTT | TTGACTTTGA | TTTAATGGGG | ATTGTGTTAC | AAAATTTCTT | GTATAACGCC | 360 |
| ATTGATGCGA | TTGAAGCCTT | AGAAGAGAGC | GAACAAGGTC | AGGTCAAAAT | TGAAGCGTTC | 420 |
| ATTCAAAATG | AATTTATTGT | CTTCACCATT | ATTGATAATG | GCAAGGAAGT | GGAAAATAAA | 480 |
| AGCGCTTTAT | TTGAGCCTTT | TGAAACCACT | AAATTAAAGG | GGAATGGCTT | AGGGTTAGCC | 540 |
| CTGTCTTTGC | AAGTCGTTAA | AGCCCATGAA | GGGAGCATTG | CGCTATTAGA | AAATCAAGAA | 600 |
| AAAACCTTTG | AAATTAAGAT | TCTTAACGCT | TCT | | | 633 |

(2) INFORMATION FOR SEQ ID NO:1464715_c2_6.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 636 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| GTGTCAGAAT TTCATCAAGT TTATGaCCCT TTGGGTAATA TTTGGCTGAG CGCTCTTGTG | 60 |
| GCCTTATTGC CGATTTTGTGTT ATTTTCTTA TCTTTAATGG TTTTAAACT CAAAGGTTAT | 120 |
| ACAGCGGCCT TTTTGAGCGT GGCCTTATCA GCCATTATTG CGGTTTTAGT GTATAAAATG | 180 |
| CCTGTTAGCA TGGTGGGTTT AAGCTTCCTT TATGGCTTTC TTTATGGCCT ATGGCTATTC | 240 |
| GCTTGGATCA TTATTGCCGC GATTTTTTTA TACAAACTCA GCGTTAAATC CGGCTATTTT | 300 |
| GAAATCTTAA AAgAAAGCGT TCAGTCCATC ACTTTAGATC ACCGCATTTT AGTGATTTTG | 360 |
| ATTGGCTTTT GtTTTGGCTC ATTTTtagAA GGGGCGATCG GCTTTGGAGG GCCTATTGCC | 420 |
| ATCACAGCGG CGATTTTAGT GGGGTTGGGg TTAAGCCCTT TGTATTCTGC TGGGTTATGT | 480 |
| TTGAtCGCtA ACACCGCTCC TGTGgCCTTT GGcgCGGTGG GTATCCCTAT AAGCGCGATG | 540 |
| GCgAGCGCGG TAGGGGTGCC AGCGAtCTTA ATTTcAGCCA TGACGGGTAA AAtCCTCTTT | 600 |
| TTTGTGAGCT TGTTAGTgCC GTTTTTTATT GTGTkT | 636 |

(2) INFORMATION FOR SEQ ID NO:14713512_f2_7.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 546 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: INVOLVED IN PENICILLIN TOLERANCE-has signal pepti

| | |
|---|-----|
| ATGGAAATTA AAATGGCTAA GGATTATGGT TTTTGTTTTG GCGTCAAAAG AGCGATACAA | 60 |
| ATCGCTGAAA AAAATCAAAA CAGCTTGATT TTTGGCTCGC TCATTCATAA CGCTAAAGAA | 120 |
| ATCAATCGTT TGGAAAAAAA TTTCAATGTG AAAATTGAAG AAGATCCTAA AAAAATCCCT | 180 |
| AAAAATAAGA GCGTGATCAT AAGAACCCAT GGCATTCTTA AACAGGATTT AGAATACTTG | 240 |
| AAAAATAAGG GGGTTAAAAT CACTGACGCG ACTTGCCCGT ATGTGATCAA ACCTCAGCAA | 300 |
| ATTGTGGAAT CCATGAGTAA AGAAGGGTAT CAAATCGTGC TTTTGGGGA CATTAAACCAC | 360 |
| CCTGAAGTCA AGGGCGTGAT CAGCTATGCC ACTAACCAGG CTTTAGTCGG CAATTCGTTA | 420 |
| GAAGAATTGC AAGAAAAAAA ATTGCAACGG AAAGTGGCTT TAGTCTCTCA AACCACCCAA | 480 |
| GCAAACCCCA AAACCTCTTG AAATCGCTTC TTATTTGGTG GARGRTGCAC TGAAGTGCGT | 540 |
| ATTTTTT | 546 |

(2) INFORMATION FOR SEQ ID NO:14714687_f1_3.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 672 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGGATCATG AGTTTTTGAT TACCATGCGT TTGAGCTTTT CTTTAGCTTT GATTACCACC | 60 |
| CTTATTTTAC TCCCTATAGG GATTTTTTTA GGCTATTTTT TAAGCCTTAA ACGCAATCTT | 120 |
| TTAACGAGCT TAACAGAAAC GCTTGTGTAT ATGCCTTTAG TTTTACCCCC AAGCGTGCTA | 180 |
| GGGTTTTATC TTCTTTTAAT CTTTTCGCCT TCTTCTTTTT TGGGAGCGTT TTTACAAGAT | 240 |
| GTGTTAAATG TGAAACTCGT TTTTAGTTTC CAAGGGCTTA TCTTAGGGAG CGTGATTTTT | 300 |
| TCCTTGCCCT TTATGGTAAG CCCTATTAAA AGCGCGTTAA TTTTCCTGCC CACTTCTTTA | 360 |
| AAAGAAGCCA GTTATAGCTT GGGTAAAGGG GAATACTACA CCCTTTTTTT TGTCCTACTC | 420 |
| CCTAACATCA AACCCAGTGT GTTGATGGCT ATCATTACAA CTTTTATGCA CACTATAGGT | 480 |
| GAATTTGGCG TGGTGATGAT GCTTGGGGGT GATATATTAG GGGAAACAAG AGTGGCTAGC | 540 |
| ATTACGATCT TTAACGAAGC TGAAGCACTC AATTATTCTA AAGCCCATCA ATACGCCTTA | 600 |
| ACGCTCACGC TTATTAGTTT TAGCCTCTTG TTTGTTACCC TATTTTTAAA TAAAAACAA | 660 |
| AGCTCGTTTT TA | 672 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGCATCCTA TAATGTTTGC CTATATCGCT AACGCGCTCG CTCAAGCTAG AAAGATCAAC | 60 |
| GGAACACTTT GCATGGCGTT TCAAAAAATA TCTCAAGTCA AAGAATTAGG CATTGATAAA | 120 |
| GCAAAGAGTT TGATAGGCAA CCTTTCTCAA GTGATTATCT ACCCCACAAA AGATACTGAT | 180 |
| GAATTAATAG AATGTGGCGT CCCATTAAGC GATAGTGAAA TCAATTTCTT ACACAACACG | 240 |
| GACATGAGAG CCAGACAAGT GCTAGTAAAA AATATCGTTA CAAACGCTTC AGCTTTTATT | 300 |
| GAAATTGATT TAAAAAAGAT TTGCAAGAAC TACTTTATAT TCTTGATAGC AATGCTGGTA | 360 |
| ATAGAAAAAT CCTCAATGAT CTTAAAAAG CAAACCAAGA AACTTATAAG GAAGAGTATT | 420 |

(2) INFORMATION FOR SEQ ID NO:14864452_c3_14.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGTGCCTGA CAGGCGGCTT GATGCGTTGG CTCAAATCGG TAAAGCCTGA ACGAATCTTG | 60 |
| CATTCTGTGG TGAATTTGT GGATATTGCC GGATTGATTA AGGGGGCGAG CAAGGGGGAG | 120 |
| GGTTTAGGCA ATCAGTTTTT AGCCAATATC AAGGAATGCG AAGTGATCTT GCAAGTGGTG | 180 |
| CGCTGTTTTG AAGATGACAA TYATCACGCA TGTGAACGA | 219 |

(2) INFORMATION FOR SEQ ID NO:15039062_f3_15.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGCATGTTG CTTGTCTTTT GGCTTTAGGG GATAACCTCA TCACGCTTAG CCTTTTAAAA | 60 |
| GAAATCGCTT CCAAACAGCA ACAGTCCCTT AAAATCCTAG GCACTCATTT GACTTTAAAA | 120 |
| ATCGCCAAGC TTTTAGAATG CGAAAAACAT TTTGAAATCA TTCCTGTTTT TGAAAATATC | 180 |
| CCTGCTTTTT ATGACCTTAA AAAACAAGGC GTTTTTTGGG CGATGAAGGA TTTTTTATGG | 240 |
| TTATTAAAGC AATTAAAAAA CATCAAATCA AACGTT | 276 |

(2) INFORMATION FOR SEQ ID NO:15126875_c3_21.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 615 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | |
|--|-----|
| ATGAAAAAGA AGCCATTGAT GTGGCGTATC TGTGCGTTAA GGAGACTTCT TCTAGGGTTC | 60 |
| AAGAGAGAGA GAGAGTTATT AAGCTTCGCT AAACATTGGA ATATCCCAAC GATTGTCGTT | 120 |
| TTCACACACA CTCAAGCCGA AGCCGGCGAT GCGTTTGTCC AAGAACTAA AGGGATCATA | 180 |
| GACGAAGAAT GGGGGTTTAA AGGTTTTGTC AGAGCCTATG TGAGGGTCAA TTCCGTTGCC | 240 |
| TTTTTCATTTA GGGGGTTGAA AGTCCCTGTT GAAGGTTTAG AAGAATTGGT AGATGAAACG | 300 |
| AAAAAATGCC TTTCAGACGC TGAAAAAAT AAGAAAAGGC ATTTCTTGAG TATTCAAAGA | 360 |
| GTTAAGATTC AAGAAAGAAA ACAGGCTATG ATAGAGGAAT GTAAAACCAT TATCCATGTT | 420 |
| GCATCAGGCG CTGCAGGAGT TGCTGGGCTT ATCCCCATAC CTTTTAGCGA TGCGCTCGCT | 480 |
| ATCGCACCCA TTCAAGCAGG GATGATCTAT AAAATGAATG ACGCTTTTGG AATGGATTG | 540 |
| GATAAATCTG TGGGCGCGAG TTTGGTCGCA GGATTGTTAG GCGTAACTG TCGCGCAAGT | 600 |
| GGGGAGGACT CTCGT | 615 |

(2) INFORMATION FOR SEQ ID NO:156587_f2_3.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: chemotaxis protein cheW

| | |
|---|-----|
| GTGCTTGGCG TGTTYAATTT AAGGGGCAAT GTCTTCCCTT TGATCAGTTT GCGTTTAAAG | 60 |
| TTTGGCTTGA AAGCCGAAAA ACAAACAAA GACACTCGTT ATTTGGTGGT ACGCCATAAC | 120 |
| GAT | 123 |

(2) INFORMATION FOR SEQ ID NO:15807794_c1_2.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 657 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| GTGAAAAGCG TTTTtagCGA AGAAAAAGAA ACGCCTGTTA CTAAAGAAAA CGGCTCTTAT | 60 |
| TTGATCGCTT ATGACCCCCT AGATGGGAGT TCAGTGATGG AGGCGAATTT CTTAGTAGGC | 120 |
| ACGATTATAG GGGTTTATGA AAAGGATTAT AAGGCGCAAA ATTTAGTTGC AAGCCTTTAT | 180 |
| GTGGTTTTTG GGCATAAAAT AGAATTGGTG GTGGCTTTAG AAGAAGTTTA TCGTTACGCT | 240 |
| TTTTATCAAA ACAAGTTTCA TTTTATAGAA ACCATCGTTT TAGAAAATAA GGGTAAAATC | 300 |
| ATCGCTAGCG GAGGCAATCA AAAGGATTTT TCYTTGGGCT TAAAAAAGGC TTTAGAAGGG | 360 |
| TTTTTTGCAG AAAATTACCG CTTGCGATAC TCAGGATCTA TGGTGGCTGA TGTCCATCAT | 420 |
| GTGTTGGTTA AAAAGGGCGG AATGTTTTCC TACCCGCAAA AGAAATTGCG AAAGCTTTTT | 480 |
| GAAGTCTTTC CTTTAGCCTT GATGGTTGAA AAAGCTAAAG GGGAAGCGTT TTATTTTGAT | 540 |
| AAGGGGGTTA AAAAGCGTTT GCTAGATCAA AGCGTAGAAA GCTACCATGA AAAAAGCGAA | 600 |
| TGCTATTTAG CCAGCCCGCA TGAAGCTCAG ATTTTAGAAA AACATTTAAA GGGAGAA | 657 |

(2) INFORMATION FOR SEQ ID NO:1581937_c3_7.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 564 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGAAAAGCA TTGGAGAAGT GATGGCGATA GGGGGCAATT TCTTAGAAGC CTTACAAAAA | 60 |
| GCGTTATGCT CTTTGGAAAA CAATTGGCTA GGGTTTGAAT CGTTAAGCAA AGATTTAGAG | 120 |
| GCGATAAAAA AGGAAATCCG CCGGCCCAAT CCCAAACGCT TGCTCTATAT TGCTGATGCG | 180 |
| TTCAGGTTGG GCGTTTCTGT GGATGAAGTG TTTGAATTAT GCCAGATTGA CAGGTGGTTT | 240 |
| TTATCTCAAA TTCAAAAAC TGTCAAAGCA GAAGAGGGCA TCAATTCTAG CGTTTTAACG | 300 |
| GACGCCAAAA AATTGAGAGG GCTTAAAAAT TTAGGCTTTA GCGATGCCAG GATTGCCACT | 360 |
| AAAATCAAAG AAAATGAAAA TTTAGAGGTC AGCCCTTTTG AAGTGGAATT AGCTAGATCT | 420 |
| AATTTACAAA TCGCGCCCCA TTTTGAAGAA GTGGACACTT GCGCGGCGGA GTTTTTATCG | 480 |
| CTCACGCTTA TTTGTATTCC ACCTATGCCC CTAACCCTTT GCCCCCTATT GGAAACAAAC | 540 |
| AAGAAAAACA AGAAAAGAAA ATCC | 564 |

(2) INFORMATION FOR SEQ ID NO:15824052_f3_6.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 693 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: transmembrane receptor

| | |
|---|-----|
| ATGTTTGGGA ATAAGCAGTT ACAGCTTCAA ATCAGTCAAA AAGATTCTGA GATTGCGGAG | 60 |
| TTAAAAAAG AAGTCAATCT CTATCAAAGC CTTTTAAATT TGTGCTTGCA TGAGGGTTTT | 120 |
| GTAGGTATTA AAAACAATAA AGTCGTTTTT AAAAGCGGGA ATCTTGCAAG CTTAAACAAT | 180 |
| TTAGAAGAAC AAAGCGTTCA TTTTAAAGAA AACGCAGAAA GCGTTAATTT ACAAGGGGTT | 240 |
| TCTTATTCTT TGAAAAGCCA AAATATTGAC GCGGTGCAGT ATTTTTCATT GGCTAAAAAA | 300 |
| ACAGGGGGTG TGGGGGAATA CCATAAAAAT GATTTGTTTA AGACTTTTGT CACGAGCTTA | 360 |
| AAAGAGGGCT TAGAGAACGC GCAAGAAAGC ATGCAGTATT TCCATCAAGA AACAGGCTTG | 420 |
| CTCTTGAATG CGGCTAAAAA TGGCGAAGAG CATTCTAATG AAGGATTAAT AACCGTTAAT | 480 |
| AAAACGGGTC AAGACATTGA ATCGCTTTAT GAAAAGATGC AAAACGCCAC TTCGTTAGCG | 540 |
| GACTCCCTCA ACCAACGGAG CAATGAAATC ACTCAAGTCA TTTCTTTGAT TGATGATATT | 600 |
| GCAGAGCAAA CCAATCTCTT AGCCCTAAAC GCCGCTATTG AGGCCGCACG AGCGGTGAAC | 660 |
| ATGGCAGAGG GTTTGCGGTG GTGGCTGATG AGG | 693 |

(2) INFORMATION FOR SEQ ID NO:16100038_c3_30.nt:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 189 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGTGGATTA TGTCTTCACT TTCTAGTTCA TTCTTTCATT CGCTCTTCTT CATCAAATCA | 60 |
| AACCCTGGCC AACTCTTAAA AGGTTGGGGT TCAAAAATCT TTTTCATAAA TAGAAAGTTT | 120 |
| GTTTTAGCAC AGTATAATCC TAGCGTTTCA ATTTTATTT TACTCAATAG GGTGTTTGGT | 180 |
| GTTGGCGTT | 189 |

(2) INFORMATION FOR SEQ ID NO:16225006_c2_6.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 459 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: Outer membrane 30K protein

| | |
|---|-----|
| GTGGGCGCTA ACCCTGTGCC GCATGCGCAA ATCTTGCAAT CAGTTGTGGA TGATTGAAA | 60 |
| GAGAAAGGGA TCAAATTAGT GATCGTGTCT TTTACGGATT ATGTGTTGCC TAATTTAGCG | 120 |
| CTCAATGACG GCTCTTTAGA CGCGAATTAC TTCCAGCACC GCCCTTATTT GGATCGGTTT | 180 |
| AATTTGGACA GAAAAATGCA CCTTGTTGGT TTGGCCAATA TCCATGTGGA GCCTTTAAGA | 240 |
| TTTTATTCTC AAAAAATCAC AGACATTAAA AACCTTAAAA AAGGCTCAGT GATTGCTGTG | 300 |
| CCAAATGATC CGGCCAATCA AGGCAGGGCG TTGATTTTAC TCCATAAACA AGGCCTTATC | 360 |
| GCTCTCAAAG ACCCAAGCAA TCTATACGCT ACGGAGTTTG ATATTGTCAA AAATCCTTAC | 420 |
| AACATCAAAA TCAAACCCCT AGAAGCTGCG GTTATTGCC | 459 |

(2) INFORMATION FOR SEQ ID NO:16251627_f2_2.nt:

72

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGGGGCTTG TTGCGAGCGG CATTAACGAT GAAGAGCTTT TAAAATGGCT TCAGGCTTTT | 60 |
| GGGTTAAGAA TGGGTCTTTG TTTTCAAGTG CTAGATGATA TTATAGACGT TACACAAGAT | 120 |
| GAAAAAGAAA GCGGTAAAC CACGCATTTA GACAGCGCTA AAAACAGCTT TGTGAATTTA | 180 |
| TTGGGGCTAA AAAAGGCAGC GGTACGCCC AAACCTT | 216 |

(2) INFORMATION FOR SEQ ID NO:16406265_f3_6.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 627 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: integral protein in inner membrane

| | |
|--|-----|
| ATGGGGTTTA ACCGCTTGGT GGATAGAGAC ATTGATAAGG ATAACCCAAG GACGAAAAAC | 60 |
| CGCCCGAGCG TGGATGGTAG GATCAGCGTT AAAGGCATGG TCATTTTITAG CGTTTCAAAC | 120 |
| GCTCTTTTGT TCGTGGGAGT GAGTTATTTT ATCAACCCTT TAGCTTTCAA GCTTTCGTTA | 180 |
| CCTTTTTTTAA TCATTTTAGG GGGTTATTCG TATTTCAAGC GCTTTTCTTC TTTGGCGCAT | 240 |
| TTTGTCGTGG GTTTGGCTTT GGGTTTAGCC CCCATTGCAG GAAGCGTGGC GGTTTTAGGG | 300 |
| GATATTCCTT TATGGAATGT CTTTTTGGCY TTAGGGGTGA TGTTGTGGGT GGCTGGGTTT | 360 |
| GATTTGCTCT ATTCTTTACA GGATATGGAG TTTGATAAAG AAAGGGGCTT GTTTTCCATT | 420 |
| CCTAGCCAAT TAGGGGAAAA ATGGTGCTTG AATCTTTCAA GGCTCTCGCA CCTTGTGGCA | 480 |
| CTGATCTGCT GGCTTTGTTT TGTGAAATGC TATCATGGGG GGCTTTTTCG GTATTGGGC | 540 |
| TTAGGGGTTT CAGCCTTGAT CTTACTCTAT GAGCAGATTT TAGTGGCCAG AGATTATAAA | 600 |
| AACATTCCTA AAAGCCTTTT TTGTGAG | 627 |

(2) INFORMATION FOR SEQ ID NO:16406581_c2_13.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|--|-----|
| GTGGAGCAAA ATAAAATCAT TAAACTCTTC ACTGTGGCGA CTATGGCGAT GATGCCCCC | 60 |
| ACATTGATTG GCACGATTWA TGGCATGAAT TTAAATTCA TGCCGGAGTT AGAATGGCAA | 120 |
| TACGGGTATC TTTTTCGCT GATTGTCATG GCGATTCTA CGATTTTGCC GGTGATTAT | 180 |
| TTCAAAAAGA AAGGGTTGGT TGAGCCTTT CATGGAATTT TTATCCTCAC TCTTAGACGC | 240 |
| TCTTTCTACA CCGCATGGCA TAGTCTCCTT GGCTACGCCA CGCTT | 285 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|--|-----|
| ATGTTTCGATT CAATCGTTTA TTTTTTCAAT AAGAGCGGGT TTGTTACCAC GCTTGTTTTA | 60 |
| GTTTGGATTT CGCTTTATTT GGTGATGACT TTATGGGTCT TTTTGTATAA AAGCATTGTA | 120 |
| TTAAAGATTG AACTCAGGCG CGAGATGCAA TCTTTGTCTA ACATTCTTAA TGGAGCGCAA | 180 |
| GACGCTCCAG AGCATTTTAT GTTTAATAAA AAAAGAAATG ATGAGACCAA AAGGTATTCT | 240 |
| AATGAATTGT TGCAGGSCTT GGAAACACCA GGTTCT | 276 |

(2) INFORMATION FOR SEQ ID NO:16440842_c3_8.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGGCGATGC TYTATTGCAT GCGGTTATTG ATGCCGATTT TAGGAGCGAT TAAAGGGGGG | 60 |
| GATATTGGCG AATGGTTCCC TGATAATGAC CCCAAATACA AAAACGCCTC TTCTAAAGAG | 120 |
| CTTTTAAAAA TCGTGTTGGA TTTTCTCAA AGCATTGGGT TTGAATTGCT TGAAATGGGA | 180 |
| GCGACCATCT TTAGCGAAAT CCCTAAAATC ACTCCTTACA AACCGGCGAT TTTAGAGAAT | 240 |
| TTGAGCCAAC TTTTGGGTTT AGAAAAATCT CAAATCAGCT TGAAAGCCAC TACAATGGAA | 300 |
| AAAATGGGGT TCATTGGCAA ACAAGAAGGG CTGTTAGTCC AAGCGCATGT GAGCATGCGT | 360 |
| TATAAACAAA AACTT | 375 |

(2) INFORMATION FOR SEQ ID NO:16459375_f1_1.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3534 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: cytotoxicity associated immunodominant antigen [H

| | |
|---|------|
| ATGATACCAA ATTTAGATAT AGAAGGAGAA ACAATGACTA ACGAAGCCAT TAACCAACAA | 60 |
| CCACAAACCG AAGCGGCTTT TAACCCGCAG CAATTTATCA ATAATCTTCA AGTGGCTTTT | 120 |
| ATTAAAGTTG ATAATGTTGT CGCTTCATTT GATCCTAATC AAAAACCAAT CGTTGATAAG | 180 |
| AATGATAGGG ATAATAGGCA AGCTTTTGAG AAAATCTCGC AGCTAAGGGA GGAATTCGCT | 240 |
| AATAAAGCGA TCAAAAATCC TACCAAAAAG AATCAGTATT TTTCAAGCTT TATCAGTAAG | 300 |
| AGCAATGATT TAATCGACAA AGACAATCTC ATTGATACAG GTTCTTCCAT AAAGAGCTTT | 360 |
| CAGAAATTTG GGAATCAGCG TTACCAAATT TTTATGAATT GGGTGTCCCA TCAAAACGAT | 420 |
| CCGTCTAAAA TCAACACCCA AAAAATCCGA GGTTTTATGG AAAATATCAT ACAACCCCCT | 480 |
| ATCTCTGATG ATAAAGAGAA AGCGGAGTTT TTGAGGTCTG CCAAACAAGC TTTTGCAGGA | 540 |
| ATTATCATAG GAAACCAAAT CCGATCGGAT CAAAATTCA TGGGCGTGTT TGATGAATCT | 600 |
| TTGAAAGAGA GGCAAGAAGC AGAAAAAAT GGAGAGCCTA ATGGAGATCC TACTGGTGGG | 660 |
| GATTGGCTTG ATATTTTTTT ATCATTTGTG TTTAACAAAA AACAATCTTC CGATCTCAAA | 720 |
| GAAACGCTCA ATCAAGAACC AGTTCCTCAT GTCCAACCAG ATGTAGCCAC TACCACCACT | 780 |
| GACATACAAA GCTTACCGCC TGAAGCTAGG GATTTGCTTG ATGAAAGGGG TAATTTTTCT | 840 |
| AAATTCCTC TTGGCGATAT GAACATGTTA GATGTTGAGG GAGTCGCTGA CATTGATCCT | 900 |
| AATTACAAGT TCAACCAATT ATTGATCCAC AATAACGCTC TGTCTTCTGT GTTAATGGGG | 960 |
| AGTCATAATG GCATAGAACC TGAAAAAGTT TCATTGTTGT ATGGAAACAA TGGTGGTCCT | 1020 |
| GAAGCTAGGC ATGATTGGAA CGCCACCGTT GGTTATAAAA ACCAACGAGG CGACAATGTG | 1080 |
| GCTACACTCA TTAATGTGCA TATGAAAAAT GGCAGTGGGT TAGTCATAGC AGGTGGTGAG | 1140 |
| AAAGGGATTA ACAACCCTAG TTTTATCTC TACAAAGAAG ACCAACTCAC AGGCTCACAA | 1200 |
| CGAGCATTGA GTCAAGAAGA GATCCAAAAC AAAGTggATT TCATGgAATT TCTTgCACAA | 1260 |

| | | | | | | |
|------------|------------|------------|-------------|-------------|------------|------|
| AATAATgCTA | AATTAGACAA | CTTgAGCAAG | AAAGAGAAAG | AAAAATTCCA | AAATGAGATT | 1320 |
| GAAGATTTTC | AAAAAGACTC | TAAGGCTTAT | TTAGACGCCC | TAGGGAATGA | TCACATTGCT | 1380 |
| TTTGTTTCTA | AAAAAGACAA | AAAACATTTA | GCTTTAGTTG | CTGAGTTTGG | TAATGGGGAA | 1440 |
| TTGAGCTACA | CTCTCAAAGA | TTATGGGAAA | AAAGCAGATA | AAGCTTTAGA | TAGGGAGGCA | 1500 |
| AAAACCACTC | TTCAAGGTAG | CCTAAAACAT | GATGGCGTGA | TGTTTGTGTA | TTATTCTAAT | 1560 |
| TTCAAATACA | CCAACGCCTC | CAAGAGTCCT | GATAAGGGTG | TGGGTGCTAC | GAATGGCGTT | 1620 |
| TCCCATTTAG | AAGCAGGCTT | TAGCAAGGTA | GCTGTCTTTA | ATTTGCCTAA | TTTAAATAAT | 1680 |
| CTCGCTATCA | CTAGTGTCGT | AAGGCAGGAT | TTAGAGGATA | AACATAATCGC | TAAAGGATTG | 1740 |
| TCCCCACAAG | AAGCTAATAA | GCTTGTCAAA | GATTTTTTTGA | GCAGCAACAA | AGAATTGGTT | 1800 |
| GGAAAAGCTT | TAAACTTCAA | TAAAGCTGTA | GCTGAAGCTA | AAAACACAGG | CAACTATGAC | 1860 |
| GAGGTGAAAC | AAGCTCAGAA | AGATCTTGAA | AAATCTCTAA | AGAAACGAGA | GCGTTTGGAG | 1920 |
| AAAGATGTAG | CGAAAAATTT | GGAGAGCAAA | AGCGGCAACA | AAAATAAAAT | GGAAGCAAAA | 1980 |
| TCTCAAGCTA | ACAGCCAAAA | AGATGAGATT | TTTGCGTTGA | TCAATAAAGA | GGCTAATAGG | 2040 |
| GATGCAAGAG | CAATCGCTTA | CGCTCAGAAT | CTTAAAGGCA | TCAAAGGGA | ATTGTCTGAT | 2100 |
| AACTTGAAA | ATATCAACAA | GGATTTGAAA | GACTTTAGTA | AATCTTTTGA | TGAATTCAAA | 2160 |
| AATGGCAAAA | ATAAGGATTT | CAGCAAGGCA | GAAGAAACAC | TAAAAGCCCT | TAAAGGCTCG | 2220 |
| GTGAAAGATT | TAGGTATCAA | TCCAGAATGG | ATTTCAAAAG | TTGAAAACCT | TAATGCAGCT | 2280 |
| TTGAATGAAT | TCAAAAATGG | CAAAAATAAG | GATTTTCAGCA | AGGTAACGCA | AGCAAAAAGC | 2340 |
| GACCTTGAAA | ATTCCATTAA | AGATGTGATC | ATCAATCAAA | AGATAACGGA | TAAAGTTGAT | 2400 |
| AATCTCAATC | AAGCGGTATC | AGTGGCTAAA | GCAACGGGTG | ATTTTCAGTGG | GGTAGAGCAA | 2460 |
| GCGTTAGCCG | ATCTCAAAAA | TTTCTCAAAG | GAGCAATTGG | CTCAACAAGC | TCAAAAAAAT | 2520 |
| GAAGATTTCA | ATACTGGAAA | AAATTCTGCA | CTATACCAAT | CCGTTAAGAA | TGGTGTAAAC | 2580 |
| GGAACCCTAG | TCGGTAATGG | GTTATCTAAA | GCAGAAGCCA | CAACTCTTTC | TAAAAACTTT | 2640 |
| TCGGACATCA | AGAAAGAGTT | GAATGCAAAA | CTTGGAATTT | TCAATAACAA | TAACAATAAT | 2700 |
| GGACTCGAAA | ACAGCACAGA | ACCCATTTAT | ACTCAAGTTG | CTAAAAAGGT | AAAAGCAAAA | 2760 |
| ATTGACCGAC | TCGATCAAAT | AGCAAGTGGT | TTGGGTGATG | TAGGGCAAGC | AGCGAGCTTC | 2820 |
| CTTTTGAAAA | GGCATGATAA | AGTTGATGAT | CTCAGTAAGG | TAGGGCTTTC | AGCTAACCAT | 2880 |
| GAACCCATTT | ACGCTACGAT | TGATGATCTC | GGCGGACCTT | TCCCTTTGAA | AAGGCATGAT | 2940 |
| AAAGTTGATG | ATCTCAGTAA | GGTAGGGCTT | TCAAGGGAGC | AAAAATTGAC | TCAGAAAATT | 3000 |
| GACAATCTCA | ACCAGGCGGT | ATCAGAAGCT | AAAgCAAGTC | ATTTTGACAA | CCTAGATCAA | 3060 |

| | | | | | | |
|------------|------------|------------|------------|------------|------------|------|
| ATGATAGACA | AGCTCAAAGA | TTCTACAAAA | AAGAATGTTG | TGAATCTATA | TGTTGAAAGT | 3120 |
| GCAAAAAAAG | TGCCTACTAG | TTTGTCAGCG | AAATTGGACA | ATTACGCTAC | TAACAGCCAC | 3180 |
| ACACGCATTA | ATAGCAATGT | CAAAAATGGA | ACAATCAATG | AAAAAGCGAC | CGGCATGCTA | 3240 |
| ACGCAaAAAA | ATTCTGAGTG | GCTCAAGCTC | GTGAATGATA | AGATAGTTGC | GCATAATGTG | 3300 |
| GGAAGTGCTC | CTTTGTCAGC | GTATGATAAA | ATTGGATTCA | ACCAAAAGAA | TATGAAAGAT | 3360 |
| TATTCTGATT | CGTTCAAGTT | TTCCACCAGG | TTGAGCAATG | CCGTAAAAGA | CATTAAGTCT | 3420 |
| GGCTTTGTGC | AATTTTAAAC | CAATATATTT | TCTATGGGAT | CTTACAGCTT | GATGAAAGCA | 3480 |
| AGTGTGGAAC | ATGGAGTCAA | AAATACTAAT | ACAAAAGGTG | GTTTCCAAAA | ATCT | 3534 |

(2) INFORMATION FOR SEQ ID NO:16603418_c3_33.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1398 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|--|------|
| ATGAAAGCGT TGAAGACTTT TTTAAAAAAA TCCCTTATTC TGTTACTAGC AATTGCCTTA | 60 |
| AACCACTTAA ACGCTGTGGC TATGATTGTG GATAATCCTA CGCAGAACGC TTGGAATGGT | 120 |
| GCTAAAAGAG CATGGGATGA AAGCAAGTGG GCTAAACATT TAGCCACTAT TACTGAAAGG | 180 |
| ATCAAGCTCG CTCAAGACAC ATTAGATAGG GCTAATCAGA CGCTTAATTC CATCAACAAA | 240 |
| GTGAATGATG TTTTGAACAA AACCAATCAA TTTCTAACAG GCAGTATTTT AAGCATCCCC | 300 |
| AATCCCATGC AGTATGTAGA AAAAATCCAA AGTTTTGCCA AGCAAGTTCA AGCCAATACT | 360 |
| GAAAGGATCA AAGAAAATGC ACAAACACTAT GATATACGCA ATCAAATTGC AGCCAAACGC | 420 |
| ATCTCTGAAA AATGCCCTGA ACTCAATTGG GATGTCAGTC AAGACGCGAG CCCTACAGAG | 480 |
| AAAAACTTAC ACCAATTTTT CACGAGCAAG GGGAAAGAAA GCGCTAACAC AAAGGCTCTA | 540 |
| AAGGATTTTG CTAACGCCAT AGGTAACACT CAAATCAGCA CGGCGAACGA TTTAGGAGCT | 600 |
| GGACTTAGAG GCAGAGCCTT ATTAGAATAC ATTTGCATTC AAAAAGGCAA TTTAGAAGCG | 660 |
| GCTAAAAAAA TCCAATTATT AGACAGCCAA ATGACTTTAG CTCTACTCAA TAACGACTAT | 720 |
| ACGGCTTATG AAAAAGCTTAG AGCTGAAAAA GAAGAATTAA AAAGACAAAT CGCTTCAAAT | 780 |
| GTGTATGCGA AAGTCAAACA GCTTGTTGTA GCTTCCCAAG ATAGAGCGTT TAGTCAAATG | 840 |
| GATAATGAGT TGGGCGTTAA AACTTTTGGG TTCAACGATG AGAATGTTAA AAAAGGTTAT | 900 |
| TGCAAGAAAG AAAACAGAAA TGGCAAAAGC GAGTGCATCC CTAACATGCT CAATGTTAAT | 960 |
| CGCTTAAAAG CGCAATTTGA TGAGCTTAAT TTAGATTATA GTAGGGATAT TGCTGGTAAA | 1020 |
| AAAGGTGAAG CAGCCGCTAA AGTGTTCAAT GACTACAAAC ACCGATTCCA ACAATTAAGC | 1080 |
| GTAGAACTG CTTTAGAAAT CGCTCAAAAT TTAAGTTTTA TGAATAAGAC GCTAGGTTTA | 1140 |
| ATGGTGCAAA TGCAAAGCTA TGCATTCAAG CAACAAATGG GCTATTTTGA AGATATTATT | 1200 |
| CCTGCTGACG CCCTAAAAGA TGACAAAGAG CATCAAGAAA ATCTTGAACA AAAACAACAA | 1260 |

| | |
|---|------|
| GAAATAGAGA AAGTCTATAG GGCTAAATTA GACGCTTATG GTTCCCTAA TGGTAGTGTA | 1320 |
| GGAAAGGCAA GTGGCGTGAA TTCAAATAGT AATAATGAAG CCCCAAGCTC TGATAATATC | 1380 |
| CAGTCGTTTA ATCCGTAT | 1398 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 189 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: D-alanyl-D-alanine carboxypeptidase

| | |
|---|-----|
| GTGATGGATG CAGAAAATGG GGAATTGCTC GTTGCAGGAA GTTACCCTGA ATACAATTTG | 60 |
| AACGATTTTG TAGGCGGGAT CAGTCAAGAC AAATGGCAAA AACTCCAAGA TGATATTTAT | 120 |
| AACCCTTTAT TAAACCGCTT CGCAATGCCT TGTATCCGCC GGGATCTGTG GTTAAAATGG | 180 |
| GCGTGGGGT | 189 |

(2) INFORMATION FOR SEQ ID NO:17089217_f3_38.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1263 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|------|
| ATGAATTTTT | TTGACACCCT | TATGGGTATG | TTTGTGAGC | CATCTCAAAA | AGTAGCCAAA | 60 |
| AGTCTTGCTG | AACATGTGGG | TAGCTTTTTT | CATGCACAAC | TCATTTTAAA | CACAATTATT | 120 |
| ACTATTTTAT | TTATGATATG | GGCGTATAAG | CGTGTGAAAG | AGGGCGATAT | GTTTGAGTTT | 180 |
| AAAACCGCTA | TGGGTGTGGT | TGTATTTATA | GCGTTTGTAG | GATTTATCAA | TTGGGGGATT | 240 |
| AAAAATCCTA | ATGATTTTAA | CACTTATTTT | ATCAATACGA | TATTCTACCC | ATCTGAAAAA | 300 |
| CTAGCCATAC | TTATCGCTCA | AAGCCTAAAT | GATGGCTTAG | AAATCCCCAC | TAACACTAAT | 360 |
| TTAAGTCCTA | GTGAAATTTT | TAGCATAGGA | AATTTAGCCT | CAAGTGCGTA | TGCAATGATA | 420 |
| GTTAATCTGT | GGGATAATGC | TTTTGATGGT | ATTAACATGT | TTAATTGGCT | CACAATGATA | 480 |
| CCTAAAATAA | TTATGTTTTT | TTTAGTGATT | TTAGGGGAAT | TATTGTTTTT | AGGCTTATTG | 540 |
| CTTATTATTG | TGTTATTAGT | TACAGCAGAA | ATTTTTATGT | GGTCAGCATT | AGGTTTAATT | 600 |
| GTATTGCCTT | TAGGTTTAAT | CCCCCAAACC | AAAGGCATGT | TATTTAGCTA | TCTTAAAAAG | 660 |
| CTCATTTCCC | TTACTCTTTA | TAAACCTTGT | ATGATGTTAG | TAGCTTTTTT | TAATTATGGA | 720 |
| ATAATCTATA | AAGTCAATAC | TTTAATCCCC | ACTAAACACG | AAGTCACACA | AGGCTTTTAT | 780 |
| GGCAATGCGG | ATAAAATGGC | AAATGAGGGA | AAAATTATTG | ATGTCTTTGG | CAATGTCTTA | 840 |
| GAAGGAGATT | GGAACTCTTA | TATAGCCCAT | AGTTCTATTG | TAGGCTTTTT | AACCATTATT | 900 |
| GTTTTAGGTT | CTGTGATTTG | TTTCTTTCTA | GTCAAACGAG | TGCCTGATTT | TATCAATAAT | 960 |
| ATCTTTGGCA | CAAGTGGAGG | CGTGGGGGCA | GTAACAGAAA | TGATGCAAAA | AATTGGCATG | 1020 |
| ACAATAGGCG | GAGCTGTATT | TGGGGGTAGT | GCAGTTATGG | TTGCTAATCA | AGTTAAGCAA | 1080 |
| GCCTATCAGA | GTGCTGGGGG | CGGACTAGCA | GGACTTCAAG | CTGGAGCTAA | AGCTTTTGGG | 1140 |
| CTTGAGCAA | TCAGTGGAGG | GGCAAGTGCT | ATGGCAAACC | ACAGGAGTGT | TAAAGCTGGG | 1200 |
| GTGAAACACT | TTGTAGCAAG | TGTTAAAAGT | GGCTTTGGAT | TTGATAATGA | TAAAAATAAT | 1260 |

AAA

1263

84

(2) INFORMATION FOR SEQ ID NO:17787558_c3_18.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: ARGININE TRANSPORT ATP-BINDING [E.coli] & homolog

| | |
|---|-----|
| ATGGATGAAC CAGAAACCAG TTTAGAGCAA AACGCTCTTA TAAGACTATC AAATCTCATA | 60 |
| AGCTTGCGCA ACACCCAACA ACTTACAAGT ATCATCGCCA CTCATGATCC TATTGTCTTA | 120 |
| GATAGTTGCG AATGGGTATT GCTCCTTAAG AATGGCAACA TTGCTCAATA CAAACCTTTA | 180 |
| AATTCTATAT TAAAATCTGT AGCTAAAACT TTAACTTTA AAGAAAAACC AACCACAAAA | 240 |
| GACTTATTAG CGTTACTAAA GGATATT | 267 |

(2) INFORMATION FOR SEQ ID NO:179677_c3_22.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 711 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|--|-----|
| GTGAAAACCT TAGGATTGTC TTCGCTTGGT GGGACTTTAG AATTTTACGA TTTTATCATC | 60 |
| TTTGTATTTT TTACAAGTAT CATTGCCAAA CACTTTTTTC CAAACACGCT TAGCCCTATC | 120 |
| TGGTCTGAAA TCAACACTTA TGGGATCTTT GCTGCAGGTT ATCTGGCGCG CCCGCTTGGT | 180 |
| GGCATAGTGA TGGCCCACTT TGGGGATAAA TTCGGTCGTA AAAACATGTT CATGCTCTCT | 240 |
| ATTTTATTAA TGGTAATCCC AACCTTTGCG CTAGCTTTGA TGCCAACTTT TAATGATTTG | 300 |
| GTGGGTTTTG GCGTGGATAG CATGGGGCTT ACCCCTAAAA ACGCTCATTA TCTTGGTTAC | 360 |
| ATAGCTCCTG TTTTTTTTRGT RCTTGTTAGG ATTTGTCAAG GCGTCGCTGT GGGTGGTGAA | 420 |
| TTGCCTGGCG CTTGGGTTTT TGTCCATGAA CATGCCCCAC AAGGACAAAA AAACACTTAT | 480 |
| ATCGGTTTTT TAACCGCTTC CGTAGTTTCT GGGATTTTGC TTGGGAGTTT GGTTTATATC | 540 |
| GGGATTTACA TGGTTTTTTGA CAAGCCTGTT GTTGAAGATT GGGCTTGGCG GGTTGCCTTT | 600 |
| GGGCTTGGAG GAATTTTTTG TATCATTTCT GTGTATTTGA GCGCTTTTTT AGAAGAAACT | 660 |
| CCCGTTTTTC AGCAAATGAA GCAGGGACGA TGCCTTAGTC AAATTCCCGC T | 711 |

(2) INFORMATION FOR SEQ ID NO:194415_c1_9.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1413 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|------|
| ATGCGCAAAT TTTTGGATGG GGCAAAAAGT GAGGTTTTAA AATACGATGT GATTTCTTTT | 60 |
| GATATTTTTG ATACCCTCCT TCTAAGACCT TTCATTAAAC CCACAGATTT ATTTTTGTAT | 120 |
| ATTGAGACTA AATACAATAT TAAAGGTTTT CATCAAGCAA GGATCCTGGC AGAAATGCAA | 180 |
| TCCAGAAAAT TAAGTAAAAG ACAAGACATT ACTCTAGATG AAATTTATCA TCAAATCCCA | 240 |
| AAAGAGTTTC ATTCATATAA GGGAGTAGAA ATCGCTACTG AAAAAGAGGT GCTTGTTCCA | 300 |
| AACTTGGAGA TGTTAGAACT CTATCGTTTC GCTAAAGAGA ACAATAAGAG AGTGATTATT | 360 |
| GTATCAGATA TGTATTTACC TTTAGAGGTT CTTGAAGATA TTTTAATTTC TAAGGGTTTT | 420 |
| GATGGTTATA CAAATTTCTA TCTTAGTAAC CATATAATGC TCACTAAACA TTCAAAGGAT | 480 |
| TTGTTTAAGC ATGTTTTAAA ACAAGAAAAT ATTACTAATA CGCAGATATT GCATATCGGT | 540 |
| GATAATTCTT GGGCAGATGA CGCTATGCCT AAAAGTTTAG GCATAGCAAC GCTATTTAGA | 600 |
| AAAAGCGTGT TGAAACAATT AGAAGAAGTT TTTCTTAAAT ACAAACATT TAATCCAACC | 660 |
| AGTGTTGCGC AAAGTTTTAT TTTAGGATCT TTATGCGTTT TTTATAAAAA TTATATTCAA | 720 |
| AAACATGAAA AATTTGATTA TTGGTTTCTT TTAGGAGCGA TGCAGGCAGG AATTGCAGCC | 780 |
| GTTGCTTATT GCCAGTTTAT CTATAAGGAG ATTCACAAAA GAAATATTGA TACTTTAGTG | 840 |
| TTTGTTGCGC GAGATGGTTA TTTATTGCAA AAAATTTTTA ATATTTTATA TCCAAATTCA | 900 |
| TATAAACTA CTTATGTCTA TGCTCCCAGA ATTTTAAAAA AAGCGGTATT TTTAGAAGTC | 960 |
| GTAGAGGGCG AGAGTTTGGA AATTTTGCGT ATTTTAGAAG GCGAAGAAGA AGTTAAAAAG | 1020 |
| AAGCAAATCA CCACCAACCA ACAGGCGTAT GTATATCTCT ATAGCAATTT TGAACATTGC | 1080 |
| CGCCATTTAG CGTTAAAATG TTTAGATAAT TACAGAAAAT ACTTGTTTTT ATCAAATTTA | 1140 |
| GAAGGAAATA TCGCTATTGT AGATACGATT ACTTTAGGCT ATTCTTCGCA AGGGTTAATC | 1200 |
| TAAAAAGCTT TAAATAAAGA AGTTTTTGGG TGCTATGTGG ATCTCCTAAG AATTTTAAAT | 1260 |

| | |
|--|------|
| TATGATTGCG TGAGTTTCTT ACCTTTTCA CACCCTAAAC CCGTTTATTT TCATAATTGG | 1320 |
| GATTTTATGG AGTTTTTGCT AACAGCCCT GAATACCCTA TTTTAAATGT AGAAAATGGC | 1380 |
| GTTCCAATCT TATCAAAAAG ACGTTTCATC TTG | 1413 |

(2) INFORMATION FOR SEQ ID NO:19531291_c1_4.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 369 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| GTGTTGAAAT TCTTTGAAGA TTCCAAACAG CTTAGCACGC CTATGGGAAA GAGCGCGGTG | 60 |
| GGGATTTTGA TTTTCCAAGA TATTGCAGCC ATTCCCATGC TTTTAATTTT GACGATTCTA | 120 |
| GGCAGTAAGG ATTCTCATGT CAATTGCTC ATTCTTAAAA CCCTTATTTT AGCGGGGATT | 180 |
| ATTTTAATTC TTTTATTATT GCCTGGAAAA AAAGGGGCTA ATCTCATCTT AGAGCAAGCG | 240 |
| AAAGACACGC GCTTGCCTGA AATCTTTATA GGCACGGATT TTAGTGATTG TTTGCAGCGC | 300 |
| GGCGGGGTTG AGCCATTTTT TTGGGTTTTT TATGTCTTTG GGGGCGTTCA TTGTGGGCAT | 360 |
| GGCGATTTT | 369 |

(2) INFORMATION FOR SEQ ID NO:19536458_f3_15.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 777 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|--|-----|
| ATGATTTTAG CCCTTTTGAT TTCTAAAGAA AAAACGCATT TAGAAGCGTT GTATTATTTG | 60 |
| AGCTATGGCG TGCTTTTAGG GGGCGTGGCT CAAATCTTAT TACACTTTTA TCCTTTAGTA | 120 |
| AAATTAGGCT TATGGGATTT ATTATTTAAA GGGTTGTTGG GTTTTAAGAC TAAAAATACA | 180 |
| AACAAAAAAG AATATCGTTT GAATAGGGCT AAAAAGGATC TAAAAGCGTT TTTCAAGCAA | 240 |
| TTCTTCCCCA GCGTCTTAGG CAATTCTAGC GCTCAGATCG CTTCTTTTTT AGACACCACA | 300 |
| ATCGCTTCTT TTCTGGCGAG CGGGAGCGTG TCTTATTTGT ATTACGCCAA TAGAGTCTTC | 360 |
| CAGCTCCCTT TAGCCTTATT CGCTATCGCT ATCTCCACAG CTCTTTTCCC TAGCATTGCG | 420 |
| ATCGCGCTTA AAAACAACCA GCAGGATTTA ATCTTACAAC GCTTGCAAAA GGCGTGGTTT | 480 |
| TTTTTGGTGG GGGTTTTGCT TCTTTGCAGC ATTGGGGGGA TAATGTTAAG CAAAGAAATC | 540 |
| ACCGAACTTT TATTTGAAAG GGGGCAATTT AGCCCTAAAG ACACCCTAAT CACTTCGCAA | 600 |
| GTCTTTTCGC TCTATCTTTT AGGCTTGCTC CCTTTTGGGC TAACCAAACCT CTTTTCTTTA | 660 |
| TGGCTTTATG CGAAATTAGA GCAAAAAAAA GCGGCTAAAA TCTCTTTAAT TTCGCTTTTT | 720 |
| TTAGGTTTAG CGGCTTCTTT GAGTTTAATG CCTTTGTTAG GGGTTTTGGG TTTGCGT | 777 |

(2) INFORMATION FOR SEQ ID NO:19541302_c1_3.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|--|-----|
| GTGCTAAAAT ACCCTACRRT GTTCATGTGT GCGGATGCGG TCATTATCAG TAAGGCGGAC | 60 |
| ATGATTGAAG TGTTTAATTT TAGGGTTTCT CAAGTCAAAG AAGACATGCA AAAATTAAAG | 120 |
| CCTGAAGCGC CCATTTTTTTT AATGAGCTCC AAAGACCCTA AAAGCTTGGA AGATTTTAAA | 180 |
| AATTTCTTTT TAGAAAAAAA GCGTGAAAAT TACCAATCCA CGCATTCGTT T | 231 |

(2) INFORMATION FOR SEQ ID NO:19556290_f3_1.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 540 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | |
|--|-----|
| ATGCTGCTTT GCGCGGAAG GAATGAGACT TTAAAAAAG CGGTGCCTAT TGGTGTGGGC | 60 |
| TTGATAGAGA GCGCGATCAA TTTAACGAGA ATGTGCCTTA AAAACCCTGA TACAGAAAGC | 120 |
| CTTATTTTTTA TAGGGAGCGC GGGGAGTTAT AGCCCAGAAA CGGAGATTTT GAGCGTGTTC | 180 |
| GAAAGCATTG AAGGCTATCA AATTGAAGAG AGTTTTAGCC ATTTAAACAG CTACACGCCT | 240 |
| TTGGATAATT TCATTCACAT AGAAACTAAA GAGCAGGCTC TTTTGTGAAAG GGTGCGTGTG | 300 |
| AATAGCAGTA ACTACATCCA CACCAGCGAA ATGTTTGCTA AAAAAATGGT TCAAAAGGGC | 360 |
| GTTTTATTAG AAAACATGGA GTTTTTTAGC GTCTTAAGCG TGGCTAAAAT TTTTCTTTA | 420 |
| AAGGCTAAAG GGATTTTTTTG CGTGAGCAAT CATGTAGGGC TTAACGCGCA TAAGGAATTT | 480 |
| AAAGAAAACC ACGCCAAAGT CAAACAGATT CTAGAAAACA TCATTGATAG TTTGATAGTT | 540 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 639 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: FLAGELLAR M-RING PROTEIN

| | |
|--|-----|
| GTGTATGAAG AAAGGATCAC TCTGGCTTCT CAAGGGATCC CTAAAACGAG TAAAGTGGGC | 60 |
| TTTGAAATCT TTGACACTAA AGACTTTGGG GCGACTGATT TTGATCAAAA CATCAAATC | 120 |
| ATTCGCGCCA TTGAGGGGGA ATTGTCGCGC ACGATTGAAA GTTTAAACCC CATTCTTAAA | 180 |
| GCCAATGTGC ATATTGCAAT CCCTAAAGAC AGCGTGTTTG TGGCTAAAGA AGTCCCTCCT | 240 |
| AGCGCTTCAG TGATGCTCAA GCTTAAGCCT GACATGAAGC TTTCACCCAC TCAAATTTTA | 300 |
| GGGATTAAAA ATTTAATCGC TGCAGCTGTG CCTAAACTCA CGATAGAAAA CGTGAAAATC | 360 |
| GTGAATGAAA ATGGCGAATC AATAGGCGAG GGCGATATAC TAGAAAACTC CAAAGAATTA | 420 |
| GCCTTAGAGC AATTGCGCTA CAAACAAAAT TTTGAAAACA TTTTAGAAAA TAAGATCGTC | 480 |
| AATATCTTAG CCCCTATTGT GGGGRGTAAA AACAAARGTRG TCRCAARRGT CAATRCGGAG | 540 |
| TTTRATTTCA RCCAAAAGAA AAGCACCAAA GAGACTTTTG ATCCCAATAA TGTCGGTAAG | 600 |
| GAGCGAGCAA AATTTAGAAG AAAAAAAGA AGGCGCTCC | 639 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 444 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| GTGATAARGA AAGGCTATAT AAGAGGAGAT CTTATGCGTA TAGTTAGAAA TTTATTTCTT | 60 |
| GTATCGTTTG TGGCGTATAG TAGTGCGTTC GCAGCGGATT TAGAAACCGG AACCAAAAAC | 120 |
| GACAAAAGA GCGGTAAAAA ATTTTACAAA CTCCATAAAA ACCATGGCTC AGAAACCGAG | 180 |
| ACTAAAACG ATAAAAGCT TTATGATTTT ACTAAAATA GCGGATTAGA AGGCGTGGAT | 240 |
| TTAGAAAAA GCCCTAACCT TAAAAGCCAT AAAAAAGCG ATAAAAGTT TTATAAACAA | 300 |
| CTCGCTAAAA ACAATATCGC TGAAGGGGTG AGCATGCCGA TTGTGAATTT CAATAAGCC | 360 |
| CTATCTTTTG GGCCTTATTT TGAAAGGACT AAAAGCAAAA AAACCCAATA CATGGACGGC | 420 |
| GGGTTGATGA TGCACATCCG TTTT | 444 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 843 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: spoIIIE gene product

| | |
|--|-----|
| GTGATGATCG ATCCCAAAT GGTGGAATTT AGCATTTATG CGGACATCCC TCATTTACTC | 60 |
| ACGCCCATTA TCACTGACCC TAAAAAAGCT ATCGGGGCTT TGCAAAGCGT GGCTAAAGAA | 120 |
| ATGGAGCGCC GATACTCTTT AATGAGCGAA TACAAGGTTA AAACCATTGA TTCTTATAAT | 180 |
| GAACAAGCCC AAAGTAACGR CGTTGAAGCG TTCCCCTATT TGATTGTGGT GATTGATGAA | 240 |
| TTAGCGGATT TGATGATGAC AGGGGGCAAA GAAGCGGAGT TTCCTATCGC TAGAATCGCT | 300 |
| CAAATGGGGC GAGCGAGCGG CTTGCACCTC ATTGTGGCGA CCCAACGCCC GAGCGTGGAT | 360 |
| GTCGTAACCG GCTTGATTAA AACCAACTTG CCTTCAAGGG TGAGTTTTAG GGTAGGCACT | 420 |
| AAGATTGATT CTAAAGTGAT TTTAGACACC GATGGGGCGC AAAGCTTACT AGGAAGGGGC | 480 |
| GATATGCTCT TTACCCCCC AGGAACAAAC GGGTTAGTGC GCTTGCATGC CCCCTTTGCC | 540 |
| ACTGAAGATG AAATCAAAAA AATCGTGGAT TTTATTAAAG CCCAAAAAGA GGTGGAATAC | 600 |
| GATAAAGATT TCTTGCTAGA AGAATCGCGC ATGCCTTTAG ACACCCCTAA CTATCAAGGC | 660 |
| GATGACATTC TAGAAAGGGC TAAAGCGGTG ATTTTAGAAA AAAAGATCAC TTCTACGAGC | 720 |
| TTTTTTACAAC GCCAATTAAA AATCGGCTAC AACCAAGCCG CCACCATTAC TGACGAATTA | 780 |
| GAAGCTCAAG GCTTTCTATC CCCAAGAAAC GCCAAAGGCA ACAGAGAGAT TTTGCAAAAT | 840 |
| TTT | 843 |

(2) INFORMATION FOR SEQ ID NO:197166_f2_7.nt:

96

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|--|-----|
| ATGAATTTTTT TTAAAATCCT TTTAATGGAG TTAAGAGCCA TTGTTTCTCA TAAGGGCGTT | 60 |
| TTATTGATCC TTATAGGCGC TCCTTTAATC TATGGCTTGT TATACCCTTT GCCTTATTTG | 120 |
| AAAGACATCG TAACGCAGCA AAAAATCGCC CTTGTAGATG AAGACAATTC CTCCTTTTCT | 180 |
| AGGCAATTAG CCTTCATGGT GCAAAGCTCC AACGAGTTAG AAATCGCTTT CTTTAGCCCC | 240 |
| TCTATGCTGG AAGCCAAAAA GCTTTTAAAA GAAGAAAAAA TTTATGGGAT CTTACACATT | 300 |
| CCCTCTCATT TTGAAGCCAA TATTTATAAA CAAAGTGCCT GTAACGATAG ATTTTATATGC | 360 |
| GAACGCCAAT TACTTTTTGA TTTATGGTGC GTTAGCGAAT GCGGTGGTGG GGAGCATCAA | 420 |
| CGCCTTAAAC GA | 432 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| GTGGGGGGCT TAGCCATGCT GGGCTTTTTT TATAATATTG AAAAAATTTT GCTCGCCACA | 60 |
| GCGACGGCTT TCTCGCAATG CGCGCCTAWT TATACGGTGC TCCTTTCCCC TTTGCTTTTG | 120 |
| AAAGAAAAGC TCAAAAGAAG CGCGTTAATT TCCGCATGCA TCGGGCTAGT GGGGGTGGTG | 180 |
| TTGATTTTCAG ATCCTAGCGT GGAAAATGTA GGACCTAGT | 219 |

(2) INFORMATION FOR SEQ ID NO:20032561_f1_1.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 933 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| GTGTGCTGGA CGGATTTGAT TCAAGGGCTT TTGATGATGA GCGCTTTAAT CGTGGTGCCG | 60 |
| ATTGTTATGA TAATCCATCT TGGAGGGATT GGAGAGGGGA TTAAAATCAT TAGAGAGATC | 120 |
| AAGCCTGAAA ACCTWTCTTT CTSGCAAGGC TCTAGCGTAG TCGCTATTAT TTCAAGCCTT | 180 |
| GCTTGGGGGT TAGGCTATTT TGGGCAACCC CATATTTTAG TCGCTTCAT GTCTATCCGC | 240 |
| TCCATTAGAG ATGTGCCTAA AGCGACCACT ATTGGGATTT CTTGGATGGT TATTTCTTTA | 300 |
| ATTGGGGCAT GCGTTATGGG GCTTTTAGGC GTTGCTTATG TACATAAATY TGACTTGAGT | 360 |
| TTAGAAGACC CTGAAAAGAT TTTCATTGTA ATGAGTCAAT TGCTCTTTAA CCCTTGATC | 420 |
| ACAGGCATTT TATTGAGCGC GATTTTAGCG GCGGTGATGA GCACGGCCAG TTCGCAACTG | 480 |
| CTTGTAAGCT CTTCTACCAT TGCTGAAGAT TTCTATGCGA CGATTTTCAA TAAAAACGCC | 540 |
| CCCCAAAAAT TAGTGATGAC GATTTCTAGG CTTTCGGTTT TAGGGGTGGC TTGCATCGCT | 600 |
| TTTTTCATTT CAACGGATAA AAACGCTAGC ATCCTCAGCA TCGTGAGTTA CGCATGGGCT | 660 |
| GGCTTTGGCG CGAGTTTGG CTCTGTGATT TTGTTTTAC TTTTTTGGTC AAGAATGACG | 720 |
| CGCATTGGCG CGATTGCTGG CATGCTCTCT GGGGCTAGCA CGGTGATTTT ATACGATAAA | 780 |
| TTTGGCAAAA GCTTTTTGGA TATTTATGAA ATCGTTCCGG GCTTTATTGT AGCGAGCGTA | 840 |
| GCTATTGTTG CGTTTAGTTT GTTTTCTAGC GTGCGATCAG GCACTAAAGA GGCCTTTGAA | 900 |
| ACCATGCTTA AAGAAATTGA GAGCTTAAAG CAT | 933 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| GTGGGGCTTT TTATCGTTTT GTTTTAAATT ATAATGAAGC ACCAAACCTC CCCCTATGCT | 60 |
| TTCACGCATA ATCAAGCCCT TGTCAC TCAA ACCCCCCCCT ATTTACGCA ACTCACTATC | 120 |
| CCTAAACCAA ATGACGCTTT AAGCGCGCAT GCGAGCTCTT TAATCAGCTT GCCTAACGAC | 180 |
| AATCTTTTGA GCGCTTATTT TAGCGGCACT AAAGAAGGGG CAAGGGATGT GAAAATCAGC | 240 |
| GCGAATCTTT TTGACAGCAA GACTAATCGC TGGAGCGAAG CCTTCATTCT TTTAACCAAA | 300 |
| GAAGAGCTTT CTCATCATTC GCATGAATAC ATCAAAAAA TTAGG | 345 |

(2) INFORMATION FOR SEQ ID NO:203192_c3_14.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 600 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: flagellar biosynthesis protein flhF

| | |
|---|-----|
| ATGCTTGTAG GGCCAACAGG CGTGGGGAAA ACGACGACTT TGGCTAAATT AGCCGCACGC | 60 |
| TATTCTAGAA TGCTGGCTAA AAAATACAAG GTGGGCATTA TCACTTTAGA CAATTATCGC | 120 |
| ATTGGGGCTT TGGAGCAATT GAGTTGGTAT GCTAATAAAA TGAAAATGAG TATAGAAGCG | 180 |
| GTGATTGACG CTAAGGATTT TGCTAAAGAA ATTGAAGCTT TGAATACTG CGATTTTATT | 240 |
| TTAGTGGATA CGACAGGGCA TTCGCAATAC GATAAGGAAA AAATTGCCGG TTTGAAAGAG | 300 |
| TTTATAGATG GGGGTATATA TATTGATGTA TCCTTAGTGC TTTCGGTTAC CACTAAGTAT | 360 |
| GAAGACATGA AAGATATTTA TGATTCTTTT GGGGTGTTAG GGATTGACAC TTTAATCTTT | 420 |
| ACGAAATTAG ATGAGAGTAG GGGGTAGGG AATTTGTTTT CTTTAGTGCA TGAAAGCCAA | 480 |
| AAGCCTATCA GTTATCTTTC TGTCGGCCAA GAAGTGCCTA TGGATTGAA AGTGGCTACT | 540 |
| AATGAGTATT TAGTGGATTG CATGCTAGAT GGCTTTAGTA ACCCTAATAA GGAACAAGCA | 600 |

(2) INFORMATION FOR SEQ ID NO:2035936_c2_13.nt:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 792 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: vacuolating cytotoxin Hpylori

| | |
|--|-----|
| GTGGGAGGAG CGAGCTTTAT TTCTGGGGGC AATGGCACGC TTTATGGCTT GAATGTGGGC | 60 |
| TATGACCGAT TGGTTAAAAG CGTGATCCTT GGGGGTTATG TGGCTTATGG CTATAGCGGT | 120 |
| TTTAACGGGA ACATCATGCA TTCTTTGGCT AATAATGTGG ATGTGGGGAT GTATGCGAGG | 180 |
| GCTTTTTTTGA AAAGAAACGA ATTCACTTTG AGCGCGAATG AACTTTATGG AGGCAATGCG | 240 |
| AGTCATATCA ATTCTTCTAA TTCCTTGCTC TCTGTGTTGA ACCAACGCTA CAACTACAAC | 300 |
| ACCTGGACAA CGAGCGTGAA TGGGAATTAC GGCTATGATT TCATGTTCAA ACAAAAAAGC | 360 |
| GTGGTGCTAA AACCTCAAGT GGGCTTGAGC TATCATTTCA TAGGCTTGAG CGGGATGAAA | 420 |
| GGTAAAATGC AAAATCCAGC TTACCAACAA TTCGTCATGC ATTCAAACCC TTCTAACGAA | 480 |
| TCGGTTTTTAA CGCTCAACAT GGGGTTAGAG AGCCGTAAAT ATTTTGGTAA AAATTCCTAT | 540 |
| TATTTTGTA CGGCGAGGTT GGGTAGGGAT CTTTGTATCA AAGCTAAAGG CGACAATGTG | 600 |
| GTGCGTTTTG TGGGTGAAAA CACTTTATTG TACCGCAAGG GGGAAATTTT TAACACTTTT | 660 |
| GCGAGCGTGA TCACAGGAGG CGAAATGCAT TTGTGGCGTT TGATGTATGT GAATGCGGGG | 720 |
| GTGGGGCTTA AAATGGGCTT GCAATACCAA GATCTTAATA TCACTGGGAA TGTGGGCATG | 780 |
| CGAGTGGCGT TT | 792 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1017 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|--|------|
| ATGGACGGCT ATGGGTTTAA AATGCAAGAC TTGGGCCAAA AACTCAAGT TATCCAACAC | 60 |
| ATCTTTGCCG GGGATGATGT GAGCGCTTTA GAAGTCAAAG AAAATGAATG CGTTAAAATC | 120 |
| RTGACTGGAG CGATGGTGCC AAAGGGAATA GAAACGATTG TTCCCATAGA ATGCATGCTA | 180 |
| GAGAGTCATA AAGATTTCGC CCTAGCTCCT AAAGATTTTA AAATTCACGC TAATATCCGT | 240 |
| CAAAAGGGCG AGAACGCTTC TTAAACAGC GTTTTAGTCC CTAAAAATAC CCGTTTGAAT | 300 |
| TATGGCCATA TCGCGCTCAT TGCCTCTCAA GGGTTCAAAG AAATCAAAGC GTTTAGAAAA | 360 |
| TTAAAAATCG CTCTCTTTAG TAGCGGCGAT GAATTAGTGC CTTTAGGGCA AAACGCCCTA | 420 |
| GAGTGCCAGG TTTATGATGT TAATTCAGTG GGTGTTTTTA ACATGCTTAA AACTACAAC | 480 |
| ACGCATTTTC TAGGGGTTTT AAAAGATGAT AAAAATTTAC AGCTTAAAAT ACTTGAATTG | 540 |
| CAAGGCTATG ATGTCATCCT TTCAAGTGCG GGGGTGAGCG TAGGGGATAA AGACTTTTTTT | 600 |
| AAAGACGCTT TGAAAGAAAG AAACGCCCTT TTTTATTACG AAAAAGTCAA TCTCAAACCT | 660 |
| GGAAAGCCGG TAACTTTAGC CCAACTCAAT CAAAGCATTA TTATAGGCTT ACCGGGTAAT | 720 |
| CCTTTAAGTT GCTTACTGGT TTTACGAGTT TTGATTCTAC CTTATTGGA GCGCTTATCC | 780 |
| TTAAATAAAG ATTTTAAATT AAAACCCTTT AAGGCTCAAA TCAATGCCCC TTAAAGCTT | 840 |
| AATAACAAAC GGACGCATTT AATCTTAGGC AACTATTCAA ACCACCAATT CATTCTTAC | 900 |
| AACAACCGCT ATGAATCAGG AGCGATTCAA GCCCTTGCGC AAGTGGATTC TATCRCTTTA | 960 |
| ATTGATGAAG GAGTGGGATT GGTTCAGGGC GAAATTGAAA TTTTAAGGTT TGAAAAT | 1017 |

(2) INFORMATION FOR SEQ ID NO:20415937_c2_15.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 438 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGCCATACG CCTTAAGAAA AAGATTTTTC AAACGCCTTT TATTGTTTTT TTTAATTGTT | 60 |
| TGTATGATAA ATTTGCATGC CAAAAGCTAT CTGTTTTCTC CTTTGCCCCC AGCGCACCAG | 120 |
| CAAATCATT AAGACAGAGCC TTGCTCTTTG GAGTGCTTGA AAGACTTGAT GCTGCAAAAT | 180 |
| CAAATCTTTT CTTTTGTATC CCAATACGAT GATAACAACC AAGATGAGAG CCTTAAAACT | 240 |
| TATTACAAGG ACATCTTAAA CAAACTCAAC CCCGTATTCA TCGCTTCTCA AACTCCAGCT | 300 |
| AAAGAAAGCT ATGAGCCTAA GATTGAATTA GCGATTTTAC TGCCTAAAAA GGTGGTGGGC | 360 |
| CGTTATGCGA TTTTAGTGAT GAACACCCTT TTAGCGTATT TTGAACACCA GAAACAACGA | 420 |
| TTTCAATATC CAAGTCTT | 438 |

(2) INFORMATION FOR SEQ ID NO:2042312_f2_10.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|--|-----|
| ATGCCTATTA ACCCTCTCTA TCTTTTCCCC AATCTTTTTA CCGCTAGCAG TATTTTTTTTA | 60 |
| GGCATGATGA GTATTTTTTA CGCTTCCAGT TACCAATTTG TCATGGCGTG TTGGTTAGTG | 120 |
| GTGGCGAGTC TTATTTTAGA TGGGCTTGAT GGGCGTGTCG CAAGGCTTAC CAAACACCAC | 180 |

(2) INFORMATION FOR SEQ ID NO:2082012_c1_2.nt:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 699 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGCTTTCAG CCTTGCTTTC TAAATGGGG ACTTACGCCT TATTACGCTT CTTGCTCCCG | 60 |
| CTTTTTCCTG AACTTTCAGA AATTTATTTA ACCCCCATAG CCATTGTGGC GCTGTGCATG | 120 |
| ATCATTTATG GAGGTTTTCT AGCCTACGCT CAAAAAGATT TAAAAACCCT CATCGCTTAT | 180 |
| AGCTCTTTCT CGCACATGGG AGTCGTGGTG CTTGGGGTTT TTTCTTTCAA TGTTGAAGGG | 240 |
| GTTTCAGGGG CGGTGTTTAT GATGTTTGCG CATGGCGTTA TCGTCATGGG ATTATTTTTA | 300 |
| CTCGCTGGTA TCTTGGAAGA ACGCGCCAGC AGTTTAGAAA TCGCTCGCTT TGGATCGATC | 360 |
| GCTAAAAGCG CTCCTGTTTT TGCAGCCTTT TTTATGATCG TTTTAATGGC GAATGTGGGC | 420 |
| ATGCCTTTAA GCATTGGTTT TGTGGGAGAG TTTTGGARCT TGTTAGGGTT TTTTGCCACT | 480 |
| TACCCTCTTT TGGCTATCAT TGCCGGGACA AGCCTCATTC TATCAGCGGT TTACATRCTC | 540 |
| ACTTCATATA AAGATGTGTT CTTTGGCAAC TTAAAAACCG GGAACAACCA AATCAGCGTG | 600 |
| TTTGAAGATT TAAACGCTCG TGAGGTAGGG GTTTTAAGCG TGATTTTAGC CTTTGATCTT | 660 |
| AATTTTAGGG ATTTATYCYA AAGCGCTTTT AAAACCGAT | 699 |

(2) INFORMATION FOR SEQ ID NO:20836042_f2_4.nt:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 96 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | |
|---|----|
| GTGGAATTGA TTAGCAATAA CCCTAACGCC AGCCAACAAT CTATCGTTAT TCCTTTGGAG | 60 |
| ACTTTTGCCT TGGCGCGAGC GTTAAAGGGA ATCTTT | 96 |

(2) INFORMATION FOR SEQ ID NO:20976500_c2_7.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGAAAATTT TTGGGACTGA TGGCGTGAGG GGTAAGCAG GGGTGAACT CACCCCCATG | 60 |
| TTTGTGATGC GTTTAGGCAT TGCTGCCGGA TTGTATTTTA AAAACATTC TCAAACGAAT | 120 |
| AAAATTCTAA TCGGTAAAGA CACCAGAAAG AGCGGCTATA TGGTAGAAAA CGCTTTAGTG | 180 |
| AGCGCTCTCA CTTCCATAGG CTATAATGTG ATCCAAATAG GGCCTATGCC TACCCCTGCG | 240 |
| ATCGCTTTTT TAACCGAAGA CATGCGCTGT GATGCGGGCA TTATGATAAG CGCGAGCCAC | 300 |
| AACCCTTTTG AAGACAATGG CATCAAGTTT TTCAATTCCT ATGGTTATAA ACTCAAAGAA | 360 |
| GAAGAAGAAA GAGCGATTGA AGAAATCTTT CATGATGAAG AATTACTGCA TTCTAGCTAT | 420 |
| AAAGTGGGCG AGAGCGTCGG TAGCGCTAAA AGGATAGACG ATGTGATAGG GCCGCTATAT | 480 |
| CGCGCATTTG AAGCACTCTY TYCCCAAACA TTT | 513 |

(2) INFORMATION FOR SEQ ID NO:2111040_f3_4.nt:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 99 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (xi) SEQUENCE DESCRIPTION:

| | |
|---|----|
| GTGCGAGCCG TGTTTGTCTT TGGTTTGAAA GCGGCGTTTT GTATAGGGAT TTTTTTCTAT | 60 |
| GGCGCTTATT ATTCCTAGA TGAGTTTTTA ATCAAGCTC | 99 |

(2) INFORMATION FOR SEQ ID NO:2149041_c2_10.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| GTGAGGAGCG GTAAAAGATT AGGCTATACC AATCAAGTGA TCACCGATAT TGTCAATATC | 60 |
| GGTATTGGGG GGTCAGATTT AGGCGCTTTA ATGGTTTGCA CCGCCCTAAA ACGCTACGGC | 120 |
| CACCCAAGAT TARRAATGCA TTTTGTGTCT AATGTGGAAT GGCACGCAGA TTTTAGACGT | 180 |
| TTTGGAAGAAA ATCAACCCGG CCAGCGCGCT | 210 |

(2) INFORMATION FOR SEQ ID NO:2150290_c1_12.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 390 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGAATCTTG TCTTTTTGTG GGCCGCTCTA GGAGGGGCTA TAGGGAGCTC GTTAAGGTAT | 60 |
| TTTGTGGGCA AAATGATGCC CAGTAAATTT TTAATGTTTG AAAGTTTCCC TTTAGGGACT | 120 |
| TTTAGCGTGA ATCTCATAGG GTGTTTTATC ATCGGCTTTA TGGGGCATTG GGCCGCTAAA | 180 |
| AAAGTTTTTG GTGATGATTT TGGGATTTTC TTTGTAACCG GAGTTTTAGG GGGTTTTACG | 240 |
| ACCTTTTCTT CTTATGGGTT AGACACTTTA AAACCTCTGC AAAAATCCCA ATACCTTGAA | 300 |
| GCCATTTCTT ATGTCTTAGG CACTAACCTT TTAGGGCTTA TTGGGGTAGC TATCGGTTGG | 360 |
| TTTTTTGGCTA AGAATTTTGT AGGCGTTAAT | 390 |

(2) INFORMATION FOR SEQ ID NO:21511555_c2_17.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 237 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGTTGGAAA AACTGATTGA AAGAGTGTTG TTTGCCACTC GTTGGTTGCT AGCCCCTTTA | 60 |
| TGCATTGCCA TGTCGTTAGT GTTGGTGGTT TTAGGCTATG TGTTCATGAA AGAGTTGTGG | 120 |
| CACATGCTCA GCCATTTARA CACCATTAGT GAAACGGATT TGGTTTTATC AGCCTTAGGT | 180 |
| TTAGTGGATT TGTTGGTTCA TGGCCGGGCT TGTTTTGATG GTGCTGCTCG CCAGTTA | 237 |

(2) INFORMATION FOR SEQ ID NO:21563752_c1_11.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGCACTATC AATTAACAAG TTTCAATATA ATACAAGATC TTTTATAAC TTGTCATGTG | 60 |
| TTAAGGATCA AAATGCGCGT GTTTGTTTGC TTTTATAGGGG TTTTGTATC TAACGGCTTG | 120 |
| GCTCGTTTTG GCTATGTGGT TTTAATCCCC CTACTCATTT TATCAGGGAG TTTAACCCCA | 180 |
| CACCAAAGCT TCCAAGTGGG TATTGCGGTG CTAATGGGCT ATGTTTTTGG GAGCTTTTTA | 240 |
| ATCCAATTTT TAAGCCCGTT AATGTCATTA SAAAGCATCG CTAAAATCAG TTTTAAATTA | 300 |
| ACACTT | 306 |

(2) INFORMATION FOR SEQ ID NO:21573938_f2_3.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

GTGGATATGA AAGACGCTGT AGGGACTTAT AAAC TAYTCA GGGCT

45

(2) INFORMATION FOR SEQ ID NO:21647676_f1_7.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3081 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: mature-parasite-infected erythrocyte surface anti

| | | | | | | |
|------------|------------|------------|------------|------------|------------|------|
| GTGTGTTT | ACCATCAGGT | TGGAGCAGGC | AAGACTTTGT | GCGCTATAGC | CAGCTGCATG | 60 |
| GAACAAAAAC | GCATGGGATT | AGTGAATAAA | ACGCTCATTG | CCGTGCCTAA | CCATTTAACC | 120 |
| AAGCAATGGG | GCGATGAATT | TTATAAGGCT | TACCCTAACG | CTAATGTGTT | AGTTGTTGAT | 180 |
| AGCAAGGACA | CCACTGAAAA | AGAAAGAGAA | CTTTTATTCA | ATCAAATCGC | TAACAACAAT | 240 |
| TATGACGCTG | TGGTTATCGC | GCACACCCAT | TTGGAATTAT | TGTCTAACCC | TAGAGGAATC | 300 |
| ATAGAAGAAT | TGAAAGAAGA | AGAGCTAGTG | AATGCTGAAA | AAAAC TTGA | AAGGCAAGAA | 360 |
| TTAGCTTATA | AAAATAACCC | TAGAGAAACT | AAAAAACCCA | ATGAAAGAGC | CTTTAAAAAC | 420 |
| AAGTTGGATA | AAATCCGTGC | TAAATACGAT | GCGATTTTAG | AAAAACAAGG | CTCTCATATT | 480 |
| GATATTAGTC | AAATGGGGAT | TGACAATTTG | ATTGTGGATG | AAGCCCACTT | ATTCAAAAAT | 540 |
| CTAGCCTTTG | AAACTTCTAT | GGAAAAAATT | GCAGGACTTG | GTAACCAACA | AGGCTCTAAT | 600 |
| CGCGCTAGAG | ATTTGTTTAT | TAAACGCGC | TACTTGCATC | AAAACGATAA | GAAAATCATG | 660 |
| TTTTTAACCG | GCACGCCTAT | AGCTAATTCC | TTGAGTGAAA | TGTATCACTT | GCAACGCTAT | 720 |
| TTAACCCCTG | ATGTGTTAAA | AGAAAGAGGG | TTAGAATTCT | TTGATGATTG | GGCTAAGACT | 780 |
| TATGGGGAAG | TGGTGAATGA | TTTTGAATTA | GACACTTCCG | CTCAAAGTTA | TAAAATGGTT | 840 |
| AATCGCTTTT | CTAAATTTAG | CGATGTGCAA | GGCTTAAGCA | CCATGTATAG | AGCTTTTGCG | 900 |
| GATATTGTCT | CTAATGATGA | TATTTTAAAG | CATAACCCCC | ACTTTGTGCC | TAAAGTGTAT | 960 |
| GGGGATAAAC | CTATCAATGT | GGTGGTGAAA | AGAAGCGAAG | AAGTGGCTCA | ATTCATTGGA | 1020 |
| GTGGCTTTAG | AAAATGGAAA | ATATAATGAA | GGCTCTATCA | TTGATAGGAT | GCAAAAATGC | 1080 |
| GAGGGCAAGA | AAAGCCAAAA | AGGGCAAGAC | AATATCCTTT | CTTGCACCAC | AGACGCTAGA | 1140 |
| AAAGTGGCTT | TGGATTACCG | CTTGATTGAC | CCTAACGCTA | AAGTAGAAAA | AGAATTTTCT | 1200 |
| AAAAGCTATG | CTATGGCAAA | AAATATCTAT | GAGAATTATT | TAGAAACTCA | TGCCACTAAA | 1260 |

| | | | | | | |
|------------|------------|------------|------------|------------|------------|------|
| GGCACACAAC | TTGGTTTCAT | AGGGCTATCC | ACACCCAAAA | CCCATAGCCA | AAAAGTCAGT | 1320 |
| TTAGAAGCGC | TAGATAACGC | TCACGAAACT | GAAAATAAAA | ATCCCCTAGA | TAAAGCTCAA | 1380 |
| GAACTTTTAG | AAAGCTTGTC | TAGTTATGAT | GAAAAGGGCA | ATCTTATCGC | TCCTAGCAAG | 1440 |
| AAAGAATTAG | AGAACGAGCT | CAAAGAGAAA | GAAGCTAAAA | GCGTCAATTT | AGATGAAGAG | 1500 |
| ATAGCTAAAG | GCTGTTCGTT | TGATGTTTAT | AGCGATGTTT | TAAGGCATTT | AGTCCAAATG | 1560 |
| GGTATCCCAC | AAAATGAAAT | CGCTTTCATC | CATGACGCTA | AAACCGAAGA | GCAAAAGCAG | 1620 |
| GATTTGTTTA | AAAAGCTCAA | TCGTGGCGGA | GTCAGGGTAT | TATTGGGCAG | TCCTGCTAAA | 1680 |
| ATGGGCGTAG | GCACTAATGT | GCAAGAAAGA | TTAGTCGCTA | TGCATGAATT | AGATTGCCCA | 1740 |
| TGGAGACCTG | ATGAATTGTT | GCAAATGGAA | GGGCGTGGGA | TAAGGCAAGG | CAATATTTTA | 1800 |
| CACCAAAATG | ATCCTGAAAA | CTTTAGAATG | AAAATCTATC | GTTACGCCAC | TGAAAAGACT | 1860 |
| TACGATAGCC | GTATGTGGCA | AATCATAGAA | ACTAAATCTA | AAGGCATAGA | GCAATTTAGA | 1920 |
| AACGCGCACA | AATTAGGCTT | GAATGAATTA | GAAGACTTTA | ATATGGGTAG | CTCTAATGCG | 1980 |
| AGCGAGATGA | AAGCAGAAGC | GACAGGCAAT | CCCTTGATTA | TTGAAGAAGT | CAAATTGAGA | 2040 |
| GCGGAGATTA | AAAGCGAAGA | ATCAAAATAC | AAAGCCTTCA | ATAAAGAGCA | TTACTTCAAT | 2100 |
| GAAGAAAGCT | TAAAAAACAA | CGCTTCTAAA | TTGGATTATC | TAAAACAGGA | ATTGAAAGAT | 2160 |
| TTAGAAACGC | TTCAAAGATC | CGTAATAATC | CCCCTCATA | CAGAGATCAA | GCTCTATGAT | 2220 |
| TTGAAAAATG | AAGAAAGTAA | GGATTATGAG | CTTATCAAAG | TTAAAGAGGT | AGAGCCTTTA | 2280 |
| AAAGAAAACG | CCTCTATGAG | TGAAGAATTA | ACGCACAAGA | AACTCAAAGA | ACAAAACAAG | 2340 |
| CAAATAGCCG | AACAAAATAA | AGAAAAGCTA | GACGCTATTA | AAAAGCAATT | TGCAAGCAAT | 2400 |
| TTGAACACCT | TGTTTGTGAA | TGAAGAAGAA | GATTATAAGC | TTTTAGAATA | CAAGGGCTTT | 2460 |
| GTGGTGAATG | CTTATAAAAC | TAAGTATCAA | GTGGAGTTTA | GTTTAAGCCC | TAAAGACAAT | 2520 |
| CCCAATATTG | CCTATAGCCC | TAGCAATATG | GTTTATAAAA | ACGATACTAT | CAACATGTTT | 2580 |
| AGCTCTTATA | ATTTCTGCGC | TGAGATCAAG | TTTGATGGGT | TTTTAAAAAG | GTTGGATAAC | 2640 |
| GCTATCACTA | AACTCCCTGA | AAAAATCAAG | GAATTAGAAA | ACTCCATTGA | AATCACGAAA | 2700 |
| AAAAATATCG | CTAAATACAC | AAGATTAGTG | GAGCAAAAAC | CTTCTTACCC | ACGACTAGAA | 2760 |
| TACCTGCAAG | CTTTAAAATG | GGATCATAAA | ACTCTAATAG | ATGATTTAGC | TAAAATGAGC | 2820 |
| AAAGACAGAA | ATTATAAGCC | TGCGTTCAAC | CCTAAATCTA | AAGAAGTCTT | AAAGAATTTG | 2880 |
| AACGCTGAAA | AAAGAGCGAG | TTTAGAGAAT | GAGAGGGAAG | AGCAAGGGGT | TAAGGGGAAC | 2940 |
| ACAAAGAGTC | ATGATGAAAT | AGAGCCAGCT | ACAGAACAAG | TGATTGAAAA | AGAAATAGAA | 3000 |
| AAAGGAGATG | AAATCGCTAA | TAATGTTGAT | TACTACGAGA | ACGAACAAGA | AGTGGAATTT | 3060 |

ACTAAATCAA TGGGTAGAAG A

3081

(2) INFORMATION FOR SEQ ID NO:21699087_f1_3.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGGCCGAAG AAGAAAAGAC CGAACTCCCT AGCGCGAAAA AAATCCAAAA AGCCAGAGAA | 60 |
| GAAGGCAATG TGCCTAAAAG CATGGAAGTG GTGGGGGTTT TTAGGGTTAT TGGCTGGGCT | 120 |
| AATGAGTATT TTTGTTTTTT TTATATGGTG GGTGGGATGG CTTTAGCGAG ATGTATCGCC | 180 |
| ATGTGT | 186 |

(2) INFORMATION FOR SEQ ID NO:21720017_c3_38.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 711 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|--|-----|
| ATGAAAACAC TCGTGAAAAA TACCATATAT TCTTTTTTGC TATTGTCTGT TTTGATGGCA | 60 |
| GAAGATATAA CAAGCGGCTT AAAGCAACTG GATAACACCT ACCAAGAGAC CAACCAACAA | 120 |
| GTGCTCAAAA ACCTAGATGA GATTTTTTCA ACCACTAGCC CTAGCGCTAA TAATAAAATA | 180 |
| GGTCAAGAAG ATGCTCTAAA CATCAAAAAA GCGGCCATTG CTTTGAGAGG AGATTTAGCG | 240 |
| TTATTGAAAG CCAATTTTGA AGCGAATGAG TTATTTTTTCA TCTCAGAAGA TGTGATTTTT | 300 |
| AAGACTTATA TGTCTAGCCC TGAACCTTTA TTAACCTATA TGAAAATCAA TCCCTTAGAC | 360 |
| CAAAAGACTG CTGAGCAACA ATGCGGAATA TCCGATAAAG TTTTAGTTCT TTATTGTGAG | 420 |
| GGGAAGCTGA AAATCGAGCA AGAAAAACAA AATATAAGAG AGCGTTTAGA AACTTCTCTA | 480 |
| AAGGCATATC AGAGCAACAT TGGAGGTACA GCTTCCTTAA TCACTGCTTC ACAGACGCTT | 540 |
| GTAGAAAGCC TAAAAAATAA AAATTTTCATC AAAGGAATCA AAAAGCTTAT GTTAGCTCAC | 600 |
| AACAAGGTCT TTTTAAATTA TTTAGAGGAG TTGGACGCAT TAGAAAGATC CCTAGAACAA | 660 |
| AGTAAGCGAC AATACCTACA AGAAAGGCAA TCAAGTAAGA TCATTGTTAA A | 711 |

(2) INFORMATION FOR SEQ ID NO:21742157_c3_4.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| GTGAGCGAAA AAGACAGGGC GTTTCTTTTA GCGAGCTTGT CTTGCGTGGA TTATGTTGTG | 60 |
| GTGTTTGGAG AAGACACGCC CATAAAATTG ATTCAAGCCC TAAAGCCTGA TATTTTAGTC | 120 |
| AAGGGAGCGG ACTACCTCAA TAAAGAAGTC ATAGGGAGCG AGTTGGCTAA AGAAACCCGT | 180 |
| TTGATAGAAT TTGAAGAAGG TTATTCCACA AGCGCTATCA TAGAAAAAAT TAAAGGACA | 240 |
| CATAATGAT | 249 |

(2) INFORMATION FOR SEQ ID NO:21976637_c3_5.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| GTGTATGACA AATCCTTGTG TAAGACCATG GCGCTAGCGT TGAAGGCTTT AGGCGTTAAA | 60 |
| AGGGCGATGG TGGTTAATGG AGGGGGGACA GGTGAAATCG TGTTGCATGA CATTACGCAT | 120 |
| GCGTGCGAAT TGAAAAATAA CGAAATTTTA GAGTATGATT TGAGCGCTAA AGATTTTGRT | 180 |
| TTRCCCCCCT CA | 192 |

(2) INFORMATION FOR SEQ ID NO:22265691_c3_14.nt:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 684 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: D-XYLOSE TRANSPORT ATP-BINDING PROTEIN

| | |
|---|-----|
| ATGCTAGTAG AAATAGAGAA TTTGACTAAA ACTTATGGGA GTTTAAAAGC GCTAGACAAT | 60 |
| ATCAGTTTGA AACTACCCAA ACAGCAATTT ATAGGGCTTT TAGGGCCTAA TGGGGCGGGT | 120 |
| AAAACCACTC TGTTAAAAAT TTTAGCCGGA TTGAATTTGA ACTATCAAGG GGAAGTGAAA | 180 |
| ATTTTAAACC AAAAGATTGG TATAGAGACT AAAAAAGCG TGGCGTTTTT AAGCGATGGC | 240 |
| GATTTTTTTAG ATCCTAAATT AACGCCTTTA AAAGCGATCG CTTTTTATAA GGATTTTTTTT | 300 |
| AGCGATTTTG ATGAATCAAA AGCCCTAAAT TTGTTAAAAC GCTTCAGCGT GCCTTTAAAA | 360 |
| AGAGAGTTCA AAGCCCTTTC AAAAGGCATG AGGGAAAAAT TGCAGCTGAT TTTAACCTA | 420 |
| TCACGAAACG CTTCTTTGTA TCTTTTTGAT GAGCCGGTGG CTGGGATTGA CCCTATTGCA | 480 |
| AGAGAAGAGA TTTTGTAGTT AATCGCTAAG GAGTTTAGCC AAAACGCAAG CTTGCTAGTC | 540 |
| TCTACGCATT TGGTGGTGGA TGTGGAAAAG TATTTAGACA GCGCGATTTT TTAAAAGAA | 600 |
| GCTAAAGTGG TGGCTTTTGG GGATGTGGGG GAATTAAAAA AAGGGTATAG CAGTTTGGAG | 660 |
| GCAGCGTATA AAGAAAGGTT GAAA | 684 |

(2) INFORMATION FOR SEQ ID NO:22303918_c1_9.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 819 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGAACAAGC TTTT TTTTAGC TTTTATTGTT GGGGGAATGC TTTTAAGTGC TGATGCTTTA | 60 |
| AACGATAAGA TTGAGAATTT AATGGGGGAG CGATCCTACC ACATGAACAA GCTTTTTTTTA | 120 |
| GAGCGTTTGT TTAAAAATCG TAAGGATTTC TATGAAATGG GGC GTTTGGA TTCCTTAAAA | 180 |
| CTACTCAACA CTCTCAAAGA AAACGGGCTT TTATCGTTTA ATTTTGACAA ACCAAGCGTG | 240 |
| TTAAAAATCA CTTTCAAGGC TTCAAGTAAT CCCCTAGCGT TTGCCAAAAG CATCAACAAT | 300 |
| TCTTTGAATA TGATGGGGTA TTCGTATGTT TTGCCTATTA GAATGCAAAG CTCTTCAGGC | 360 |
| GAGAATGTTT TTTCATACGA GCTTAAAACG GAATACGTTT TAGACCCTAA CATTTTGATA | 420 |
| GAGACGATGA AAAGGCATGG TTTTGATTTT ATGGATATTA GACGGGTGTC TTAAAGGAG | 480 |
| TGGGAATACG ACTTTGCCTT ACAAAGATC AAGCTCCCTA ACGCGAGAGC CTTAGTTTTG | 540 |
| AGTAGCGATC CTGTGGAGTT TAAGGAAGCG AGCGGGAAAT ATTGGCTGAG CGTGAATCAA | 600 |
| AACGCGTATT TAAAAATAAG CTCCAATAAC CCTTTGTGGC AACCCAAAAT CATTTTTTAT | 660 |
| GATGAAAAC TAAAGATCAT TCAAATCATT GCTAAAGAAA ACAGACAACA AGAAATCGCT | 720 |
| CTTAACTTGC TTGATGGCGT GCGTTTTATC CATATCACTG ACGCAAAAAA CCCTATCATT | 780 |
| TTAAAAAATG GGATTAGCGT GGTTTTTGAT GCGATGCCT | 819 |

(2) INFORMATION FOR SEQ ID NO:22370182_c1_12.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: *H.influenzae* lic-1 operon licA-licD genes

GTGTCTCGCC CGTTCAAAC GATCAAAAAA CCCCACAAC CCCCT

45

(2) INFORMATION FOR SEQ ID NO:22441050_c3_5.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 201 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|--|-----|
| ATGATCGCTG TATTACCGCC CTTGTTTTCT ATGGGGAGCT TTGATGAGTG GATTTATAGG | 60 |
| GGGCTTGTGG CTTTAATGGT GAGCTGTCCT TGC GCGTTAG TGATTTCTGT GCCTTTAGGG | 120 |
| TATTTTGGAG GCGTGGGAGC GCGAGCCGA AAGGGGATTT TAATGAAAGG AGTGCATGTT | 180 |
| TTAGAGGGTG CTTACCCAAA C | 201 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 969 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|--|-----|
| GTGCAACACT TCAATTCCT CTATAAAGAT TCTTTATTTT CTATCGCTTT ATTCACTTTC | 60 |
| ATTATCGCTC TTGTGATTTT ATTAGAACAG GCTAGAGCGT ATTTACCCCG AAAGAGAAAC | 120 |
| AAAAAATTTT TGCAAAAATT CGCCCAAAT CAAAACGCCT ATGCGAGCAG CGAGAATTTA | 180 |
| GACGAGCTTT TAAAGCATGC TAAAATTTCC AGTTTGATGT TTTTAGCTAG GGCGTATTCT | 240 |
| AAAGCGGATG TGGAAATGAG CATTGAAATC TTAAAAGGGC TTTTGAATCG CCCCTTAAAA | 300 |
| GATGAAGAAA AAATCGCTGT TTTAGATTTA TTGGCTAAAA ATTATTTTAG CGTGGGGTAT | 360 |
| TTGCAGAAAA CAAAAGACAC CGTGAAAGAA ATTTTGCGCT TTTCCCCAAG GAATGTGGAA | 420 |
| GCGTTGTTGA AGCTTTTGCA TGC GTATGAA TTAGAAAAAG ATTATTCAAA GGCTTTAGAA | 480 |
| ACTTTGGAAT GTTTGAAGA ATTAGAGGTG CCTAAAATTG AAACGATTAA AAATTACCTC | 540 |
| TATTTAATGC ATTTAATAGA GAATAAGGAA GATGCGGCTA AAATCTTGCA TGTTTCAAAA | 600 |
| GCGTCGTTAG ATTTGAAAAA AATCGCTCTG AATCACTTAA AATCGCATGA TGAAAATCTT | 660 |
| TTTTGGCAAG AAATTGATAC AACCGAACGG CTAGAAAATG TGATCGATCT TTTATGGGAT | 720 |
| ATGAATATCC CTGCTTTTAT TTTAGAAAAA CATGCCCTTT TGCAGGACAT CGCGCGATCT | 780 |
| CAAGGGTTGC TTTTGGATCA CAAACCTTGC CAAATTTTGT AATTAGAGGT TTTACGCGCT | 840 |
| CTATTGCATA GCCCTATAAA AGCGAGTCTG ACTTTTGAAT ACCGCTGCAA GCATTGCAAA | 900 |
| CAAATCTTTC CTTTTGAAAG CCATAGGTGT CCTGTGTGTT ACCAGTTAGC GTTTATGGAT | 960 |
| ATGGTGGCT | 969 |

(2) INFORMATION FOR SEQ ID NO:22453166_c2_2.nt:

124

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGGAACACC TTACAAGGGG AATTAAGCAC

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | |
|--|-----|
| GTGGTTATCT TAGGCTCRCA TGGCAAGGAA GAGTATTACG CTAGCAAGAT TGCAGCCCCC | 60 |
| ATTTTTTAAAG AAATCACCGA AATTTTAGTG CGTTACAATT ACCTATCGCC CTCTATTGCG | 120 |
| ATTCAAAACG CTTTGGA AAAA AAACCGCTTA AAA | 153 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 237 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGAAAAAGG TTATTGTGGC TTTAGGCGTT TTGGCGTTCG CAAATGTTTT AATGGCAACC | 60 |
| GATGTTAAGG CTCTTGTAAG AGGTTGTGCC GCTTGCCATG GGGTTAAGTT TGAAAAGAAA | 120 |
| GCTTTAGGTA AAAGCAAAAT CGTTAACATG ATGAGCGAAA AAGAGATTGA AGAGGATCTT | 180 |
| ATGGCTTTTA AAAGCGGTGC CAACAAGAAT CCTGTCATGA CCCGCAAGCT AAAAAAT | 237 |

(2) INFORMATION FOR SEQ ID NO:22667967_f1_2.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: influenzae type B lipooligosaccharide

| | |
|---|-----|
| ATGGGGATTG CAACCAGTCT CATCAGTGAG GTTTCTAAGT TTTATTACGC TTAAAAATAC | 60 |
| CATGCGAAAT TTATGAGCTT GGGGGAGCTT GGGTGCTATG CGAGCCATTA TTCGTTGTGG | 120 |
| CAAAAATGCA TAGAGCTCAA TGAAGCGATC TGTATTTTAG AAGACGATAT AACCTTGAAA | 180 |
| GAGGATTTTA AAGAGGGCTT GGATTTTTTA GAAAAACACA TCCAAGAGTT AGGCTATGCG | 240 |
| CGTTTGATGC ATTTATTGTA TGATGCCAGC GTGAAAAGTG AGCCT | 285 |

(2) INFORMATION FOR SEQ ID NO:22687687_c2_2.nt:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 462 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (xi) SEQUENCE DESCRIPTION:

| | |
|--|-----|
| ATGCACCTTA AAAGTGGGGC TGTTTTTATC TCTGATGCGC ATTTTTTGCC CAAAAGCCCT | 60 |
| CATTTAATCC ATACGCTTAA AGAACTTTTA AGCGCCAAAC CCCCACAAGT CTTTTTCATG | 120 |
| GGCGATATTT TCCATGTTCT TGTGGGCTAT TTACCCCTAG ATAAAGAGCA GCAAAAAATC | 180 |
| ATTGATTTAA TCCATGCGTT GAGCGAAATT TCACAAGTCT TTTACTTTGA AGGCAACCAT | 240 |
| GATTTTTTCCA TGCGTTTTGT ATTCAATTCC AAAGTAATGG TTTTGTAGCG CCAAACCAA | 300 |
| CCCGCATTAT TCCAGTATGA TAACAAACGC TTTTGTAGTAG CCCATGGGGA TTTATTCATC | 360 |
| ACTAAAGCGT ATGAATTTTA CATCACGCAG CTCACTTCCA CTTGGGCTAG ATTTTTTTTA | 420 |
| ACTTTTTTTAA ATTTATTAAG TTTTAAACC TTATACCCTT TT | 462 |

(2) INFORMATION FOR SEQ ID NO:22704567_c2_27.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 939 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | | | | | | |
|------------|------------|------------|------------|------------|-------------|-----|
| GTGCAACCGA | TGAAATCTAA | AAAACTTTAT | TTAGCTTTAA | TCATAGGGGT | TTTATTAGCG | 60 |
| TTTTTAACCC | TATCTTCATG | GCTAGGTAAT | AGCGGTTTAG | TGGGGCGTTT | TGGGGTGTGG | 120 |
| TTTGCCGCAA | TCAATAAAAA | ATATTTTGGG | TATCTTTCAT | TGATTAATTT | ACCCTATTTG | 180 |
| GCGTGGGTTT | TATTCCTTTT | ATACAGGGCT | AAAAACCCTT | TTACAGAAAT | CGTTTTAGAA | 240 |
| AAAACTTTAG | GGCATCTATT | AGGCATTTTA | TCTTTACTCT | TTTTGCAATC | TAGCCTGTTG | 300 |
| AATCAAGGGG | AAATCGGCAA | CAGCGCGCGT | TTGTTTTTAC | ACCCTTTTAT | AGGGGACTTT | 360 |
| GGGCTTTATG | TGCTGATAAT | GCTTATGGTA | GTTATCTCTT | ATTTAATTTT | ATTCAAACCTG | 420 |
| CCCCCTAAAA | GCGTTTTTTT | CCCTTATATG | AACAAAACAC | AAAGCCTTTT | AAAAGAGATT | 480 |
| TACAAACAAT | GCTTGCAGGC | CTTTAGCCCT | AATTTTAGCC | TGAAAAAAGA | GGGTTTTGAA | 540 |
| AACACCCCAT | CAGATTCTCA | AAAAAAAGAA | ACCAACAACG | ACAAAGAAAA | AGAAAACCTC | 600 |
| AAAGAAAACC | CTATTGATGA | AAACCACAAC | ACCCCTAACG | AAGAATCGTT | TTTAGCGATC | 660 |
| CCTACCCCT | ATAACACGAC | CTTAAATAAT | TCAGAGCCGC | AAGAAGGCTT | AGTCCAAATT | 720 |
| TCCCCACACC | CCCCTACCCA | TTACACCATT | TACCCTAAAA | GAAACCGATT | TGATGATTTG | 780 |
| ACTAACCCCA | CTTTAAAAGA | ACCTAAGCAA | GAAACCAAAG | AAAGAGAACC | CACGCTAAAA | 840 |
| AAAGAAACGC | CCACCACACT | CAAACCTATC | ATGCCCATAT | CCGCATCCAC | ACAGAAAATC | 900 |
| ATGACAAAAC | RGAAAACCAC | AAAACCCCTA | ACCACCCCA | | | 939 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 957 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|--|-----|
| GTGATGTTAA GTAGAGACAT TGTCCAATAT TCCAAGATCC GCACCGAGTT ATACGCCTAC | 60 |
| CTCACTTATT TGTTTTTCGCA CAATATCCGC AACCACCTTC CTGAAATCAC TTTGGATTAT | 120 |
| TTAAACAGGC AAATCAGTAA GATGCAAGCT GAAATCAAAA TGGCAAAAAG TTTTTTTGTT | 180 |
| TTAGACGCTA AGGGCATGCT CATGCTTAAG CCAAGCCAAT TTAAAGAGCA GGGGCATAAG | 240 |
| GAAGGGCTAT TAGAGCATGA TTTAACAGAA GGGATTGAAT TAGAATCGCA TGTCAGTTTT | 300 |
| AGCGATAAGT ATTATTTTTTA TCAAGCCGTG AATGAAAAGC GTTGCATTTT AACCGACCCC | 360 |
| TATCCTTCTA AAAAAGGGAA CCATTTGGTA GTGAGCGCGT CTTACCCGGT GTATGATCAA | 420 |
| AATAACGATC TAGCGTTTGT GGTGTGCTTG CAAATCCCTT TGAGGGTGGC GATTGAAATC | 480 |
| AGCTCGCCTT CAAAGTATTT TAAAACTTTT AGCGAAGGGA GCATGGTCAT GTATTTTATG | 540 |
| ATTTCTATCA TGCTCACTTT AGTGTCGCTG CTTTTATTCTG TGAAATGCAT TTCTAGCTTT | 600 |
| TGGACAGCGA TCGTGCATTT TAGCAGTTTT GACATTAAAG AAGTGTTCCA CCCCATTGTG | 660 |
| CTTTTAACCC TAGCTTTAGC CACCTTTGAT TTGGTCAAGG CGATTTTTGA AGAAGAAGTG | 720 |
| TTGGGTAAAA ATAGCGGGGA CAACCACCAT GCGATCCACC GCACCATGAT CAGGTTTTTA | 780 |
| GGCTCTATCA TTATCGCATT AGCCATTGAA GCGTTAATGC TCGTGTTTAA ATTCAGCGTG | 840 |
| AGCGAGCCGG ATAAAATCAC TTATGCGGTG TATTTGGCTA TCGGCGTGGC GGTGCTTTTG | 900 |
| ATCAGTTTGG CGATTTATGT TAAATTCGCT TATAGCGTGT TGCCCAAACG AGAACGC | 957 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|--|-----|
| ATGGTTATAC ATGAAAAAAT CAAAAGCCGC TTTTCTAGGA ATTGGTCTTT AAGGAATAGG | 60 |
| GGCAGGCATT TTGCATCTTC AAGCGTGTAT TTTTCTCAC TTCTTGTCAT TACAGCGGTT | 120 |
| AATAGAAGTA GTGCAGTTGC TTGGTTATTG ATGCCTGAAC ATTTGATTGG GTGGTTTTTG | 180 |
| ATTTCTTTTA GTGGGGAATT TGTAGCAGAC ATGGCGTTTG GCAAAAAAAG TAAGATTTTT | 240 |
| AAAACCCGCT TTGGAATTTT TATTGTGAGC GGC GTTTCAC TATTGCTTGG CGCTTACCAG | 300 |
| CGCTTTTATT TTTTGTATGG TTTGGCTTTA TTAATTGGTG GGCTGTCTTT TTTA | 354 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|--|-----|
| ATGTTTAAAA GCAGATTAAA TTCATGGATT TTATTAGGGA TTTTAGGGGT TTTAGTGGTG | 60 |
| GTTTTTTTGGG ATGTCATAAA ATACAAAATA GAAGATTTCG AACATGATCA TTATCTATCA | 120 |
| CAAGTGAAAG AAAGGGAAGA ATATTATAAA AACCACATAG AAGAAGCTTT GAAAAAGGAT | 180 |
| AGCGAATGCT TTGAAAAAGG AGGCGATAAA GTGGATTGCT CGGCTGCTAT GAGAATAGCT | 240 |
| GCTGGTGAAA GAAATAGAAG AATGTTAGAG ATTAAA | 276 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 414 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGGTATTTT GGGGCGCTGT TTTCTTTTTA TGGGATCGAA CGGCATGGAA GCGCTTAATG | 60 |
| GTGTTTTTGA ACAGCTTGAW TTYCATGCTT GCGGCCTTGA GTTTGGGGTC GTTTTTAGGG | 120 |
| GCATGGATCA AAAATGAAGC CCACACCACT CAAATCGTTT TGATTTCTTC TTTGCCCTTG | 180 |
| ATTTTTATGA TGGGTTTTGT GTGGCCTTTT GAATCCTTGC CCTCTTATTT GCAAGTCTTC | 240 |
| GTTCAAATAG TGCCTGCTTA TCATGGGATC AGTTTGCTCG GGCGATTGAA TCAAATGCAT | 300 |
| GCGGAATTTA TAGATGTTTC TATCCATTTT TACGCGCTTA TTGCGATTTT TATCGTGAGT | 360 |
| TTTATAGGGT GCGTGTTCAA ACTCAGCTCT TTAAAGAAAG CTTGTGAAAA CGCT | 414 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 762 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|--|-----|
| ATGCATGAGC AAGGTTCTAT AAGCTTTTSTA GGCGRACAGG GAGCTAAAAG ATTATTATAC | 60 |
| ATACTCTACA AGCTCGCATT TAATGCTAAG TCTAATAAGA TTGCCCTAGA TAGACATTAC | 120 |
| GCCAAAATGT TTTTGCAAGT TGTAGCAAGA ACTCTAATAA AGAATGTCAA TATATTAGAA | 180 |
| GAGCAAGGTT TTATTGAAGT CATTAAAGGA AAACAAAGAT ACTTGTATGT GTATCTTAAA | 240 |
| GATTACAGAG AATTAGAATG CTTAGTGAAG AGCAAGATGG CTAAGTATGT GATGTATTTA | 300 |
| AGACAATTCT TTGATTATTT GGATAGAAAA AGGCGTTATG GCTTTGATTT TACGCTTAAA | 360 |
| AACCTAGCCT TTGCTAAGAC CAAAGAAAGC TTACCCAGAC ATTTAAACGA TAAAGACTTA | 420 |
| AAGAGTTTTT TAAAAACACT CTTAGACTAT AAGCCAGCTA CAAGCTTTGA AAAACGCAAT | 480 |
| AAGTGTATTC TACTTATTGT AATACTTGGG GGACTTAGAA AATGCGAAGT GTTAAACATA | 540 |
| GAATTAAAAC ACATTCAAGT AGAAGAGCAA AACTACTCTA TTTTAATTCA AGGTAAAGGT | 600 |
| AGAAAAGAGA GAAAAGCTTA TATTA AAAAG AGTTTGTAG AACCAAGCTT GAATGCTTGG | 660 |
| ATTAGTGATG ATTACAGACT AAAATATTTT AATGGAGCAT ATCTCTTTAA AAAGGATAAG | 720 |
| CAAAAATCAC AAAATTCTTT AACGCTTTAT AATTTATCCC CT | 762 |

(2) INFORMATION FOR SEQ ID NO:23441078_c3_9.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 555 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| GTGGTCTTTA AAATTTTAAG TTTATGGTTA GGGGTGTTTT GTTTCCTTAG GGCTACGCAT | 60 |
| TTATACTTAG GCGAAGAACC CAAATATAAA GACAATTTCA CGCATTTTGA ATACGCTAAC | 120 |
| CCTAACGCTA GAAAAGGCGG TGTTTTGAGA AATGACGCTA TAGGGACTTT TGATAGCCTT | 180 |
| AACCCTTTTG CGCTTAAAGG CACTAAAGCC GAAGGCTTGG ATCTCATTTA TGACACTTTA | 240 |
| ATGGTGCAAA GCTTAGACGA ACCTTTTGCA GAATACCCCT TAATCGCTAA AGACGCCGAA | 300 |
| GTGGCTAAGG ATAACAGCTA TGTGATTTTT ACCCTAGATA AAAGAGCGAG ATTCAGCAAT | 360 |
| AACGCTCCCA TTTTAGCGAG CGATGTGAAG TTTAGCTTTG ATACGATAAT GAAATTAGGA | 420 |
| TCGCCCCTTT ATAGGCAGTA TTACCAAGAT GTTAAAAAGG CGGTTATCTT AGACAAGCAC | 480 |
| CATGTTAAAT TCATTTYCAA AACCCTGAA AATAAAGAAT TGCCCCTCAT TTTAGGGCAG | 540 |
| TTGCAGATCT TTTCC | 555 |

(2) INFORMATION FOR SEQ ID NO:23442642_c3_16.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| GTGGCCATGA TAGATTGCGC GATTATTGGA GGTGGTCCTG CAGGTTTGAG TGCGGGGCTT | 60 |
| TATGCCACTA GAGGCGGTGT TAAAAACGCC GTTTTATTTG AAAAAGGAAT GCCTGGGGGG | 120 |
| CAAATCACTG GCAGTAGTGA GATTGAAAAT TATCCGGGCG TTAAGGAAGT GGTGAGCGGA | 180 |
| TTGGATTTCA TGCAACCA | 198 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 546 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| GTGGGGAAAA GCTTGAGATA CAGCTTGAAT TTAGATCTCA ATCAAAAAGC CGATTTGTTT | 60 |
| TTCACCGAAT TAGAGCCAAC AGGTCTCACG CTCTCCCCCA TCATGAAACG CTTTACTATC | 120 |
| AAAGGCGATT TTGATTCAGG GCTAAAATCC TATGACATGA GCTACATGTA TGCGAGCCTT | 180 |
| CAAGCTATAA GCGCGATCAG GAGATTACCC TTAGGGCTTT ATGATGGGGT GCATGTCTAT | 240 |
| TCTAAAACGC CCATGAAGGA TATTGAAAAA TTACGCAACG CTTTAAAAAC AATCAACCAC | 300 |
| CATGGCATAG GCATTGAAGG GTGGTGGCAA CAAAACGGGA ATTTTTTCTC GGCGATGGAA | 360 |
| TTGGAAAAAA GAGCGTTATT CATTGTGCTC ATGCTCATTA TTTTAATGGC GTCTTTGAAT | 420 |
| ATCATCAGCT CGCTTTTAAT GGTGGTGATG AACAGGCGTA AAGAAATCGC CCTACTCTTT | 480 |
| AGCATGGGGA GCAGTCAAAA AGAAATCCAA AAAACCTTTT TTTATTTGGG TAATATCATT | 540 |
| AGTTTA | 546 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 741 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|--|-----|
| ATGAAAAAAA CTTTTTTTGAT CGCTTTAGCG CTTACGGCTT CTCTTATAGG CGCTGAAAAC | 60 |
| ACCAAATGGG ATTATAAAAA TAAAGAAAAT GGCCCGCACC GCTGGGACAA ATTGCACAAA | 120 |
| GATTTTGAAG TGTGCAAAAG CGGTAAAAGC CAATCGCCCA TCAACATTGA GCATTACTAC | 180 |
| CACACGCAAG ATAAAGCCGA TTTGCAATTC AAATACGCCG CTTCTAAACC TAAAGCGGTC | 240 |
| TTTTTCACCC ACCATACTTT AAAGGCTTCG TTTGAGCCGA CTAACCACAT CAATTATAGA | 300 |
| GGGCATGACT ATGTGTTGGA TAATGTGCAT TTCCACGCC CTATGGAGTT TTTAATCAAT | 360 |
| AATAAAACCA GGCCTTTGAG CGCGCATTTT GTGCATAAAG ACGCTAAAGG GCGTTTGTTG | 420 |
| GTGTTAGCGA TTGGTTTTGA AGAAGGGAAA GAAAACCCCA ACCTTGATCC TATTTTAGAA | 480 |
| GGCATTCAAA AGAAACAAAA TCTTAAAGAG GTGGCTTTAG ACGCTTTCTT GCCTAAAAGC | 540 |
| ATCAATTACT ACCATTTTAA CGGCTCTCTC ACCGCTCCTC CTTGCACAGA GGGGGTGGCA | 600 |
| TGGTTTGTCA TAGAAGAACC TTTGGAAGTT TCTGCCAAAC AATTGGCTGA AATCAAAAAA | 660 |
| CGCATGAAAA ATTCGCCCAA CCAACGCCCC GTCCAGCCTG ACTACAACAC CGTGATCATT | 720 |
| AAAAGCTCGG CTGAGACCCG C | 741 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1266 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|--|------|
| ATGAAAATTT CTTTATTGGG GCATGGAAAA ACCACTCTAG CCCTAGGGCG TTTTTTTTAAA | 60 |
| AAAAACCATA ATGAAGTCAA ATTTTTTTGAT GATAAATTCC CTGCATTTTT TAAGGATAGC | 120 |
| GAGGGTTTTTC TTTGCTACCC TAGTAAGGAT TTAAACCCTA ATGATTCCCA ACTAGAAATC | 180 |
| GTCAGCCCTG GCATTAGTTT CACGCACCCT TTAGTCATGA AAGCCAAGCA TTTAATGAGC | 240 |
| GAATACGATT ATATTGATAG TTTGTTTGAT CATTCTTTCA CGCCTACGAT GATAAGTATT | 300 |
| AGCGGCACTA ACGGGAAAAC CACCACGACC GAAATGCTCA CCACACTTTT AGAAGATTTT | 360 |
| AAGGCTGTGA GTGGGGGGAA TATCGGCACG CCCTTGATTG AATTGTTTGA AAAACGATCG | 420 |
| CCCTTGTTGGG TGCTAGAAAC AAGCTCCTTT TCTTTGCATT AACTAATAA GGCTTACCCT | 480 |
| TTAATCTACT TGCTCATCAA TGTGGAAGCC GATCATTTGA CTTGGCATTG CAATTTTGAA | 540 |
| AATTATTTGA ACGCTAAACT CAAGGTTTTA ACATTGATGC CTAAAACTTC GCTCGCTATC | 600 |
| CTCCCTTTAA AATTCAAAGA ACACCCTATT GTTCAAAACT CGCAAGCGCA AAAAATCTTT | 660 |
| TTTGACAAAA GCGAAGAGGT TTTAGAGTGT TTAAAAATCC CTTCTAACGC CCTTTTTTTT | 720 |
| AAGGGAGCGT TTTTATTAGA CGCGGCTTTA GCCCTTTTAG TTTATGAGCA ATTTTTAAAA | 780 |
| ATAAAGAATT TAAAATGGCA AGATTATAGA GAAAACGCCC TTAAAAGACT GAACGCTTTT | 840 |
| AAAATCGGCT CGCATAAAAT GGAAGAATTT AGGGATAAAC AAGGGCGTTT GTGGGTAGAT | 900 |
| GACAGCAAAG CCACGAATAT TGATGCCACC TTACAAGCCC TAAAAACCTT TAAAAACCAA | 960 |
| AAAATCCATT TGATTTTAGG GGGCGATATT AAAGGGGTCA ATTTAACCCC CCTTTTGTAA | 1020 |
| GAGTTTAAAA ACTATAAAAT AAGCCTTTAT GCCATAGGAT CAAGCGCTTC TATCATACAA | 1080 |
| GCCTTAGCGT TAGAATTTAA TGTTTCTTGT CAGGTTTGTT TGAAGTTAGA AAAAGCGGTT | 1140 |
| CAAGAAATTA AAAGCGTTTT ATTACAAAAT GAAGTCGCTT TGCTTTCACC TAGCGCGGCC | 1200 |
| AGTTTGGATC AATTTTCTTC GTATAAAGAA AGGGGTGAAA AATTCAAAGC GTTTGTTTTA | 1260 |

AAAGAT

1266

(2) INFORMATION FOR SEQ ID NO:23492181_c2_6.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: iron(II) transport system

| | |
|---|-----|
| ATGAAAGAAA TCATTGTCGC CCTTGTGGGC CAGCCTAATG TGGGGAAATC GTCCTTAATC | 60 |
| AACGCTTTGA GTAACSCCCA TTTRAAAGTG GGGAATTTTA CCGRGGTTAC CGTGGATAAA | 120 |
| ATGGAAGTGA GTTTGATCCA WAAAGATCAT CAARTSWYTM TC | 162 |

(2) INFORMATION FOR SEQ ID NO:23515833_f1_3.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | |
|--|-----|
| GTGCATCGTT TTTCTAGAAA CCCATGCGCA TCTTGCAATC GCGCTCGCTC TTGTTCGAGA | 60 |
| CTATCTCGCT CATTAGTGAG CGCGGTAAC TGGTGGTTGA GCTTGTCGTT TTCGGTGGTT | 120 |
| AGTGCTTTAT TTTCTTTAGT CAGCTCGGTG ATTTTATGGG TTAGCTCGGT GTTTTCTCTT | 180 |
| TTTAGCCTTT CTTTTTCTGT TGTCAATTCT CTTTTTTCTT CAGTCAGCCG ATCTCTGGCT | 240 |
| GCTAATAAGC GTGTGTTTTT TTTAGCTAAA ATGTCTTTTT CCGTTTTTCAG TTCTGCTTTT | 300 |
| TCTTTAGTGA GCTTGTTATT GTTTTGCCAT AAT | 333 |

(2) INFORMATION FOR SEQ ID NO:23526667_f2_4.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 411 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGCAAAAAA TGGGCGTTGT CTCTTATTCC GTGTTTCAAG CGTTTGAAAA GGCTTTGAGT | 60 |
| CGGTTTAAAG AGGGCGTTGT TTTGATTGTG GATTCTTTAA GGCGTTTGAT TATGGGGAGC | 120 |
| GCTTCAGTTA AAGAATTGAG TGGGGTAATA GGCATTGTGG GGGCGTTAAG CCATGCCAAT | 180 |
| AGCGTGAGCA TGCTTTTGTG GTTTGGGGCG TTTTATCTA TCAATCTAGG GATTTTAAAT | 240 |
| TTATTACCCA TTCCAGCCTT AGATGGGGCG CAAATGCTAG GGGTCGTTTT TAAAAATATT | 300 |
| TTTCATATCG CTTTGCCAAC GCCCATACAA AATGCGTTGT GGCTAGTGGG GGTGGGGTTT | 360 |
| TTGGTTTTTG TCATGTTTTT AGGGCTTTTT AATGACATTA CTCGTTTGCT A | 411 |

(2) INFORMATION FOR SEQ ID NO:23531562_c2_11.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| GTGATGGCTT TGTGAAAAT TAGTGTGGTA GTTCCTGAGG GGGAAGTTTA TACAGGAGAG | 60 |
| TTTAAAAGCG TTGTGTTGCC AGGAGTGGAA GGGGAATTTG GGGTGCTTTA TGGGCATAGC | 120 |
| AACATGATCA CCTTGCTTCA GGC GGGAGTG GTTGAGATTG AAACCGAAAA CAAAAAGAG | 180 |
| TACATTGCTA TCAATTGGGG TTATGCAGAA GTTACTAATG AACGGGTGGA TATTTTAGCC | 240 |
| ATGGAGCGG TCTTTATTAA AAAAGGATCA GATGACAGAG ATGATGCTAT CTCTAGGGCT | 300 |
| AAAAAGCTTT TAGAGGACGC AAGCTCTGAC AGGTTAGCGG TCTCTAGCGT GCTGGCTAAG | 360 |
| ATTGAGTCTC TT | 372 |

(2) INFORMATION FOR SEQ ID NO:26366312_f3_9.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: UDP-N-ACETYLMURAMYL-TRIPETIDE SYNTHETASE

| | |
|---|-----|
| ATGGGAGCGA TAGCGAGTTG TTACGCGCAT CAAATCATCT TAACTTCAGA CAATCCTAGA | 60 |
| AGCGAAAACG AAGAAGACAT CATTAAGGAT ATTTTAAAAG GCATCAATAA TTCTTCTAAA | 120 |
| GTCATTGTAG AAAAAGACCG AAAAAGGCC ATTTTAAACG CTTTAGAAAA TTAAAAGAC | 180 |
| GATGAGGTGT TGTTGATTTT AGGCAAGGGC GATGAAAACA TTCAAATCTT TAAAGACAAA | 240 |
| ACGATTTTTT TTAGCGACCA GGAAGTCGTT AAAGATTATT ATCTCAATTT AAAACAAGGA | 300 |

(2) INFORMATION FOR SEQ ID NO:23535937_f1_2.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: UDP-N-ACETYLMURAMYL-TRIPETIDE SYNTHETASE

| | |
|---|-----|
| ATGTATTCCT TGCTCTTAGA TTTGAATAAA AAGACCGCTC TTTTAGGCAC AAGAGGGTTT | 60 |
| TTTATCGACG ACAAACACAT CAAAGAAAAG GGCTTGACCA CGCCCACTCT TTTAGAGCTT | 120 |
| TATAGCGATT TGGAAGAAGC GATTCGTTTA AAATGCGAAT ACTTCATTAT GGAGGTGAGC | 180 |
| TCCCATGCGA TTGTCCAAAA CGCATCGCTG GGCTTGATTT CGCTCTTAAA ATTCTCAÇCA | 240 |
| ATATCACAAG CGATCATT | 258 |

(2) INFORMATION FOR SEQ ID NO:23564012_c2_3.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGAAAACGA ACTTTTATAA AATTAAATTA CTATTGCTT GGTGTCTTAT CATTGGCATG | 60 |
| TTTAACGCTC CGCTTAACGC TGACCAAAC ACGGATATAA AAGATATTAG TCCTGAAGAT | 120 |
| ATGGCGCTAA ATAGCGTGGG GCTTGTTTCT AGAGATCAGC TAAAAATAGA GATCCCTAAA | 180 |
| GAAACCCTAG AGCAAAAAGT GACCATACTC AATGACTATA ATGATAAGAA TGTTAATATC | 240 |
| AAGTTTGACG ACATAAGTTT AGGGAGTTTC CAACCTAATG ATAATCTAGG TATCAATGCG | 300 |
| ATGTGGGGCA TTCAAATCT TCTM | 324 |

(2) INFORMATION FOR SEQ ID NO:23573294_c1_11.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 720 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGATTGATA SCCTTGATGG GGCAAAAGAT GCACAATTGA TAAAAAAGC TTACGCGTTT | 60 |
| TTGTGTTTAG GAGGCGATGG CACGATTTTA GGGGCTTTAA GAATGACGCA TGCTCACAAT | 120 |
| AAGCCATGCT TTGGGGTGAG GATTGGGAAT TTAGGGTTTT TGAGCGCGGT TGAATTGAAC | 180 |
| GGGTTGAAAG ATTTCTTACA AGATCTCAAG CAAAACAGGA TCAAATTAGA AGAGCATTTG | 240 |
| GCTTTGGAGG GCCGTATTGG AAACACTTCT TTTTATGCGA TCAATGAAAT CGTGATCGCT | 300 |
| AAAAAAAAAG CTTTAGGGGT TTTAGACATC AAAGCGTGCG CGGGCCATAC GCCCTTTAAC | 360 |
| ACTTATAAAG GCGATGGGCT TATCATTGCC ACGCCCCTAG GCTCAACCGC TTATAATTTG | 420 |
| AGCGCTCATG GGCCCATTTG GCATGCTTTA AGCCAAAGCT ATATTTTAAC GCCCTTGTGC | 480 |
| GATTTTTCTT TAACGCAACG CCCTTTAGTG TTAGGGGCGG AATTTTGCTT GAGTTTTTGC | 540 |
| GCTCATGAAG ACGCTCTTGT GGTATTGAT GGGCAAGCCA CCTACGATTT AAAAGCCAAC | 600 |
| CAACCCCTAT ACATTCAAAA AAGCCCCACG ACCACCAAGC TCTTACAAAA AAATTCAAGG | 660 |
| GATTATTTTA AAGTGCTTAA AGAAAAGCTG TTATGGGGGG AAAGCCCTAA CAAAAAAGA | 720 |

(2) INFORMATION FOR SEQ ID NO:23598962_c1_17.nt:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 549 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | |
|-------------|------------|------------|------------|------------|------------|-----|
| ATGATAGTGG | GTTTGATAGG | GGTTGTGGAA | AAAATCTCTG | CTTTAGAAGC | GCATATAGAA | 60 |
| GTGCAAGGGG | TTGTTTATGG | GGTGCAAGTT | TCTATGCGAA | CGGCTGCTTT | GCTCCAAACG | 120 |
| GGCCAAAAAG | CGCGTTTGAA | AATCTTACAA | GTGATTAAAG | AAGATGCGCA | TCTTTTATAC | 180 |
| GGGTTTTTTAG | AAGAGAGCGA | AAAAATTCTC | TTTGAAAGGC | TTTTGAAAAT | CAATGGGGTA | 240 |
| GGGGGGCGTA | TCGCTTTAGC | CATTCTTTCA | AGCTTTTCGC | CGAATGAATT | TGAAAACATT | 300 |
| ATCGCTACTA | AAGAAGTCAA | AAGACTCCAG | CAAGTCCCAG | GCATAGGGAA | AAAGCTCGCC | 360 |
| GATAAGATCA | TGGTGGATTT | GATTGGCTTT | TTCATTCAAG | ATGAAAACAG | ACCCGCGCGC | 420 |
| AATGAAGTCT | TTTTAGCCCT | AGAGAGTTTG | GGCTTTAAAA | GCGCTGAAAT | CAATCCAGTT | 480 |
| TTAAAAACCC | TAAAACCCCA | TCTCAGCATA | GAGGCAGCGA | TTAAAGAAGC | CTTACAGCAA | 540 |
| CTGCGCTCT | | | | | | 549 |

(2) INFORMATION FOR SEQ ID NO:23610905_c1_15.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 462 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| GTGGGGGTTT TGTTRGCGTT GTTTTTCTTT TATGCGAAAA ATAACCTTTT GGAAAACACC | 60 |
| CAAATACGCA TGCAATACAC CGCTGATGCG ATCGCTAAAA GCCTTTTAGA ATTAAATAAT | 120 |
| GCCTCTTCTT TAGAGCCTTT AAAAATCTTA GAAGAACGAT TCAAAAACAC CCCCTTTGTT | 180 |
| TTGTTGGACG CAGACAACAG AGTCAAGTTT TCTAATATCG GGGTGTTTGT GGCCTCTTTT | 240 |
| AAAAATGACG CCTTAATCAA AACCCCTTAT TTTGCGCTTA AAAAACAGGG CTTTACCTC | 300 |
| ACAGACAGCG CCCCAACTAA CCGCTTAGGG GTTTCTAAAA TCATTATTGC AGAAGAAGAA | 360 |
| ATTCAAAAAA TCTTTATCCC CCTTTATAAA ATGATAGGCT ATGTGTTTTT GGGCGCGAGT | 420 |
| TTGTTTGTCTG CGCTAATAGC CATGTGGCTT TATAAAATCC CA | 462 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 864 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|--|-----|
| GTGGTAATAA TGATTTTAGT CTGCTTTTTA GCTTGCTCGC AAGAGAGCTT TATCAAAATG | 60 |
| CAAAAAAAG CCCAAGAGCA AGAAAATGAC GGCTCTAAAC GCCCCAGCTA TGTGGATTCTG | 120 |
| GATTATGAAG TCTTTAGCGA AACGATTTTT TTACAAAACA TGGTGTATCA GCCTATAGAG | 180 |
| GAAAGAAACG CTTTTTTCCA ACTGACTAAA GATGAAGACA ATTCTTTTAA CCCTGAAAAT | 240 |
| TCCGTGATTT TACTGAATGA GCCAAGCGAT AATAGTGAAA AAAACCTACT CTCATACCCA | 300 |
| AACGATCCCA ATAACAATGA AGACAACGCT AATAATAGTC AAAAAAATCC GTTCCTTTAC | 360 |
| AAGCCCAAAA GAAAAACAAA AAACCCAAAA CTCATTGAAT ATTCCCAACA AGATTTCTAC | 420 |
| CCCCTAAAAA ATGGGGATAT TATCATGAGT AAAGAAGGGG ATCAATGGTT GATAGAAATC | 480 |
| CAATCCAAAG CCTTGAAGCG TTTTTTAAAA GATCAAAACG ATAAAGATCG CCAGATCCAA | 540 |
| ACTTTCACCTT TTAATGACAC TAAAACGCAA ATCGCGCAAA TTAAGGGCAA AATTTCTTCG | 600 |
| TATGTTTATA CCACCAATAA CGGTAGCTTG AGTTTAAGGC CYTTTTATGA ATCGTTTTTG | 660 |
| TTAGAAAAAA AGAGCGATAA TGTTTATACG ATAGAGAATA AGGCTTTAGA TACTATGGAG | 720 |
| ATTTCAAAGT GTCAAATGGT GTTAAAAAAG CATTCAACCG ATAAATTAGA CAGCCAGCAT | 780 |
| AAAGCCATCA GTATTGATTT GGATTTTAAA AAAGAGCGCT TTAAGAGCGA TACGGAATC | 840 |
| TTTTTAGAAT GTCTTAAGGA AAGT | 864 |

(2) INFORMATION FOR SEQ ID NO:23631317_c3_34.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1260 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | | | | | | |
|-------------|-------------|------------|------------|------------|-------------|------|
| ATGGCCGCTC | CACTACTTGC | TCTGCCCTTT | CTTTCTAACC | CTTTAGTGCT | TGGTGCTTTA | 60 |
| GCTGTCATAG | GAGTGGGTGC | TTACTTGTAT | CCCAATAAGC | AAGATTCTTT | AGTTGTGCAA | 120 |
| GCAGATGGGC | TTTATAGTGA | AATTCTTGGG | TTTTTCATTT | CGTTTTCTAG | CAAGATCTTG | 180 |
| AAAGGAATTG | GTGAGCCTTT | AGCCAATGTT | ATCCAACCTT | TTGGTATGGT | TTTAGGAATG | 240 |
| CTTTTAATCC | TTTGTATTTC | CTTTAAACGC | TATCAAAACA | ATGATTTATT | TGAAATCAAA | 300 |
| ACCTTTTTTAA | TGCTTTTTTGT | GTTTGTAGGA | TACCTTTCTT | TGTACCATTA | TGCTTTTTAAA | 360 |
| TCTGATGGTT | CTAGTAGCGG | TAATGGTCGC | TCCAGTTTTG | CCTTTCAAAA | TCATGTAACA | 420 |
| GAAATTTTTTG | ACACGCCTGC | TAAGTTGCTA | AATGCTGGGA | TTTCTAATGT | GGTTAAGGAA | 480 |
| TATCAAACAA | ATAGTGCAAG | AGAACACAAG | AATATAGACA | CGCACCACAG | TATCACTAAC | 540 |
| GCTAATATTT | CATTCCATGT | CAGACAAATT | TTAACGAGTT | TGAATAAACT | ATATGAAGAC | 600 |
| TTCAAAATTA | ATAATGGACT | ATCGCTAAAA | ACCCTTATTG | CAGCTGTTTT | GTTATTAGTT | 660 |
| ATTTTAGGAT | TAGAATTGTT | TTTATTGTTC | AAAGTTTTCT | GTTATGTTTT | TATGACTTAT | 720 |
| TTAGAAAAAA | TTATTTACTT | GTCTTTGGTT | ATTTTCATGC | TACTGCTAGG | GTTTTTTCAG | 780 |
| CAGACTAGAG | GTTTTTTAGT | GTCTTATGTG | AAAAAAATTA | TTTCATTGAC | TTTTTACATG | 840 |
| CCTTTGTTGT | TGCTATTAGT | GTTATTCAAC | TCTTTTGCAT | TACAATACGC | AATCAAAGTG | 900 |
| GGAGGGAGCA | ATGAAATAGT | GGCTAAATTT | GGCATTATTG | TAGCAATAGG | AATTTCACTG | 960 |
| ACATTTATTC | AAAAAGTCCC | CGAAATGATT | AACGCTATCT | TTGGCACACA | AGGTGGTCTA | 1020 |
| ACGGATGCTA | AAAGCTTCAT | ATATCAAGGT | GTGCAAATGG | CTAGTGCTGG | AGCTGGAGCC | 1080 |
| ATAGCTGGAA | GTCTTAAGAG | TGTGGGTCGT | TCAGCATTTG | GTAGAACGCT | AGAAGCTTAT | 1140 |
| AAAGACGCAA | AATCTACGAT | AAACAGCACT | ACGGCTAACA | TGAGAGACAT | GCCAGGACAT | 1200 |
| TCTGGTGTTA | GAGTGGGTGT | GGAGACGATT | GAACCTCCCA | AGTCTCATAG | AGCTAGCAAA | 1260 |

(2) INFORMATION FOR SEQ ID NO:23646885_c1_12.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| GTGTTAAAAT TTCAAAAATT ACCCTTATTG TTTGTTTCCA TTCTTTATAA TCAAAGCCCT | 60 |
| TTATTGGCTT TTGATTATAA GTTTAGTGGG GTAGCGGAAT CTGTTTCTAA AGTGGGGTTT | 120 |
| AACCATTCCA AACTCAATTC CAAAGAAGGG ATTTTCCCTA CAGCCACCTT TGTAACCGCC | 180 |
| ACGATCAAGC TTCAAGTGRA TTYCAAATCT GCTCCC | 216 |

(2) INFORMATION FOR SEQ ID NO:23728388_f2_6.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 615 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGGGTAATC ATTTTCTCTAA ATTAGGATTT GTTTCTAGCGG CTTTAGGGAG CGCGATAGGT | 60 |
| TTAGGGCATA TCTGGCGCTT CCCCTATATG ACTGGGGTGA GTGGTGGGGG TGCTTTTGTT | 120 |
| TTATTGTTTT TATTTTTATC CTTAAGCGTT GGTGCGGCGA TGTTCATCGC TGAAATGCTA | 180 |
| TTAGGACAAA GCACGCAAAA AAATGTAACA GAAGCTTTTA AAGAGCTTGA CATTAACCCT | 240 |
| AAAAAACGCT GGAAATACGC AGGGATCATG CTTATTTCTG GACCTTTAAT ACTGACTTTT | 300 |
| TATGGCACTA TTTTAGGTTG GGTGCTTTAT TATTGGTGA GTATTAGTTT TAATTTGCCT | 360 |
| AGCAGTATCC AAGAATCTGA ACAAATTTTT ACTCAAACCTT TGCAGTCTAT AGGGTTACAA | 420 |
| TCCATAGGGC TTTTCTAGCGT TTTATTCATA ACCGGATGGA TTGTTTCTAG GGGGATTAAA | 480 |
| GAAGGCATTG AAAAATCTCA TTTGGTTTTA ATGCCCTTAC TCTTTGCCAC TTTTTTTGGT | 540 |
| TTGCTTTTTT ATGCGATGAG CATGGATTCT TTTTCTAAAG CTTTCCATTT CATGTTGATT | 600 |
| TCAAGCCAAA AGATT | 615 |

(2) INFORMATION FOR SEQ ID NO:23831562_f2_19.nt:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 984 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (xi) SEQUENCE DESCRIPTION:

| | | | | | | |
|-------------|-------------|------------|------------|------------|-------------|-----|
| ATGGAAAAAG | TTTGC GTGAG | CGCATGGGGG | TTGCCTAAGA | TTTTAGAAGA | AAGATTAAAA | 60 |
| GAAAAATATG | GCGATGATTG | GGAAAAACAT | GTTAAGGCTA | AAGCAATAAA | CGAAGAAGAG | 120 |
| CTTGAAGAAC | AAGTCAAAGC | TAAAGCCAAA | GAGCAACAAA | AGACACAAAG | AGAAAAAACA | 180 |
| CTCAATGGAT | TTTTAAAAAA | AGTTGGTTTA | AAAAAGCGTG | ATATGTTACA | AAGCACTATG | 240 |
| TTATTTGATG | AAGTCAAAGA | AGCTGATGTG | CTTTTTCAAG | CAGAGCGTAA | AATTGGCGAT | 300 |
| TGGATTTTTA | GCAGTGCGGT | GTTCTTTTTT | GCTCTAGCCC | TTATAGAAGC | CATTATTATT | 360 |
| GTATGCTTAT | TGCCGTTAAA | AGAAAAAGTG | CCTTATTTAG | TAACCTTTTC | AAACGCTACA | 420 |
| CAAAATTTTG | CCATAGTCCA | AAGAGCAGAC | AAGAGCATCC | GTGCTAATCA | AGCGCTTG TG | 480 |
| AGACAATTGG | TAGCGTCTTA | TGTTAATAAT | AGAGAAAATA | TTTCAAGTAT | AAAAGAGCAA | 540 |
| AACGAAATAG | CCCACGAAAC | CATTAGGTTG | CAAAGCGCAT | TTGAAGTGTG | GGATTTTTTTT | 600 |
| GAAAAACTGG | TTTCTTATGA | GCATAGCATT | TACACTAATA | TAAATCTAAC | ACGAAAAATT | 660 |
| AGCATTATCA | ATATCGCTTT | AATCAGTAAA | ACCCAAGCCA | ATATTGAAAT | ATCCGCACAA | 720 |
| CTTTTTTCATA | AAGAAAAGTT | AGAAAGCGAA | AAGCGTTATA | GAATAATTAT | GACCTTTGAA | 780 |
| TTTGAACCTA | TTGAAATTGA | TACAAAATCT | GTTCCCCTAA | ACCCTACAGG | CTTTATTGTT | 840 |
| ACAGGTTATG | ATGTA ACTGA | AATTGCGATT | TTAAAAGATT | TAGATGAGAA | AAATAAAGTC | 900 |
| AAAGATGATG | GTGTGAAATC | TAGGATTATC | CATGTCGAGA | AAAAAGACCC | TCATATGAGC | 960 |
| CAGTATAAAG | ATGTTAAGGA | GCAA | | | | 984 |

(2) INFORMATION FOR SEQ ID NO:23867207_c3_6.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|--|-----|
| ATGCTGCATA AGGCTAAGGT GGGCATCGTG TTTCAGGCGC TTTTAGGGAT TTTTTCGCTG | 60 |
| TTTTTATTGT TGTTTTACTT GAGCGCGTTT TTAATGGTGG CTTTAAAGA CACTAAACGC | 120 |
| ATGTTTATAA GCGTTTTAAT AGGGAGCGTG GTGTTTCCTTT GGAGCGATCT ATTGGTCTTT | 180 |
| GTAGGGTTTA AAAATATCAG CTTTGTTTTG GATATTGGTT ATGAAATC | 228 |

(2) INFORMATION FOR SEQ ID NO:23880087_c3_16.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGCCGTTTT TGAAAACTG GATCTGGAGT TTAAAGATGG CTTTGAGCGC GATTAGTGGG | 60 |
| GCTAGTGGGG TGGGGAAAAG CGTCCTTATT GCGAGCCTTT TAGGGGCGTT TGGGCTTAAA | 120 |
| GAGAGCAACG CTTCAAACAT TGAAGTGGAA TTGATCGCGC CTTTTTTAGA CACGGAAGAA | 180 |
| TACGGCATTT TTAGAGAAGA TGAGCATGAA CCCTTAGTTA TTAGCGTGAT TAAAAAGAA | 240 |
| AAAACACGCT ATTTTTTAAA CCAAACAAGC CTATCTAAAA ACACGCTCAA AGCGTTATTA | 300 |
| AAGGGGCTTA TTAAACGCTT ATCTAACGAC AGATTCAGCC AGAATGAACT CAACGATATT | 360 |
| TTAATGCTCT CTTATTAGA TGGCTATATC CAAAATAAAA ATARGCGTTT AGCCCCCTTT | 420 |

(2) INFORMATION FOR SEQ ID NO:23912707_c2_16.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 924 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | |
|--|-----|
| ATGCCACAAA ACCAGCTTGT GATCACCATC ATTGATGAAT CAGGCTCTAA GCAACTCAAA | 60 |
| TTTTCTAAAA ATTTAAAACG CAACCTCATC ATTTCTGTTG TCATTCTTTT ATTGATCGTG | 120 |
| EGGCTTGGCG TGGGGTTTTT AAAATTTTTTA ATCGCTAAAA TGGATACGAT GACAAGCGAG | 180 |
| AGGAATGCGG TTTTAAGGGA TTTTAGGGGT TTGTATCAAA AAAATTACGC CCTAGCGAAA | 240 |
| EAGATTAAAA ACAAGCGAGA AGAGCTTTTTT ATTGTGGGGC AAAAGATCCG TGGGCTAGAA | 300 |
| TCCTTGATTG AAATCAAAAA GGGGGCTAAT GGGGGAGGGC ATCTCTATGA TGAAGTGGAT | 360 |
| TTAGAAAATT TGAGCTTAAA TCAAAAACAT TTAGCACTCA TGCTCATTCC TAATGGCATG | 420 |
| CCCCTAAAAA CTTATAGCGC TATCAAACCC ACTAAAGAAA GGAACCACCC CATTAAAAAG | 480 |
| ATTAAGGGCG TTGAATCCGG GATCGATTTT ATCGCGCCAT TGAACACGCC TGTGTATGCG | 540 |
| AGCGCTGATG GGATTGTGGA TTTTGTGAAG ACTCGTTCTA ATGCGGGGTA TGGGAAC TTG | 600 |
| GTGCGCATTG AACATGCGTT TGGTTTCAGC TCCATTTATA CGCACTTAGA TCATGTCAAT | 660 |
| GTGCAGCCTA AAAGCTTCAT CAAAAAAGGG CAGTTGATTG GCTATAGCGG GAAGAGCGGT | 720 |
| AATAGCGGCG GCGAAAAATT GCATTATGAA GTGCGGTTTT TGGGTAAAAT TTTAGACGCA | 780 |
| EAAAAATTCC TAGCATGGGA TTTGGATCAT TTTCAAAGCG CTTTAGAAGA AAATAAATTT | 840 |
| ATTGAATGGA AGAATCTGTT TTGGGTTTTA GAAGACATCG TCCAGCTCCA AGAGCATGTG | 900 |
| EATAAAGACA CCTTAAAAGG TCAG | 924 |

(2) INFORMATION FOR SEQ ID NO:23912807_c1_7.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1017 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: phosphomannomutase

| | |
|---|------|
| ATGATCACTG GCTCTCACAA CCCCAAAGAA TACAACGGCT TTAAAATCAC GCTCAATCAA | 60 |
| AACCCGTTTT ATGGCAAGGA CATTCAAGGCT TAAAAAACA CGCTTTTAAA CGCAAAGCAT | 120 |
| GAAATAAAGC CCCTAAAAGA AACGCCAGAG AAAGTCAATG CCCTAGAAGC GTATCATCGC | 180 |
| TATTTGATCA AGGATTTTAA GCATTTAAAA AATCTTAAAT ACAAATCGC CCTGGATTTT | 240 |
| GGTAATGGCG TGGGGGCGTT AGGATTAGAG CCGATTTTAA AGGCTTTAAA CATTGATTTT | 300 |
| AGCAGCCTTT ATAGCGATCC TGATGGGGAT TTTCTAACC ACCACCCAGA CCCTAGCGAA | 360 |
| GCGAAAACT TAAAAGACTT AGAAAAACAC ATGCGAGAAA ACGCTATTTT AATAGGCTTT | 420 |
| GCTTTTGATG GCGATGCGGA TAGGATTGCG ATGCTAAGCT CTCATCATAT CTATGCGGGC | 480 |
| GATGAATTAG CGATTTTATT CGCTAAACGC TTGCATGCTC AAGGCATCAC CCCTTTTGTG | 540 |
| ATCGGCGAAG TCAAATGCTC TCAAGTGATG TATAACGCAA TCAATACTTT TGGTAAGACG | 600 |
| CTCATGTATA AAACCGGGCA TAGCAATTTA AAAATCAAGC TCAAAGAAAC TAATGCGCAT | 660 |
| TTTGCGGCTG AAATGAGCGG GCATATCTTT TTAAAGAAC GCTATTTTGG CTATGATGAC | 720 |
| GCTCTTTACG CATGTTTAAG GGCTTTGGAG TTATTGCTTG AACAAAGTCC AAGCGACTTG | 780 |
| GAAAACACCA TTAAAAACCT CCCCTATTCC TACACCACGC CTGAAGAAAA AATCGCCGTG | 840 |
| AGCGAAGAAG AAAAATTGTA AATCATTCGC AACTTACAAG AAGCGCTTAA AAACCCGCCA | 900 |
| AGCCATTTCC CTACAATCAA AGAAATCATC AGCATTGATG GCGTGAGAGT GGTTTTTGAA | 960 |
| CATGGCTTTG GGCTTATTCG CGCAAGCAAC ACCCACCCCC TATTTAGTCA GCCGCTT | 1017 |

(2) INFORMATION FOR SEQ ID NO:23915877_f1_2.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 621 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|--|-----|
| ATGTCCAAGA ACCTTCAAAA GAAGAATCCA AAGAAGAGTT TYCCACAAGC CCAGAAAGCC | 60 |
| ATAAGGGAGA TGAAAATGTT TGAAACCATT GCYTTTTTATT TCTTTGCGAT CCTTACTTTA | 120 |
| AGCATGGCGT TAGTGGTGAT CACAACCACA AATATCCTCT ATGCCATTAC CGCTCTCGCT | 180 |
| AGTAGCATGG TTTTATATTC TGCTTTTTTC TTTTACTGG ACGCTGAGTT TTTGGGCGTG | 240 |
| GTGCAAATCA CGGTGTATGT GGGTGCGGTC ATTGTGATGT ATGCGTTTGG CATGATGTTT | 300 |
| TTCAACTCCG CTGCAGAAGT AGTTGAACGC AAGCAAAGCC CTAAAATCTT GTGCGTTCTT | 360 |
| TCATTGCGG TGGCGCTGTT GCTCACCTTG ATTTTAAGCG CTCCTAGCAT TGSSGAAAAC | 420 |
| CTTTCTAAGC AAGTCAATTC CAACGCTATT GATGCGCAA TYCCYAACAT TAAAGCGATT | 480 |
| GGTTATGTGC TTTTCACCAA TTACCTCATT CCCTTTGAAG CGGCGGCTTT AATGCTTTTA | 540 |
| GTCGCTATGG TTGGAGGCAT CGCTACAGGG ATTCAAAAAA TCCATGGGAA AAATCACACG | 600 |
| CAATTTATAA AGGAATCTCT A | 621 |

(2) INFORMATION FOR SEQ ID NO:23945317_c2_15.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 753 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| ATGGGTGCAA | TTTTATCTAT | TTTAAACTT | GAAATCAAAT | CTTATCTCAC | CAATACAAGC | 60 |
| GCGCTATTTT | GGACTTTTAT | TTATCCTATT | TTAATGCTCC | TATTACTAAT | TTTTGTTTTT | 120 |
| TCAAAAAATA | CCACTGAAAT | TTTTTACTTT | AATAACATTA | TAGGTCTAAT | GGGACTTCTT | 180 |
| ATTATTTCTA | GCGCGATCTT | TGGTCTCACA | CAAGCTATAA | CAAGCTCTAG | ATCGCATAAT | 240 |
| ATATTCTTAT | TCTACATGCT | ATCACCAGCA | ACTTTCAAAC | AAATAACTCT | AGCATTAATC | 300 |
| GCTTCAAGAC | TAATCGTTGT | AATCCTATAT | GCTTTTATCT | TTATTGTTCT | CTCTTTTTAT | 360 |
| GCGCTCAATA | TCATCACTAT | TCTTAATTTT | AAAGCGCTTA | TTTTGGGGTT | TATTAGCATT | 420 |
| TTTTCAAGCG | CATTGTTTTG | TTTTTGCTTG | GCAATTTTGT | TAGCTAGAAT | TTTTCAAAAC | 480 |
| GAACAAAGCA | TCTTAGGATT | TTGTAATATC | ATCAATCTCT | ATGCGCTAAT | GTCTTGTAAT | 540 |
| GTTTTTGTTT | CTTTAGAATA | CCTACCTAAT | ATTGGTCAAT | TATTTATCAA | AACATCTATT | 600 |
| TTTTACTACC | TTAATCAACT | TCTAATCAAA | GCTTTTCAAG | GGATTGATAC | TATACTGGTT | 660 |
| TTAGCAACTT | CAACATTTTT | CATTATTGGT | GGCATTATTT | TATTTTACT | AAGCGCTAAT | 720 |
| CGCATGTTAC | TAACACCAAA | AGAACGCATG | CGT | | | 753 |

(2) INFORMATION FOR SEQ ID NO:23958179_c2_4.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGGCAGGCA CACAAGCTAT ATATGAATCA TCTTCTGCAG GATTCTTATC GCAAGTCTCC | 60 |
| TCAATCATCT CAAGCACAAG TGGTGTGCGA GGGCCATTG CAGGAATAGT AGCGGGCGCT | 120 |
| ATGACAGCAG CGATTATTCC TATTGTTGTG GGATTTACTA ATCCGCAAAT GACCGYTATY | 180 |
| ATTRACCCAA TAYAATCAAA GCATCGC | 207 |

(2) INFORMATION FOR SEQ ID NO:24003758_c3_32.nt:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 336 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: spoIIIE gene product

| | |
|---|-----|
| GTGAGCCGTA TTTTAGGCTT GAGCGATGAT TTAGCGATGA CTTTATGCGC TGAATCCATC | 60 |
| CGCATTCAAG CCCCTATCAA AGGTAAAGAT GTCGTTGGTA TTGAAATCCC TAACAGCCAA | 120 |
| AGCCAAATTA TTTATTTAAG AGAAATTTTA GAAAGCGAAT TGTTTCAAAA ATCCAGCTCG | 180 |
| CCTCTAACCC TAGCTTTAGG CAAAGACATT GTGGGTAACC CTTTCATCAC GGATTTAAAA | 240 |
| AAGCTCCCCC ACTTGCTCAT CGCCGGCACG ACAGGGAGCG GTAAGAGCGT GGGCGTGAAT | 300 |
| GCGATGATTT TATCCTTACT TTATAAAAAA CCCCCC | 336 |

(2) INFORMATION FOR SEQ ID NO:24036302_f3_3.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 456 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|--|-----|
| ATGGATGAAA GSCTCGTTTA TGGGGTGATT TGCATGCCCA GTCAGGTTTT TGCCAACACC | 60 |
| GGCACTAACG TGAGCATCAT CTTTTTTTCAA AAAACGCCAA GCGCAAAGGA AGTGATCTTG | 120 |
| ATTGACGCTT CCAAACCTCGG CGAAGAATAC ACCGAAAACA AAAACAAAAA AACGCGCTTA | 180 |
| AGGCCAAGCG ATATGGATTT GATTTTAGAA ACTTTCCAAA ATAAAGCCCC AAAATCGGAT | 240 |
| TTTTGCGCTC TGGTTTCTTT TGATGAAATT ACAGAAAAAA ATTATTCTCT AAACCCCGGG | 300 |
| CAGTATTTCA CTATAGAAGA CACGAGCGAG ACAATCAGCC AAGCGGAGTT TGAAAACCTG | 360 |
| ATGCAACAAT ATTCAAGCGA ACTAGCGAGC CTTTTTGATG AAAGCCAAAA TTTGCAACAA | 420 |
| GAGATTTTAG AAACTTTAAA AGGGGTTAGG TTTGAG | 456 |

(2) INFORMATION FOR SEQ ID NO:24070250_c1_11.nt:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 339 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: chemotaxis protein cheY

| | |
|---|-----|
| ATGAGAAGAA TTATTAAAAA CACACTTTCA CGCTTAGGCT ATGAAGATGT TTTAGAAGCT | 60 |
| GAGCATGGGG TGGAAGCTTG GGAAAACTA GACGCTAATG CGGACACTAA GGTGCTTATT | 120 |
| ACGGATTGGA ACATGCCTGA AATGAACGGG TTGGATCTCG TTAAAAAGGT GCGTGCGGAT | 180 |
| AACCGATTTA AGGAAATCCC TATCATTATG ATCACCACAG AGGGCGGTAA AGCTGAGGTC | 240 |
| ATTACGACTT TAAAAGCGGG CGTGAATAAC TACATTGTGA AACCTTTTAC CCCCCAAGTT | 300 |
| TTGAAAGAAA AATTAGAGGT TGTTTTAGGG ACAAACGAT | 339 |

(2) INFORMATION FOR SEQ ID NO:24078837_f3_7.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 549 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGGCAGAAG AACAAAGAAA TACCGCGCAA CAACCCCAAA AAAAAAGCAA AGCCCTTTTA | 60 |
| TTTGTCATTA TTGGAAGCGT GCTAGTGATG CTTTTATTGG TGGGGGTGAT TATCATGCTG | 120 |
| CTTATGGGGA ATAAGGAAGA ATCTAAAGAA AACGCTTCTA AAAACACCCA AGAAGTCCAA | 180 |
| GCTAATCCTA TGGCGAACAA GAATCAAGAA GCCAAAGAAG GCTCTAATAT CCAGCAATAT | 240 |
| TTGGTGCTTG GGCCTTTGTA TGCGATTGAT GCGCCTTTTG CGGTGAATTT GGTCTCTCAA | 300 |
| AATGGCAGAC GCTACCTTAA GGCTTCTATT TCGCTAGAAT TGAGCAATGA AAAGCTTTTG | 360 |
| AATGAAGTCA AGGTTAAAGA CACGGCGATT AAGGACACGA TTATAGAAAT TCTATCGTCT | 420 |
| AAAAGCGTGG AAGAAGTGGT TACTAACAAA GGCAAAAACA AGCTTAAAGA TGAAATTAAG | 480 |
| AGCCATTTGA ATTCGTTTTT GATTGATGGC TTTATTAAAA ATGTCTTTTT CACTGATTTC | 540 |
| ATTATCCAA | 549 |

(2) INFORMATION FOR SEQ ID NO:24089087_c1_16.nt:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 105 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGGGGTGTT TTAGCACCAT TTGTTGTAAG GGTTTAACGC TTAGCGTTGG TGGATTTTTG | 60 |
| GTGATGATGA GATTCTTAAT ATTCAAAGAT TTTTGCAAAG ATTTT | 105 |

(2) INFORMATION FOR SEQ ID NO:24104558_f1_1.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2106 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: VirB4 homolog

| | |
|--|------|
| GTGGCGCGTC TTGTGGTTAA AAGGCGTAAA ATTGATTATA AACAAAGCAT TCAATCTGAC | 60 |
| TCTCAATACT TGCAAGCGAS CTTGAATCAG TTTGAAAATA AAGAAGTGTA TGAGAATCAG | 120 |
| TATTTTTTTAG TTTTAGAAAG CACTCACTCT TTGCATGGCG TTTTGGAGCA TAAGAAAAAA | 180 |
| TCTTTCATGC ACGCTAATAG AGAAAATTTT AAGGATATTC TCTCTTATAA AGCGCATTTT | 240 |
| TTGCAAGAAA CTTTAAAAAG CTTAGAAATC CAGCTCAAAA ACTATGCCCC CAAACTCTTA | 300 |
| AACTCTAAAG AGGTTTTGAA TTTTATGCA GAATATATTA ATGGGTTTGA ACTCCCTTTA | 360 |
| AAACCCCTAG TAGGGGGGTA TTTGAGCGAT AGCTATATCG CTAGTTCTAT CACTTTTGAA | 420 |
| AAAGATTATT TCATTCAAGA AAGCTTTAAT CAAAAACCT ATAACCGCTT GATTGGCATT | 480 |
| AAAGCTTATG AGAGCGAAAG GATCACTTCT ATAGCGGTGG GAGCGCTTTT ATACCAAGAG | 540 |
| ACGCCTTTGG ATATTATCTT TTCCATAGAG CCTATGAGCG TCAATAAAAC GCTGAGTTTT | 600 |
| TTAAAAGAGA GGGCCAAGTT TAGCATGTCT AATCTTGTTA AAAACGAGCT ATTAGAATAC | 660 |
| CAAGAATTAG TCAAAACCAA ACGATTATCC ATGCAAAAAT TCGCCCTAAA CGTTCTTATC | 720 |
| AAAGCCCCCA GTTTGGAGGA TTTAGACGCT CAAACCAGCT TAATTTTAGG GCTTTTATTT | 780 |
| AAAGAAAACCT TAGTGGGCGT TATAGAACT TTTGGCTTGA AAGGGGGGTA TTTTTCCTTT | 840 |
| TTCCCTGAAC GCATCCATTT AAACCACCGC TTGCGTTTTT TAACCTCTAA AGCCCTAGCG | 900 |
| TGTTTGATGG TGTTTGAAAG GCAAAATTTA GGTTTTAAGG CTAATTCATG GGGGAATAGC | 960 |
| CCTTTGAGCG TGTTTAAAAA TTTGGATTAT TCCCCTTTTT TATTCAATTT CCACAACCAA | 1020 |
| GAAGTGAGCC ATAATAACGC TAAAGAAATT GCCAGAGTGA ATGGGCATAC TTTAGTTATA | 1080 |
| GGGGCAACCG GAAGCGGTAA AAGCACGCTG ATTAGCTATT TAATGATGAG CGCTTTAAAA | 1140 |
| TACCAAAACA TGCGCCTTTT AGCTTTTGAC AGGATGCAAG GGTGTGATTC TTTCACCGAA | 1200 |
| TTTTTTTAAAG GGCATTACCA TGACGGCCAA TCTTTTAGTA TCAACCCCTT TTGTTTAGAG | 1260 |

| | | | | | | |
|------------|------------|------------|-------------|------------|------------|------|
| CCTAATTTGC | AGAATTTAGA | ATTTTTGCAA | TCCTTTTTTT | TGAGCATGTT | GGATCTTGCC | 1320 |
| CCTTCAAGGG | ATAAAGAAGC | CTTAGAAGAC | ATGAATGCGA | TTTCTGGCGC | GATTAAGAGC | 1380 |
| CTTTATGAGA | CCTTATACCC | CAAAGATTTT | AGTTTGCTGG | ATTTTAAAGA | AACGCTTAAA | 1440 |
| AGAACCTCAT | CTAACCAATT | GGGCTTGAGT | TTAGAGCCGT | ATTTGAATAA | CCCCCTTTT | 1500 |
| AACGCTTTGA | ATGACGCGTT | CAACTCCAAC | GCTTTTTTTAA | ATGTGATAAA | CCTAGATGCG | 1560 |
| ATCACCCAAA | ACCCTAAAGA | CTTAGGGCTT | TTAGCCTATT | ACTTGTTTTA | TAAGATCTTA | 1620 |
| GAAGAGTCTA | GGAAAAACGA | CAGCGGCTTT | TTGGTTTTTT | TAGACGAATT | TAAATCCTAT | 1680 |
| GTGGAAAACG | ATTTGTTAAA | CACTAAAATC | AACGCTTTAA | TCACGCAAGC | CAGGAAAGCT | 1740 |
| AATGGCGTGG | TGGTGTTGGC | CTTGCAAGAC | ATTTACCAAC | TTAGCGGGGT | TAAAAACGCC | 1800 |
| CATAGTTTTT | TAAGCAACAT | GGGACTCTC | ATTTTGTATC | CGCAAAAAAA | CGCTAGGGAA | 1860 |
| TTGAAACACA | ATTTCAATGT | GCCTTTGAGC | GAAACTGAAA | TTTCTTTTTT | AGAAAACACC | 1920 |
| CCTCTGTATG | CCAGGCAGGT | TTTAGTCAAA | AATCTGGGTA | ACGGGAGTTC | CAACATGATT | 1980 |
| GATGTGAGTT | TGGAGGGCTT | GGGGTGTTAT | TTGAAAATCT | TTAATTCAGA | TTCCAGTCAT | 2040 |
| GTCAATAAAG | TGAAAGCGTT | ACAAAAAGAC | TACCCTACAG | AGTGGCGTGA | GAAACTTTTG | 2100 |
| AAGAGT | | | | | | 2106 |

(2) INFORMATION FOR SEQ ID NO:24132293_f1_2.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 879 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: methyl-accepting chemotaxis protein; transmembran

| | |
|--|-----|
| ATGCAAGAAG ACTGGCAAGC CGTCCAAGAC ACCATTAAAG TGGTTTCAGA TGTGAAAGCG | 60 |
| GGGAATTTTG CGGTGCGCAT CACGGCTGAA CCCGCAAGCC CTGATTTGAA AGAATTGAGA | 120 |
| GACGCGCTAA ATGGGATCAT GSAYTATTTG CAAGAAAGCG TAGGGACTCA CATGCCAAGC | 180 |
| ATTTTCAAAA TCTTTGAAAG CTATTCTGGC TTGGATTTTA GAGGGCGGAT CCAAAACGCT | 240 |
| TCGGGTAGGG TGGAATTGGT TACTAACGCT TTAGGGCAAG AAATCCAAAA AATGCTAGAA | 300 |
| ACTTCGTCTA ATTTTGCCAA AGATCTAGCG AACGATAGCG CGAATTTAAA AGAATGCGTG | 360 |
| CAAAATTTAG AAAAGGCTTC AAAC TCCCAA CACAAAAGCC TGATGGAAAC TTCCAAAACG | 420 |
| ATAGAAAATA TCACCACTTC CATTCAAGGC GTGAGCTCTC AAAGTGAAGC CATGATTGAA | 480 |
| CAAGGGAAAG ACATTAAAAG CATTGTAGAA ATCATTAGAG ATATTGCCGA TCAAACGAAT | 540 |
| CTATTAGCCC TAAACGCTGC TATTGAAGCC GCACGAGCCG GCGAGCATGG CAGAGGCTTT | 600 |
| SCGGTGGTGG CTGATGAGGT GAGGAAGCTC GCTGAAAGGA CGCAAAAATC CCTCAGTGAG | 660 |
| ATTGAAGCCA ATATTAATAT TCTCGTTCAA AGCATTTCAG ACACGAGCGA AAGCATTTAA | 720 |
| AACCAGGTTA AAGAAGTAGA AGAGATCAAC GCTTCTATTG AAGCCTTAAG ATCGGTACT | 780 |
| 3AGGGCAATC TAAAAATCGC TAGCGATTCT TTAGAAATCA GTCAAGAAAT TGACAAAGTC | 840 |
| ICTAACGATA TTTTAGAAGA TGTGAATAAA AAGCAGTTT | 879 |

(2) INFORMATION FOR SEQ ID NO:24215_c1_7.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGCCTAAAA GTTTCACCTT ACCGACTTTC GTGTGGTGTT TGTTTGTGGG GGTTATCTTA | 60 |
| AGGAACGCTT TGTCGTTTTT TAAAATCCAT AGCGTGTTTG ACAGAGAGGT TTCAGTTATA | 120 |
| GGGAATGTGA GCTTGAGCCT GTTTTTAGCT TACGCT | 156 |

(2) INFORMATION FOR SEQ ID NO:24218968_f3_2.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 546 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: HYPOTHETICAL ABC TRANSPORTER

| | |
|--|-----|
| GTGGGGCCTTT TAAATTCTAA GCGGTTCAAA CCCTACCGCA AGATTTTGCA AATGGTGTTT | 60 |
| CAAGACCCCT ACGCATCATT AAACCCTCGC TTAAGCATT C AAAGCATTTT AATAGAAGCT | 120 |
| TTGCGCTTTG CTTACCCTAA AGCTTCACAA CAAGAATGGC ACCATTTAGC TGAACCTTGC | 180 |
| TTAGAAGAAG TGTGTTTAAA CCCTGAATTG CTTAACTTTT ACGCTTATGA GCTCAGCGGA | 240 |
| GGGGAGCGCC AAAGAGTGGC GATCGCTAGA GCGATTGCCT TAAAACCTAG AATCATTCTT | 300 |
| TTAGATGAGC CAACCTCTGC TTTAGACAAA AGCATTCAAA AAAGCGTGTT GGAATTATTG | 360 |
| TTGAATTTAC AAGAAAAGCA GGATTTGAGC TATTTGTTTA TCAGCCATGA TTTAGATGTG | 420 |
| ATCAAAGCTT TTTGCGATAG GGTGTTAGTG GTGAGTGAGG GGAAAATCGT GGAAACAGGC | 480 |
| GCTATTGAAG AGGTGTTTGA CAACCCCAAA CACGCTTATA CCAAGCGTTT GTTGGAATCC | 540 |
| AGGCTT | 546 |

(2) INFORMATION FOR SEQ ID NO:24219012_cl_3.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 753 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|--|-----|
| GTGAGTTTGA TTAAAGTTAG TGGTGATAAA AAAGTGATTG AGGTTTCTAT TCCTTTAACT | 60 |
| TCCATTTTCAG GCAAAGCGCG TGTGAAAATC AGACATGCCT TTAGCGATTG TGGTATTTCA | 120 |
| ACAGCGACTA GAAAAATCCC TTTTAGTTTA AAGCATTATG TAGAGTGGCA GATCGGTTAT | 180 |
| GATGTCCCCA TTAAAGATAA AGAAAAATTT GAACTCACTA CTTTAAAAGA TGAAAAATAT | 240 |
| CATTTTTTTAG GGGCTAATAA TAAAGTAAAA ACTCTTTATG AATTGAGCGA AATGATTTAT | 300 |
| TACGCTAAGC GATTGGGTTT AATCAGTTTA GAAAATTTAG AAAATACTTT AAAATTTTTTA | 360 |
| GAAAAACAAA AACAATTTAT AGAAGATAAT TTTATGATTA CAAGAGAAAG ATTTAGATCG | 420 |
| CATCAATTTG GTGGCATGGA TTTTGAAGTC TCACGCATTT CTTATCCTTT GTCATTCAT | 480 |
| TCTTTTGATG ATAATGAGTT GAGCGAAATA GTTATTAAGG AACAACAATA TGGCTCTAAA | 540 |
| ACCCAAGCCA TGCTGTATTT TTGCTTTTCT ATTTTGGAGT TAAAAACCGC TACCCCCTTA | 600 |
| TTAAACAGAA CCGCTATGCC CAAAGAACAT GCCCTTTTGA TTATCCATGA AACCAACGCT | 660 |
| CTTGTGTTTT TAGAAATGCT TAAAATTTTT GGAAGTTTAA GCCAAGTGCA CCATAACGAT | 720 |
| GTGTTWAAGA TTTTWGAAAA AATACTTCAA AAT | 753 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: major surface LPS-antigen

GTGATCACGG CGTGTTTAA TAGYGAAAAA ACCATTGAAG ACACCATTCT TTCCGTGCTT 60

AATCAAACCTT ATAAAAACAT TGAATACATC ATTATAGATG GGGCTAGCGC GATAGCACTT 120

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|--|-----|
| GTGTTTGTAG GGCTTTATCA TGGGGCAAGC ATCTTTGATT TAAAATTGA AGTCTATCTT | 60 |
| ACTATGCTAA TCTCTTTAAT GCCCTTTGTG GCTACGATTT ATATCAATTT CCCAAAAACC | 120 |
| ACAGAAACTT CGCATGGCTA TGCGAGATGG GCTAATGTTA AAGATATAGA ATGCTTTAAA | 180 |
| ATTTTGTAGCA AAGAGGGCTT TTGTAAAGTG GTGCATAGAT TAGGGGTGCA ATTTGATAAT | 240 |
| GGCTTTATTC TAGGTAAATT TGGTTTTCCA AAGCTTAGAA ATGTGTGCTA TGACAAGCCC | 300 |
| TTAGGAACGA TGATTGTTGC ACCCCCTGGT GCGGAAAAAC TGCATGTGTG GCTTTGCCAA | 360 |
| ATTAT | 366 |

(2) INFORMATION FOR SEQ ID NO:24230058_f1_1.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGAAACGCC TTGCTGTTGC GCTTATTTTG GTGTTGGGAG TGGTGTGGGG GAAATCCTTG | 60 |
| CCTAAGTGGG CAAAAGATTG CTCAAAAGAG ATGCGGATTG AAAAGACCCA AACCAAAGAT | 120 |
| GAAAAAATTT TAGTGTGTGG GATGAGCGAT ATATTGCTTT CAGATATGGA TTATAGCTTG | 180 |
| TCCTCAGCCA GACAAAACGC CTTAGAGAAA GTGATGGAAG CTTTCAAGGG GGATAGAATA | 240 |
| GAGATTAAGG CTGGTGAGCT AAAGGCCACT TTTATTGATA CGGATAAAGT TTATGTGCTT | 300 |
| CTAAGAATCA CTAAGAAGCA TGTCGCTTTA ATGAATGAG | 339 |

(2) INFORMATION FOR SEQ ID NO:24238762_c3_33.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1311 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|--|------|
| ATGAACCCCC AGATTCAACC CGCCACTAAA AAACCCTTAA AATCCCTTTT AGCCGCTAGT | 60 |
| TCAGGCAATT TAGTGGAATG GTATGATTTT TACGCTTATG CGTTCCTTGC TCCTTATTTC | 120 |
| GCTAAGGAAT TTACCCACAC CAATGACCCT ACTCTAGCGC TCATCTCAGC TTTTFTAGTT | 180 |
| TTTATGCTAG GGTFTTTCAT GCGCCCTTTG GGGAGTTTGT TTTTGGTAA ATTGGGGGAT | 240 |
| AAAAAGGGGC GTAAAACTTC CATGGTGTAT TCCATTATCC TTATGGCGCT AGGCTCTTTC | 300 |
| ATGCTCGCAT TGCTCCCCAC TAAAGAAATC GTAGGGGAAT GGGCGTTCTT GTTTTATTG | 360 |
| TTAGCCAGGC TTTTACAGGG CTTTAGCGTG GGAGGAGAAT ATGGCGTGGT CGcCACTTAT | 420 |
| CTCTCTGAAT TAGGCAAGAA TGGTAAAAAA GGTTTTTATG GCTCTTTCCA ATATGTAACT | 480 |
| TTAGTGGGAG GGCAACTCTT AGCTATTTTT TCGCTCTTTA TCGTTGAAAA CGTTTACACG | 540 |
| CATGAGCAAA TCAGCGCGTT TGCTTGGCGT TATTTATTCG CTTTAGAGGG TATATTAGCC | 600 |
| CTACTCTCGC TCTTTTTGAG AAATATCATG GAAGAACTA TGGATAATGA AGCGACTCCT | 660 |
| CAAAAAAGA CTAATGTAAA TAATACAAAA GAAACCCATA TCAAAGAAAC CCAAAGAGGC | 720 |
| AGTTTAAAGG AATTGCTCAA CCATAAAAAA GCCTTAATGA TAGTCTTTGG GCTAACTATG | 780 |
| GGAGGGAGTT TGTGCTTTTA CACTTTTACG GTGTATTTAA AAATCTTTTT AACCAACAGC | 840 |
| TCATCGTTTA GCCCTAAAGA AAGCAGTTTT ATCATGCTTT TAGCGCTCTC TTATTTTCATC | 900 |
| TTCTTACAAC CCTTATGCGG GATGCTTGCG GATAAAATCA AACGCACCCA AATGCTGATG | 960 |
| GTFTTTGCGA TCACAGGGCT TATTGTAACG CCTATTGTCT TTTATGGTAT CAAGCATGCC | 1020 |
| ACTAGCGTGT ATGAAGCCCT ATTTTATGAA ATACTCGCAT TGAGCAGCAT GAGTTTTTAC | 1080 |
| ACTTGCATTG CTGGGGTTAT TAAGGCGGAA TTATTCCCTG AACATGTGCG AGCGCTTGGC | 1140 |
| GTGGGTTTAG CCTATGCGAT CGCCAATGCG CTTTTTGGAG GGAGCGCGAG TTATATAGCG | 1200 |
| TTAGAGTTCA AACAGCATGG TTTTGAAGAG GGGTTTGTGG GCTATGTCAT GTTGAGTATT | 1260 |

GTTATCTTTA TGGTTATGGT TATCATATTC CCTAAAAAA CCTATTTGGA G

1311

(2) INFORMATION FOR SEQ ID NO:24298127_c3_12.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: phosphoglucomutase

| | |
|---|-----|
| ATGGACATTA GCATTTT TAG AGAATACGAT ATTAGAGGCA TTTACCCAC CACTTTAGAT | 60 |
| GAAAATACGG CTTT TAGTAT CGGCGTGGAG TTGGGAAAA TCATGCGAGA ATACGATAAA | 120 |
| AGCGTGTTTG TAGGGCATGA CGCAAGGGTG CATGGGCGTT TTTTGTTTGA AGTTTTGAGC | 180 |
| GCGGGGCTGC AATCAAGCGG CTTGAAAGTG TATGATTTAG GGCTAATCCC CACACCGGTA | 240 |
| GCGTATTTTG CGGCCTTTAA TGAAATAGAC AATATCCAAT GGCCC | 285 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| GTGTGCGACA TTTTTTCTGA TGGCGTTTTA TTGGACAAAG CGTTAGTGAT TTATTTCAAA | 60 |
| GCCCCCTATA GTTTCACCGG TGAAGATGTG TGCGAAATCC AATGCCATGG AAGCCCCCTT | 120 |
| TTAGCGCAAR ATATCCTTCA AGCTTGCTTG AATTTAGGGG CTAGGCTCGC TAAAGCGGGG | 180 |
| GAATTTAGCA AAAAAGCCTT TTAAACCAT AAAATGGATT TGAGCGAGAT TGAAGCGAGC | 240 |
| GTTCARCTCA TCCTTTGTGA AGRTGAAAGC GTTTTAAACG CTCTAGCCAG GCAGCTTCAA | 300 |
| GGGGGA | 306 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGTTTAAAA AAATGTGTTT GAGCCTGCTA ATGATAAGCG GTGTTTGTGT GGGGGCAAAG | 60 |
| GATTTGGATT TCAAGCTGGA TTATCGCGCG ACTGGGGGGA AATTCATGGG GAAAATGACG | 120 |
| GACTCTAGTC TTTTAAGTAT CACTTCTATG AACGATGAAC CGGTGGTGAT TAAAAACCTT | 180 |
| ATTGTCAATA GGGGAAATTC AGTCGAAGCG ACTAAAAAAG TAGAACCCAA ATTTGGCGAT | 240 |
| AAGTTTAAAA AAGAAAAACT CTTTGATCAT GAATTAAAT ACTCGCAACA GATATTTTAC | 300 |
| CGCCTGGATT GCAAGCCTAA CCAATTGTTA GAAGTTAAAA TCATCACGGA CAAGGGCGAA | 360 |
| TATTACCATA AATTTTCCAA A | 381 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1506 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SULFATE TRANSPORT ATP-BINDING PROTEIN CYSA

| | |
|--|------|
| ATGACCTTGA AGCCATATCC AACCAAAGAG ACTGGTCTTG CTAGCCAATT ATCTGGGCAC | 60 |
| TGGTTTTTTC AGCTTTCGTT ATTTAATAAA ACAAACCTTA ATCCTAATAA AATTTGGATT | 120 |
| CCTTTAGAGT TCAATAAAAG ATCAAAAATA AAGTTTGATA AAGATTTAGA AATCTATTTT | 180 |
| GATAGTCATG AATCGTTCAA TATCTCTAAA AAATACTTGC AAGAAATAGA TCAAGAATCA | 240 |
| CTAAAAAAGA TCAAACAATC AAAAGATTTT TTTTCAATTC AAAAAATAGA GAGTAAGCAT | 300 |
| GATAATAACG ATATACTGCA ACTTGAATTT TTTGAGAATG ATACAAGTTT TCTTTTTGCT | 360 |
| AAAGGAAGTT TTGCAGAAAT TTTAGAATAC AACATGCAAT TAAAAATAGA TTCTTTAATT | 420 |
| ACAAAAGAAT TTAATAAGCT TTTAGCGATC GTTCAAGATA GTCCCCAAGA TAGTTACCAA | 480 |
| TTAAAAATTC GTGTCCGACA TAACAATAAG CTTCTTAGAG AGAAATATAC GGAACATGAA | 540 |
| ATAAACTTG AAGTTTATGA TTGCAGAAAA TCCCACGATC ACAATGAGCC AATCATCTTA | 600 |
| AGCCAGCAAA GCACCGGCTT CCAATGGGCG TTTAATTTCA TGTTTGGCTT TCTTTATAAT | 660 |
| GTGGGATCAC ATTTTAGTTT TAACCATAAT ATTATCTATG TCATGGACGA GCCAGCCACT | 720 |
| CATTTGAGCG TGCCAGCCAG AAAGGAGTTT AGGAAATTTT TAAAAGAATA CGCTCATAAA | 780 |
| AATCATGTTA CTTTTGTTTT AGCCACCCAT GACCCCTTTT TAGTGGATAC GGATCATTTA | 840 |
| GATGAAATAA GGATTGTGGA AAAGGAAACA GAAGGCTCTG TAATTAAGAA TCACTTTAAC | 900 |
| TATCCCCTAA ATAATGCAAG CAAAGACTCC GACGCTTTGG ACAAATCAA ACGCTCTTTA | 960 |
| GGAGTGGGCC AGCATGTTTT TCATAACCCC CAAAAACACC GAATCATTTT TGTAGAAGGC | 1020 |
| ATCACGGATT ATTGTTATTT GAGCGCTTTT AAATTGTATT TGC GTTACAA AGAATACAAG | 1080 |
| AGACAACCCCA TTCCTTTCAC TTTCTTACCC ATTTCAGGGC TTAAAAACGA TTCAAACGAT | 1140 |
| ATGAAAGAAA CCATTGAAAA ACTTTGCGAG TTAGACAATC ACCCTATTGT TTTGACAGAC | 1200 |
| ATGACAGAA AATGCGTTTT TAACCAACAA GCAACGAGCG AACGATTTAA AAGAGCTAAT | 1260 |

| | |
|--|------|
| GAAGAAATGC ATGATCCCAT CACCATCCTA CAACTCTCAG ACTGCGATAG GCATTTCAAA | 1320 |
| CAAATTGAAG ATTGTTTCAG CGCAAACGAT AGAAACAAAT ACGCTAAAAA TAAGCAAATG | 1380 |
| GAATTGAGCA TGGCTTTTAA AACAAAGGCTT TTGTATGGCG GAGAAGATGC GATAGAAAAA | 1440 |
| CAAACAAAAA GAAATTTTTT AAAATTATTC AAATGGATTG CATGGGCTAC AACTTGATC | 1500 |
| AAAAAC | 1506 |

(2) INFORMATION FOR SEQ ID NO:24395801_f2_3.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| GTGTATTTTT TTCTGGCATT GAGCGGGGAA AAAGTCTTAC TGCCCGTCAT TGGCGGTTTA | 60 |
| GAAAAAACG CGCTAGAAGC CGGGCTGTTA AAGGGGGATA GAATCCTTCT ATCAACCATC | 120 |
| AAAAAA | 126 |

(2) INFORMATION FOR SEQ ID NO:24396937_c2_11.nt:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1050 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | |
|------------|------------|------------|------------|-------------|------------|------|
| ATGGAAAATT | TTAAACTCAT | CAACTTTTTT | ACCGGTCAAA | ACGATGCGGG | TAAAACCAAT | 60 |
| CTTTTAGAAG | CTCTTTATAC | CAACACAGGC | CTTTGTGATC | CTACTGCCAA | TCAAGTCAGT | 120 |
| CTTCCTCCTG | AACATGCCGT | GAATATTAGT | GAATTCAGAA | AAATCAAAC | CGATGCCGAC | 180 |
| AACCTAAAAA | CCTTTTTTTT | TCAAGGAAAC | ACCGCTAATC | CCATTAGTAT | CCGCACTGAA | 240 |
| TTTGAACATG | CTACTATCCC | TCTTACTATC | CAATACCCCA | CACAAACCAG | TTACAGCAAA | 300 |
| GACATCAATT | TGAATAGCGA | TGATGCTCAT | ATGACAAACC | TTATAAACAC | AACAATAACG | 360 |
| AAGCCACAGC | TCCAATTTTC | CTACAATCCA | TCCCTTTCCC | CCATGACAAT | GACTTATGAA | 420 |
| TTTGAAAGGC | AAAACCTAGG | TTTAATCCAT | TCTAATTTAG | ATAAAATCGC | TCAAACCTAT | 480 |
| AAAGAAAATG | CGATGTTTAT | TCCTATAGAA | TTATCTATTG | TTAATTCTCT | TAAAGCATTG | 540 |
| GAAAATTTAC | AATTAGCAAG | CAAAGAAAAA | GAATTGATTG | AAATCCTACA | ATGTTTCAAC | 600 |
| CCTAATATTT | TAAATGCTAA | TACAATAAGA | AAGTCTGTCT | ATATCCAAAT | CAAAGATGAA | 660 |
| AACACACCGC | TAGAAGAAAG | TCCCAAAAGG | CTTTTAAATT | TGTTTG GTTG | GGGTTTTATC | 720 |
| AAATTCTTTA | TTATGGTGAG | CATTCTTATA | GACAATCGTG | TCAAGTATCT | TTTTATTGAT | 780 |
| GAAATAGAAA | GCGGTTTGCA | CCATACAAAA | ATGCAAGAGT | TTTTAAAAGC | TCTGTTTAAG | 840 |
| TTAGCTCAAA | AATTACAGAT | TCAAATTTTT | GCCACCACGC | ACAATAAGGA | ATTTTTATTA | 900 |
| AACGCCATCA | ACACGATATC | CGATAATGAA | ACGGGAGTTT | TTAAAGACAT | AGCCTTGTTT | 960 |
| GAGCTTGAAA | AAGAAAGCGC | TTCTGRCTTT | ATCAGACACA | GCTATTCTAT | GCTAGAAAAA | 1020 |
| GCGCTTTATA | GGGGTATGGA | GGTTAGAGGC | | | | 1050 |

(2) INFORMATION FOR SEQ ID NO:24406401_f3_32.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1395 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|--|------|
| ATGGATTTTA AAAAATGCCC TAATTTTGAA AAAAAATGTG CGTTTCTTTG TTTCTCAAAT | 60 |
| TTGGTTTTTAC TTATTGAAAT CCACTCTAAA GGACTACACA TGCAAAAAAA GAAACCCAAG | 120 |
| AACCCGCAAC CGAATTTATT TAGCATCTTA GATAAGGGCG ATGTTGCAAC AAACAATCCT | 180 |
| GTTGAAGAGT CAGACAAGGC CAATAAAATA CAAGAGCCAC TCCCTTATGT CGTGAAAACG | 240 |
| CAAATCAATA AAGCAAGCAT GATTTCTAGA GATCCTATTG AATGGGCAAA GTATTTAAGC | 300 |
| TTTGAAAAAC GAGTCTATAA GGATAATAGT AAAGAAGATG TCAATTTCTT TGCCAATGGT | 360 |
| GAGATAAAAG AAAGTTCTCG TGTTTATGAA GCGAATAAAG AAGGGTTTGA AAGGCGCATC | 420 |
| ACTAAAAGAT ACGATCTGAT TGATAGAAAT ATTGATAGAA ATAGAGAATT TTTTATAAAA | 480 |
| GAAATTGAAA TTCTAACCCA CACAAACAGC TTAAAAGAAT TGAAAGAGCA AGGGTTAGAA | 540 |
| ATCCAATTGA CCCACCATAA TGAAACGCAT AAGAAAGCCT TAGAAAATGG CAATGAAATC | 600 |
| GTAAAGAAT ACGACCATCT TAAAGATATT TACCAAGAAG TAGAAAGAAC AAAAGATGGT | 660 |
| GGATTGGTAA GAGAAATAAT CCCCAGTATT TCTAGCGCTG AGTATTTCAA GCTTTACAAC | 720 |
| AAACTGCCTT TTGAATCAAT AAACAATGAA AATACCAAAC TGAATACTAA CGACAATGAA | 780 |
| GAAGTTAAAA AACTAGAATT TGAATTAGCT AAAGAAGTGC ATATTTTAAT CCTAGAGCAA | 840 |
| CAATTGCTTT CAGCAACAAA TTATTATTCT TGGATAGATA AAGATGATAA TGCGAATTTT | 900 |
| GCTTGGA AAA TGCATAGGCT TATCAATGAA AATAAACTCA AAGAAAACCA TCTCAGCGCC | 960 |
| AATAACGCTA ATAAGATTAA GCAATTTTTC TTTAATAATG GTTCTATTTT AGGCTGGACT | 1020 |
| AAAGAAGAAC AAAGCGCTAT ACAAGAAAAC AGAGATTATT CTTTAAGAAG CGCTCTTTTA | 1080 |
| AGTTTAGAAG AAATCGCTCA AGCAAAAATT GAATTGCAAA AATACTATGA AAGCGTTTAT | 1140 |
| GTTAATGGTG ATGGGAATAA AAGAGAAATC AAGCCTTTTA AAGAAATTTT AAGAGACACC | 1200 |
| AACAATTTTG AAAAAGCTTA TAAGGAGCGT TATGACAAAT TGGTAAGCTT GAGTGCAGCA | 1260 |

| | |
|---|------|
| ATCATTCAAG CTAAAGAGGG TGGTAATGAG CGACAAAATT CTAGTGCAA TAACAATAAC | 1320 |
| CCTATTAAAA ATACAATAGA GACTAATACT TCTAACAATA TTATTCAAAA TAATGATAAT | 1380 |
| ATAATCATCC AAATT | 1395 |

(2) INFORMATION FOR SEQ ID NO:24407533_c1_9.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|--|-----|
| ATGGCGCTTG AAGTGGTTTT ATGGGATTTT GATGGCGTGA TTTTGTGACAG CATGCATTTA | 60 |
| AAATATGAAG GGTTTAAGGC GTTGTTTCAA AAGCATGGCA ACGATAGTAA AGAGGGTTTG | 120 |
| AAACAATTTG AAGTTTATCA CTATCAAAGT GGGGGGATTT CAAGGAATGA AAAGATCCAA | 180 |
| TATTTTTATA ACGAGATTTT AAAAACCCTT ATCGCTCAAG AAGAAATAGA TGCATTAGCC | 240 |
| CTAGAGTTTG GCGCTATCAT AGAGCAAAAG CTTTTTGATA GGGGGCATTT GAATAGCGAR | 300 |
| GTGATGGCGT TTATTGATAA GCATTATCAA AATTATATTT TCCATATCGC TTCAGCGGCC | 360 |
| TTGCATAGCG AATTGCAAGT GTTGTGCGAG TTTTtaggga TTAactaagta TTTTAAGAGC | 420 |
| ETTGAAGGGA GTCCGCCTGA TAAACCCAAG ATTATCGCTA ATATCATTCA AAAATACGCC | 480 |
| TATGACCCAA GCCGTATGCT AATGATAGCG ATAGCGTCAA TGATTATGAA AGCGCTAAGG | 540 |
| CTAATAAAGT GGCgtttttg GGCTATAACA GCAAGGTTT | 579 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 423 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|--|-----|
| ATGCTCAAAA AAAAGATTGA TTTGCATAAA GATTCTATTA GGAAGCTCTT TTTTATTAC | 60 |
| TTCATCCCTT TAGTTTTTTC TATGATCTCA CTTTCTACTT ACTCTATGGT AGATGACATG | 120 |
| TTTGTGGGCA AAAAAGTGGG TAAAGAAGCT ATCGCTGCGG TCAATATCGC ATGGCCTATT | 180 |
| TTTCCAGGAC TCATTGCGTA TGAATTGCTT TTTGGTTTTG GGGCAGCGAG CATTGTGGGG | 240 |
| TATTTTTTTAG GTCAAAATAA AACCCATAGG GCTAGGCTTG TGTTTAGCAG CGTGTTTTAT | 300 |
| TTTGTCGCTC TAAGCGCCTT TATTTTGAGC ATGGCGTTAT TGCCTTTTAG CGAAAATATC | 360 |
| GCGCAGTTTT TTGGGAGCAA TGACGCTTTA TTGAACATGT CAAACGCTAT ATTGAAATCA | 420 |
| TTT | 423 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| GTGAAATGTT TATTAATAAA AAAATCACTT CTATTTCAC TGAAACCATT GCCGGACCTA | 60 |
| AAAACGACTA CCCCTATTTT AGCGCCTATG AGCGTGGTGG CTGGGAGGTT GRCTSCSCAT | 120 |
| TTAGTCCAGC ATTATTTACT GGCTTTAGAG CATGTTAAAG GGTTTATGGG TAAGGGGGTC | 180 |
| ATACTAGGGG GTTTGTCGGG TGCSCAAAGG GCTAAAATCG TCGTAATTGG AGGCGGTGTG | 240 |
| GTTGGCATGG AGAGCGCGAA AGTCTTAARC CAAATGGGGR CTAAAGTAAC GATTTTAGAA | 300 |
| TTAGACTACG CTAAATTACA AAACCACCCT TATTATCATT TGTATGATTT AGAAGTCTTA | 360 |
| AGCGTGAATG AAGCCAATAT CATTCAAGCC TTAAACGGGR CGGTGGGGCT AGTGGGAGCG | 420 |
| GTRCTGGTTA CARCGAGCCA AACCCCTAAA GTGRTCTTAA GAAGGCATTT AAAATAC | 477 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1128 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|------|
| ATGCTTGCAA AAATCGTTTT TAGCTCATTG GTTGCGTTTG GAGTTTTGTC GGCTAATGTG | 60 |
| GAGCAGTTTG GTTCATTTTT CAACGAGATA AAAAAAGAAC AAGAAGAAGT GGCCGCAAAA | 120 |
| GAAGACGCTC TTAAAGCTCG CAAGAAGCTC TTAAACAATA CGCATGATTT CTTAGAAGAC | 180 |
| TTGGTTTTTA GAAAACAAAA AATCAAAGAG CTTGTGGATT ACAGAGCTAA AGTTCTTTTA | 240 |
| GATTTAGAAA ACAAGTACAA AAAAGAAAAA GAGGCTCTAG AGAAAGAGAC AAGAGGTAAA | 300 |
| ATCCTTACTG CTAAGTCAAA GGCTTATGGT GATCTAGAGC AAGCCTTAAA AGATAACCCT | 360 |
| CTTTATAAGA AACTTCTTCC TAACCCTTAT GCTTATGTTT TAAACCAAGA AACATTCACG | 420 |
| CAAGAAGATA AGGAGCGTTT GAGTTATTAC TACCCCAAG TGAAAACGAG CAGTATTTTT | 480 |
| AAAAAACTA CCGCTACCAC TAAAGATAAG GCTCAGGCTT TGCTTCAAAT GGGTGTGTTT | 540 |
| TCTTTAGATG AAGAGCAAAA CAAAAAGCG AGCCGATTAG CTTTATCTTA CAAGCAAGCG | 600 |
| ATTGAAGAAT ATTCCAATAA CATTTCTAAT TTATTGAGCA GAAAAGAATT GGATAATATA | 660 |
| GATTATTACT TGCAGCTTGA AAGAAACAAA TTTGACTCCA AAGCAAAAGA TATTGCTCAA | 720 |
| AAAGCCACCA ACACGCTTAT TTTTAACTCG GAACGCTTGG CGTTTAGCAT GGCGATTGAT | 780 |
| AAGATCAATG AGAAATACTT AAGGGGCTAT GAAGCTTTTT CTAAGTTGTT GAAAAATGTC | 840 |
| AAAGATGATG TGGAGTTGAA TACTTTGACT AAAAAGTTCA CCAATCAAAA ATTGAGTTTC | 900 |
| GCACAAAAAC AAAAATTGTG TTTGTTGGTT TTAGACAGCT TCAATTTTGA TACCCAATCC | 960 |
| AAAAAATCTA TATTAAAAA GACTAATGAA TACAATATCT TCGTAGATAG CGATCCTATG | 1020 |
| ATGAGCGACA AAACAACAT GCAAAAAGAA CACTACAAGA TATTTAATTT CTTCAAAACA | 1080 |
| GTGGTTTCTG CATAACGGAA CAATGTTGCC AAGAATAACC CCTTTGAA | 1128 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1056 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|------|
| ATGGATTTCG TAGGGTTTGA AGATTTAAAA TGCAAAGACA AAGAAAAGTC TCAAAAAGTT | 60 |
| TTTGTGATCC GTAACGATAA GTTAGGCGAT TTTATTTTAG YGATTCCCGC TTTAATCGCT | 120 |
| CTCAAGCATG CTTTTTTAGA AAAAGGCGTA GAAGTGTATT TGGGCGTGGT TGTGCCTAGC | 180 |
| TATACCACCC CAATTGCTTT AGAATTCCCT TTCATTGATG AAGTTATCAT AGAAGACAAC | 240 |
| CATTTAGCCA CCACCCYCAA AAACCGCTCC ATTGACGCTC TTATCTTTTT ATTTTCTAAT | 300 |
| TTTAAAAACG CCAAAGTCGC TTTCAGTTTG AGAAAATCCA TCCCTTATAT CCTAGCCCCA | 360 |
| AAGACCAAAA TCTATTCTTG GCTTTATCAA AAGAGAGTGC GCCAAAACCG CTCTTTATGC | 420 |
| TTAAAAACCG AATACGAATA CAATTTGGAC TTAATCCATG CGTTTTGTAA AGACTACGAT | 480 |
| CTCCCTAACG CTCAACTTAA AAAAATCGCA TGGAAGCTTA AAGACAAATC CAAAGAGCGA | 540 |
| TCCATCATCG CTTCAAAACT CAACGCTAAT GTTGATCTAT TGTGGATTGG CGTGCATATG | 600 |
| CATAGCGGAG GCAGTTCGCC CGTATTGCCC GCTTCGCATT TCATTGAGTT GATTGCAATC | 660 |
| TTGCATGAAA AATTAAGTTG TGAGATCATT CTTATTTGCG GGCCAGGCGA GAGAAAAGCC | 720 |
| ACAGAAGAAC TCCTTAAAGA AGTCCCTTTC GCTCACCTCT ATGATACGAG CCATAGTTTA | 780 |
| GTGGATTTAG CCAAATTGTG CGCGAATTTA AGCGTCTGTA TCGGGAACGC TTCAGGCCCT | 840 |
| TTGCATGTGA ACGCTTTATT TGACAACCAA TCTATCGGGT TTTACCCTAA CGAACTCACC | 900 |
| GCCTCTATTG CCAGATGGCG GCCTTTCAAC GAACAATTTT TAGGCATCAC CCCGCCTAAT | 960 |
| GGCTCAAACG ATATGGGTTT GATTGACATT CAAAAGAAA GCGAAAAGAT TATGGGATTT | 1020 |
| ATCACAAAAA ATCTTTCTCA TCACATGCAA GAAAGA | 1056 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| GTGGGTGTCT TATCCCTCAA AATAGAGGCA ATTTCTAATT TTTATGGGTT ATGCGTTTTA | 60 |
| GGGGTGTTGT TAGCATGTTT TTATCTTTTA GACGCTTATT ATCTCATGCA AGAAAGGCTG | 120 |
| TTTAGGGAGC AATACCAATG GCTAATAAAA AACCGACTTA AAACCGATGA AAGGCTGTTT | 180 |
| GAAGTCTTCC CTATTCATCA AACTTGCCAA TCAACGCAAT TCTTATCGCC ATGCGTTCGT | 240 |
| TTAGTCTTTT CCCCTATTGG GCGT | 264 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|--|-----|
| ATGTCTTTAG GGGCAGTGGT CAGCTCACTC CTTTGCCATA AGTTAGAGGG GGCAATATTA | 60 |
| GATCTGAGAG CGTATCGTTS RARAGCTTAT TATCACGAAA ATAAAGATAC YTTGCTTATT | 120 |
| AAAGGCAAAA AACGCCTTCT TTACAATTAT ATTAAAGCCC ATATTGYTTT AAACCTTGCTA | 180 |
| TGGACAATTA GAAATCGCAC GTRATCATTG GGAAAATTTA CTCAAAATCC AACCGAACAA | 240 |
| CCGCCCACGA ATAACCACAC CATTCAATGG AAAAACRGAA AACATTCTAA TGGACAGAAT | 300 |
| TTTAGTGATT GGTAT | 315 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|--|-----|
| ATGAAAAAAAA CAACCCTCTT TGTATTGGGC TTATTATTCA ATAGCTCTTT AAGCGCTGTT | 60 |
| GATGGGATTT CTCAAACCGA GCCTTCTTCT TTGAATTGCG CTGAAGATAG CCTGCCTTTG | 120 |
| AACCATTCTA ACGCCCAAAA ACTCTCTTTA AAAAACGCAT GGAATAGGGT GTTGTCTAAT | 180 |
| CATGAAGGCT TGCATGCGCA GAATACGCCA TTAAGCGAGC GAGTAAAA | 228 |

(2) INFORMATION FOR SEQ ID NO:24416083_f3_16.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 294 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| GTGAAAAAAG TAGAATCCAT GAATGTGGTG CCTTTCATTG ACATCATGCT TGTGTTGTTA | 60 |
| GTGATCGTGC TCACAACGGC GTCTTTTGTG CAAACTTCAA AGCTTCCTAT TAGCATTCCT | 120 |
| CAAGTGGATA AGGATAGCAC TGATTCTAAA GATGTGTTGG ACAAAAAACA AGTTACGATC | 180 |
| GCTATTTCTA ATAAGGGTTC TTTTATTTT GACGATAAAG AAATCAGCTT TGAAAATTTA | 240 |
| AAACACAAGG TTTCCACTTT GGCTAAAGAC ACCCCTATTG TCTTTGCAAG GCGA | 294 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 486 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|--|-----|
| ATGGGATCTT ACACATTCCC TCTCATTTTG AAGCCAATAT TTATAAACAA AGTGCCTGTA | 60 |
| ACGATAGATT TTTATGCGAA CGCCAATTAC TTTTGTGATT ATGGTGCGTT AGCGAATGCG | 120 |
| GTGGTGGGGA GCATCAACGC CTTAAACGAT GAAATCAGGT TCAAACGCAA CGCCCAAATA | 180 |
| GAAGAAGCTG AATTAGGGAC AGACGGGATT AAGATTAAGC CTATCGCTTT GTATAACCCT | 240 |
| AGTGAGGGGT ATTTGAATTA CGCGCTCTCT AGCGTGTTTA TTTTCATCTT ACACCAGGTG | 300 |
| ATGCTCATTG CAAGCAGCAT GTTTACTAGC TCCAGGCGTT TGGAATTGGC CCTTTTAGAC | 360 |
| AAGAAACAAA TCGCTTTAAG GCTGTGCGCA AGACTCTTGG TGTTTCATGGG GGCGTTTAGC | 420 |
| GTTTTTGTTT TATGGTATTT TGGGGCGCTG TTTTCTTTTT ATGGGATCGA ACGGCATGGA | 480 |
| AGCGCT | 486 |

(2) INFORMATION FOR SEQ ID NO:24427340_f1_1.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| GTGATTATGA CTAAGCTTGA TGGCACTTCT AAGGGCGGAG CGATTTTARG CGTGCTGTAT | 60 |
| GAGTTGAAAT TACCCATTCT TTATTTAGGA ATGGGCGAAA AAGAAGACGA TTTGATCGCT | 120 |
| TTTGATGAAG AACGCTTTAT AGAAGATTTG GTTGATGCGG TGTTTGTGGA ACAA | 174 |

(2) INFORMATION FOR SEQ ID NO:24441412_f3_3.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| GTGTGTGGGG CTCATGGAAA GAGCAGTATC ACGGYCATGT TGAGCGCGAT TTGCCCCGCT | 60 |
| TTTGGASSGA TTATTGGGCG GCATTCTAAA GAGTTTGATT CCAATGTSSG AGAGAGCGCG | 120 |
| GATATGAGTT TGGTTTTTGA ASCCGATGAA AGTGATTCAA GTTTTTTTAT TTTCCAACCC | 180 |
| TTTTTGC GCG ATTGTGCC | 198 |

(2) INFORMATION FOR SEQ ID NO:24492192_c2_9.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: ONE OF THE DIFFERENT ANTIGENIC SEROTYPES OF PROTE

| | |
|---|-----|
| GTGAATGAGT TAAAAAACTC TAAGCAAGTT TTAGGGAATG GGAAAGCCGA TCTGAGCAAC | 60 |
| GAAAACACCA AGGTAAGGCA GACTAAAACA RATCTGACTG AAAAAAATCA AAGGCTAACC | 120 |
| ACAGAAAAAA CAGAATTAAA TAACAAGATT ACTGGGTTAG CCACAGAAAA AGAAAGGTTA | 180 |
| GCCGCAGACA AAGAAAACCT AACTAAAGAA AGCAGACAAA GAAAACCTAA C | 231 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 555 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGGATTTAC AACAAATTGA TGAGCTAGAA AATAAGTTTG AAGAACAAGA AGAACAAGCC | 60 |
| CAAGATACCC CCCTAAAACA AGAGCCTAGC ACAAAGGAAG TAAAAATCCC TAAAAAAAGG | 120 |
| GGGCGTAAAA AAAGCTTGTT AGATGAAGAT AAGAAAAAGA GCTTTAACAT TGCCTTTAGT | 180 |
| CCTTGTGTGA TAAAAGAACT TAATGAATTT TTGCTAGAAT TTGGCTCATT TAAAGAGACA | 240 |
| CGAAGCACTT TTATTGAAGA AGCGCTTATT AGGCATTTAA AACACAGAAA AAACACCCAA | 300 |
| GAGCAAAAGC TTTTAAAGCA ACTAGAAAGA TTACAAAACA AAGAAAAGGG AATAATGAAA | 360 |
| ACAATGAACT TGAATGAATT TTTTACGCAT AAGATAATCT ATAAAGACAC CCCTTTAAAG | 420 |
| TTTAAGGATA CACTAGAACA AGAAATCAGC CAAGCTAGTT TAGTAGAGAA GTTAATCTTA | 480 |
| GCTAATATCT TAGCCAATAT GGTGTTTGCT AAGATAAGCA ATGAGAATGC CCCTAAAATT | 540 |
| CTTATTTTCA CGGCT | 555 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGGGGTGCT ATGGGATAGG CATTAGCCGG TTGCTCAGCG TGATTTTAGA GCAAAAAAGC | 60 |
| GATGATCTAG RCTGTGTGTG GACGAAAAAT ACCGCTCCTT TTGATGTGGT GATCGTGGTT | 120 |
| TCTAACCTGA AAGATGAAGC GCAAAAAAAA CTCGCTTTTG AAGTGTATGA AAGACTGCTC | 180 |
| CAAAAGGGCG TTGATGCGCT GTTAGATGAC AGAGACGCTC GTTTTGGGGC GAAGATGAGG | 240 |
| GATTTTGAAT TGATTGGGGA ACGATTAGCC TTGATTGTTG GGAAGCAAAC TTTAGAGAGT | 300 |
| AAGGAATTTG AATGCATCAA ACGCGCTAAT TTAGAAAAGC AAACGATCAA AGACATAGGA | 360 |
| ATTAGAAGAA AAAATTTTAG AAATGTTAGC GAGCGAATAA GGGGAGGGAA TGGAAAAAYT | 420 |
| AGTGATTGGC TC | 432 |

(2) INFORMATION FOR SEQ ID NO:2458267_f1_1.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|--|-----|
| ATGGAAATAC AACAAACACA CCGCAAAATC AATCGCCCTT TAGTTTCTCT CGTTTTAGCA | 60 |
| GGAGCGTTGA TTAGCGCCAT ACCGCAAGAG AGTCATGCCG CCTTTTTTCAC GACCGTGATC | 120 |
| ATTCCAGCCA TTGTTGGGGG TATCGCCACA GGCCTGCTG TAGGAACGGT CTCAGGGCTT | 180 |
| CTTAGTTGGG GACTCAAACA AGCCGAAGAA GCGAATAAAA CCCCAGATAA ACCCGATAAA | 240 |
| GTTTGGCGCA TTCAAGCAGG AAAAGGGCTT | 270 |

(2) INFORMATION FOR SEQ ID NO:24609431_c2_15.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 804 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGTCAGAAA AAGAAAGACT GAATGAAGTG ATCTTAGAAG AAGAGAATAA TGGGAGTGGT | 60 |
| ACTAAAAAGG TGTTTTTGAT CGTGGCCATA GCCATTATCA TTTTGGCGGT GCTTTTAATG | 120 |
| GTGTTTTGGA AAAGCACCAG AGTCGCTCCT AAAGAGACTT TTTTACAAAC CGATAGTGGC | 180 |
| ATGCAAAAAA TAGGCAACAC TAAAGATGAG AAAAAAGACG ATGAGTTTGA AAGCTTGAAT | 240 |
| ATGGATTCTC CCAAACAAGA AGACAAGTTA GACAAAGTGG TGGATAATAT TAAAAACAA | 300 |
| GAGAGTGAAA ATTCTATGCC CATTCAAACC GATCAAGCTC AAATGGAGAT GAAAACAACA | 360 |
| GAAGAAAAAC AAGAATCTCA AAAAGAATTA AAAGCTGTTG AGCCTATTCC CATGAGCACT | 420 |
| CAAAAAGAAT CTCAGGCTGT GGCTAAAAAA GAAACCCCCC ATAAAAAGCC TAAAGTAGCG | 480 |
| CCAAAAGATA AAGAAGCGCA TAAAGRTAAA GCTAAGCATG CAGCTAARGA GCCAAAAGTC | 540 |
| AAAAAAGAAG CTCGTAAAGA AGTTTCTAAG AAAGCTAATT CTAAAACCAA TCTTACTAAA | 600 |
| GGGCATTATT TGCAAGTGGG GGTTTTTGCG CACACGCCCA ACAAAGCCTT TTTACAAGAG | 660 |
| TTTAATCAAT TCCCCATAA AATTGAAGAT AGGGGGGCTA CTAAACGCTA CCTYATAGGY | 720 |
| CCTTATAAGA GCAAGCAAGA AGCCTTAATG CATGCCGATG AAGTCAGCAA GAAGATGACT | 780 |
| AAACCGGTTG TCATAGAAGT GCGG | 804 |

(2) INFORMATION FOR SEQ ID NO:24609593_f2_2.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: ferric enterobactin transport protein fepC

| | |
|---|-----|
| GTGGAATATT ATGCGTTTAA TTTCAGCGTG TTGGATTTTG TCTTAATGGG GAAAGCGACG | 60 |
| CATTTGAATC TGTTGCTAT GCCTAAAGCT AAGCACATTA AAGAAGCCAC GAGCGTTTTA | 120 |
| GAGCGCTTGG ATTTAGAGTC CTAAAAAGAT CAAGGCATTA ACGATTTGTC CGGCGGTCAA | 180 |
| AGGCAGATGG TACTTTTAGC CAGAAGCTTG TTGCAAAGAA CGCCCTTATT GTTACTGGAT | 240 |
| GAGCCTACGA GTGCGTTAGA TTTAAAAAAC CAAGCCCTTT TTTTGTATGC GATTAAAGAT | 300 |
| GAGATGAAAA AACGAGAATT GAGCGTTTTA GTCAATATCC ATGATCCCAA TTTGGTTGCC | 360 |
| AGGCACTCCA CGCATGTGGT CATGCTCAAA GATAAAAAAC TTTTTTTGCA AGCTTCCACG | 420 |
| CCAATCGCTA TGACTTCACA CAATTTAAGC GCGCTTTATG ACACGCCCCT ARAAGCGATC | 480 |
| TGGCATGATG ATAAGCTTGT GGTGTATGCG TTG | 513 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGATGGCAC ATTCACTTAT TTTGGTTTCA AAAACATCAC TCTCCAACCT GCTTATTTTT | 60 |
| GTGGTTCAAC CTGATGGGAA ATTGAGCATG ACTGATGCCG CCATTGATCC TAACATGACT | 120 |
| AATTCAGGAT TGAGATGGTA TAGAGTTAAT GAAATTGCAG AGAAGTTTAA GCTCATTAAA | 180 |
| GACAAAGCCC TTGTAACAGT GATCAATAAA GGCTATGGGA AAAATCCATT GACAAAAAAT | 240 |
| TACAATATCA AAAACTATGG TGAATTGGAG CGTGTGATTA AAAAGCTCCC TCTTGTGAGA | 300 |
| GATAAA | 306 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 711 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| GTGCTGAATG AAGAGCAAAA TTCATTAGAA GAAAAAGGGG GCGAAAACAA AAACGAAAAA | 60 |
| AAAACCCCCC TAAAGGGCAT TCATTCTAAA ATCCCCTCTT TGAAGCAGGC TTTGGAGCAG | 120 |
| ACGATTAGTA AAATCAAAAG CTCTAAAGAG TTTTTCAAAC AGCTTCTACA CAATAAAAAA | 180 |
| AAGCTTTATA TCGCGCTTGG AATATTGCTT TCACTCATCG CGCTCATTGT GGCTTTGAGT | 240 |
| TTGTTACTAG GGCATAAAAA AGAAAATAAA CAAACTTCTT TACAAACTAA TACCGCCACC | 300 |
| ACCAATAACG AAACGCCTAA CGACACCAAT AACGCAGAAG CCGAAGGGCA AATAGAAAAT | 360 |
| TTAGACTTGC CTGATTTAAT CGGCAAAGAC TCTTTGAAAA GAAACGATGA AAGCCAAGTG | 420 |
| BATGCGATGA TGCAAAAAGC GAGCCTTTTG TATGAGCAAG GGCAAAAAGA TGAAGCCTTG | 480 |
| CATTTGTTTG ATAAGATCGC TTCTTTCTCG CAAGGGATTG CGAGCCATAA TCTAGGGGTG | 540 |
| ATTAAATTCA AAGAAAAGGA TTTTAATGGG GCGTTGGATT TGTTTGATTC CAGTATCGCT | 600 |
| TCTAAAGAAA ACGCGAGCGT GRGCGCGATT GATGCGTTAG TTACGGCTTA TCATTGCAA | 660 |
| BATGCGGATT TGTATTATCA TTATCTAAAA ATTGTRAAGA GACACTTGT A | 711 |

(2) INFORMATION FOR SEQ ID NO:24651083_c2_5.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 675 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGAATACAA GCTTATTGAC CCAAGCACAG GTTTTAAGCT CTAAAGAAAA TCAAATCCAT | 60 |
| CGCCTTTTGT TAGAGCTTTT AGAAGAGGCT AAGCTTCATT TTGAGCCTAA GCTTTATATC | 120 |
| ATTAACGCCC CTTACATGAA CGCTTTTGCG AGCGGGTGGG ATGAATCTAA TTCCCTTATC | 180 |
| GCTCTTACAA GCGCTTTAAT AGAGAGGTTA GATAGAGACG AATTAAAAGC CGTGATCGCT | 240 |
| CATGAGCTCA GCCACATACG GCACAACGAC ATCCGCTTGA CCATGTGCGT GGGGATTTTG | 300 |
| AGCAATATCA TGCTATTGGT GGCTAATTTT AGCGTGTATT TTTTCATGGG GAATCGCAAG | 360 |
| AATAGCGGGG CGAATTTAGC CCGAATGATT TTATGGGTTT TACAGATCAT CTTGCCTTTT | 420 |
| TTAACGCTCC TTTTGCAAAT GTATTTGAGC CGCACACGAG AATACATGGC CGATAGCGGG | 480 |
| GCGGCGTTTT TAATGCATGA CAATAAGCCC ATGATCAGAG CCTTACAAAA GATTTCTAAC | 540 |
| GATTACACCA ACAACGATTA TAAAGAAATA GATAAAAATA GCACCCGATC AGCGGCCTAT | 600 |
| CTTTTAAACG CTGAAATGTT TAGCACCCAC CCTAGTATTA AAAATCGTAT CCAATCCTTA | 660 |
| AGAAAGCGTG TGATC | 675 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1605 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|------|
| ATGTTTAATA TTAAAAGGAC TTTTSTAATA ACGATCATAA GTTTTTTTTCT CATTGTTTCCT | 60 |
| AATTGGTTGA AAGCTATTGA TTTGCCCAT TTTTCAAATC TCAAAATTTA CCAAACAGTT | 120 |
| TATTGCATGC TGATACCGAG TTATGTTTTA ACCAACAAAA GTTTTGCAGA TATTTTGACA | 180 |
| GGCTATACAT CTATTGGTGC ATCAGGGAGT GGAAAGAGTT CAGGGCAGGG TGTGATCGAA | 240 |
| GCGCTTAGCA CACCATTAGC CACAAGTTTA GCCGCTAGCA ATCTGGTGAA ATATTTGAAT | 300 |
| ACTTTAGGTC CTTTATGGGG ATCGGCGTGG GCAAGTGTTG CTACAGCTAT ACAAGGTTTT | 360 |
| GCTCTAACGC CATCAAGTGG CTGTAATTTT GGTGGAACG CATTGATAAA TAAAAACATA | 420 |
| GATGTATCCA TGGATAGCGT ACTAGACAAT TTGAGCAACA AGATTCAGAA TTTTACCAAA | 480 |
| GGCGGTGTTG AGGACAATGT GAAAGGCAAT ATTCTTTTAC AAATAATTGG CTCAATAACC | 540 |
| GCTCAAGCTT CTACGAATAT TACAGCTGAT GGTTTAATTT GGCTGATTGG TAAAGAATTC | 600 |
| ACTGCAAATA AACTGCAAAA CAACACTATA GCCATGCTTG CTTTGGCCGC ATTAGAATCT | 660 |
| GTTGTCAAAG GAGCGGACGC TGCTGTTCTT CCTGCATATG GTGTAGTCAA TCTGCCTGAT | 720 |
| ATTATCATAG GGCAAGGGTC ATATCTTGAT TTTGTTTCTT ACCTAATTTA TATTGTTTTT | 780 |
| GGGATTTTTG TTTTATTTT TTTTATGAAA TTGAGAGATA TTTCAAACGG CATTGAGATT | 840 |
| AACATAGGTT TTGAATACAT GCGATTTGTT GGGGGGACAT TATTCAAAAT GGCGATGGTC | 900 |
| TCTTTTATCG CCTATGCAGG TTTTGGTTAT CTTTATAAAA TCTCTTATTC TATTTATTTT | 960 |
| GGTTTAGCAG GTGCTTTTGG GCTGAATCAA GTTCTTTTTT GGGCTTTAGA TTTAGTGCTG | 1020 |
| AATTACACTG TTAATTCAAT TTTACCTGCG GTAAGAGCTG TTTTTTCTAA TGTTGGCAAC | 1080 |
| AACGCTCCTA GTTTGTTACA AGGCTTGCAA GTGGCAGGTA TTTCTTTATT CGCTATTTTT | 1140 |
| ATGCAAGTAA CTATCATTAT GAGAATAAGC ACTGTTGTTG TGAAACCTTT GATAGCGGGG | 1200 |
| GCTTTTAGCG GTATTGTTTT CCCTATTGCA GTATGTTTGA TCGTGCTAGA TTGGTTCAAA | 1260 |

| | | | | | | |
|------------|------------|------------|------------|------------|------------|------|
| GATTCTATGA | AAAACATATT | GATATGGTTT | ATTAATAATC | TGTTTATCTT | GGTTCTAGCT | 1320 |
| ATTCCTATTT | TGCTCTTTGG | TGTTTTGGCA | TTATTGGCAT | TCAATTTGAC | CATAACGCCC | 1380 |
| TCTGTTGCTA | TACAAAACAT | CAATCAAGGG | GGATTGGGTA | TCGATTCAAC | TATTGCGAGT | 1440 |
| TTGATCACTC | TATTTATTTT | AAAAGGTTTC | ATAGAGACGA | TTATTGAGAG | CGTCAATGCG | 1500 |
| ATCGTTAACA | CCATTTTCAG | CTCTGTCTCT | ATGGATGGTA | GCAGAATGGA | TAGAGAAAGA | 1560 |
| GATGCCTTAA | TGGTGGGAAG | AGTTGGTGGA | TCTATGTTTA | AAGGA | | 1605 |

(2) INFORMATION FOR SEQ ID NO:24803280_f3_7.nt:

2/2

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGGCGTTTT GGCAGGCTAT CCGGTGGTGG ATTTTAAAGT TACCCTTTAT GATGGGAGCT | 60 |
| ACCATGATGT GGATTCTTTC AGAAATGGCG TTTAAAATCG CTGGYTYTAT GGC GTTTTAAA | 120 |
| GAAGCGAGTC GTGCGGCTAA CCCGGTTTTA CTAGAGCCTA TGATGAAAGT GGAAGTGGAA | 180 |
| GTCCCTGAAG AATACATGGG CGATGTGATT GGCGATTTAA ACAGAAGAAG AGGGCAAATC | 240 |
| AATTCTATGG ACGATAGATT AGGTTTGAAA ATCGTGAATG CTTTCGTGCC GTTAGTGGAA | 300 |
| ATGTTTGATT ATTCTACGGA TTTGCGATCA GCCACTCAAG GGCGTGGGAC TTACTCTATG | 360 |
| GAGTTTGACC ACTATGGCGA AGTGCCTAGC AATATCGCTA AGGAAATCGT GGAAAAACGC | 420 |
| AAAGGC | 426 |

(2) INFORMATION FOR SEQ ID NO:24806290_f1_1.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 459 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGCAGAATT TGCCGGGTAT GGCGAGAGCG GCGATGCTAA CCACATCATC AGCCCCAGCC | 60 |
| CCTGAGGGTG AAGGGGCTTT TAGAGCCATG AAAATGGCTT CAGAAATGGC GAAAGTGGAA | 120 |
| GTAGGCTATG TGAACGCCCA TGGGACAAGC ACGCATTATA ACGATTGGTA TGAAAGCATT | 180 |
| GCGTTAAAAA ATGTGTTGGC TCTAAAGAAA AAGTCCCTCC TGTTAGCTCC ACTAAAGGGC | 240 |
| AGATTGGGCT TGCTTGGGTG CTGCGGGGTT AGAAGCCGTT ATTCTATCAT GGCCATGAAY | 300 |
| CAAGGGATCT TACCTCCTAC CATTAATCAA GAAACGCCTG ACCCAGAATG CGAYCTGGAT | 360 |
| TATATCCCTA ATACAGCCAG AGAAAAGCAA GTGAATGCGG TGATGAGTAA CTCATTTGGT | 420 |
| TTTGGTGGCA CTAATGGTGT TGTGATTTTC AAAAAAGCC | 459 |

(2) INFORMATION FOR SEQ ID NO:24818802_f1_1.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGATACTAA AAAATTTGAT TTTGTTATTT TTAGCAAAGA GAAAACTTAT TTTCATAGAA | 60 |
| GCTAATTTTT ATACCATTAG TGGGAGCAAG CTTAATGAAG TCGCAAGATC CTATCAAGAC | 120 |
| TTAGCTTTAA AATTTGAAGC ATTTCTAAT TACGAATTTA TTTGGATAAC TGATGGCATA | 180 |
| GGTTGGCTAG ACGCTAAAAG CAAGCTCCAA GAAGCTTACA AATCTGTAGA AATCTATAAC | 240 |
| TTAAGCTATG TGAATGATTT TATATCAAAG GTGCAAAAA | 279 |

(2) INFORMATION FOR SEQ ID NO:24882763_f1_1.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGGAATCAC AACTCATGAA ACTCGCCATT GAAACTTATA AAATCACTTT GATGATTTCT | 60 |
| TTACCGGTAT TATTAGCGGG CTTAGTGGTG GGGCTGTTAG TCAGTATTTT TCAAGCGACC | 120 |
| ACCCAAATCA ATGAAATGAC TTTGTCTTTT GTGCCTAAGA TTTTAGCCGT GATTGGGGTG | 180 |
| CTGATTTTAA CCATGCCGTG GATGACGAAC ATGCTTTTAG ATTACACCAA AACCTTAATC | 240 |
| AAGCTCATTC CTAAAATCAT AGGC | 264 |

(2) INFORMATION FOR SEQ ID NO:25398250_c2_22.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|--|-----|
| ATGAAATTTT TTACAAGAAT CACTGACAGC TACAAGAAAG TTGTAGTAAC TTTAGGGCTA | 60 |
| GTGGTAACAA CCAATCCTTT AATGGCGGTC ACCAGTCCTG CAACAGGCGT TACTGAGACT | 120 |
| AAAAGTTTGG TTATTCAGAT CATTTCTGTT CTAGCGATCG TAGGTGGTTG CGCTTTAGGG | 180 |
| GTCAAAGGCA TAGCAGATAT TTGGAAAATC TCTGATGACA TCAAAAAGAGG TCAGGCGACT | 240 |
| GTTTTTTGCTT ACGCGCAACC CATAGCTATG TTAGCGGTGG CAGGTGGCAT TATCTATTTG | 300 |
| AGCACTAAGT TTGGCTTCAA TATTGGCGAG AGTGGAGGAG CTAGC | 345 |

(2) INFORMATION FOR SEQ ID NO:2548562_c3_11.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 573 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | | | | | | |
|------------|-------------|-------------|-------------|------------|------------|-----|
| ATGAAAAATC | CCCAAGCTAA | TGTTTTTAAAA | CTCTTTTTTAA | ATCAAGTGGC | TGACCAAAAA | 60 |
| TACATAGATA | TGAATGATGA | AAAAAACTAT | GACCCAAGAG | AACCTGAACC | CCCTTATGGA | 120 |
| ACAAAAGGGG | CGTTAGATGA | GATTATAAGG | ACAGATGCTA | GGAGTTGGGC | AAACACTCCT | 180 |
| GATGATGAAT | TTGGGAGCAT | TATGTCTTCT | TTTAAGCGTT | TTATGTATGT | CTATAAAGAC | 240 |
| CCAAAAGTGC | GTGAAGCTAC | TTCTAAAATG | AGCTTTGATT | ATGAAGAATT | AAGAACGGGC | 300 |
| AATATCAGTA | TTTACATTGT | AATCGCTCAA | ATTGATATAG | GCACACTTTC | TTCTTTAGTA | 360 |
| AGAGCCTTTT | TAGAGAGTAT | TGCTAAAAAC | CTTATGGTCA | AAGAAAGCTC | TAAACCTGAA | 420 |
| GAGCGTATTT | TTATCATTGC | TGATGAATTT | GTTAGATTTG | GTAAGTTGCC | TTTCTTGTTA | 480 |
| GAAATGCCAG | CACTTTGTCTG | CTCTTATAAT | GTTGTCCCCT | TATTCATCAC | GCAAGATTAT | 540 |
| GCTATGATTA | GAAATACTAT | AGCGATGATG | ATT | | | 573 |

(2) INFORMATION FOR SEQ ID NO:25501501_c2_60.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1053 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|--|------|
| ATGATAAGTG AGATTATTAA GTTTC AATTA AAAGGAATAA AAATGATTAG ATTAAAAGGT | 60 |
| TTGAATAAAA CTTTAAAAAC AAGCTTATTA GCTGGGGTTT TACTAGGTGC TACTGCTCCC | 120 |
| TTAATGGCAA AGCCTTTATT AAGCGATGAA GACTTATTGA AACGAGTAAA ACTACACAAT | 180 |
| ATCAAAGAAG ATACGCTGAC TAGCTGTAAT GCTAAGGTGG ACGGCTCTCA ATACTTGAAT | 240 |
| AGTGGTTGGA ATTTATCTAA AGAATTTCCG CAAGAATATA GAGAAAAGAT TTTTGAATGC | 300 |
| GTAGAAGAAG AAAAACATAA ACAAGCCCTT AATTTAATCA ATAAAGAAGA CACTGAAGAT | 360 |
| AAAGAAGAAC TTGCAAAAAA AATCAAAGAA ATTAAAGAAA AAGCTAAAGT TTTAAGGCAA | 420 |
| AAATTTATGG CTTTTGAAAT GAAAGAACAC TCTAAAGAAT TCCCAAATAA AAAGCAACTT | 480 |
| CAAACCATGC TTGAGAACGC TTTTGATAAT GGAGCTGAAA GTTTTATTGA TGATTGGCAC | 540 |
| GAACGCTTTG GGGGTATAAG TAGAGAGAAT ACTTATAAAG CACTTGGCAT TAAAGAATAT | 600 |
| AGTGATGAAG GAAAGATATT AGCCTTTGGC GAAAGAAGTT ATATTAGACA ATATAAAAAA | 660 |
| GATTTTGAAG AAAGCACTTA TGATACTAGA CAAACCTTAT CTGCTATGGC TAATATGAGT | 720 |
| GGCGAAAACG ATTATAAAAT TACTTGGTTA AAACCCAAAT ATCAGCTCCA TAGTTCAAAT | 780 |
| AATATTAAAC CCTTAATGTC AAACACAGAG TTGTTAAATA TGATAGAGCT AACCAATATC | 840 |
| AAAAAAGAAT ATGTTATGGG CTGTAATATG GAAATAGATG GTTCTAAATA TCCCATTCAT | 900 |
| AAAGATTGGG GATTTTTTTGG TAAGGCAAAA GTCCCAGAAA CTTGGAGAAA TAAGATTTGG | 960 |
| GAATGTATTA AGAATAAAGT AAAGTCCTAT GACAACACTA CCGCTGAAAT AGGAATAGTT | 1020 |
| TGGAAAAAAA ATACTTATTC TATCTCTCAT CAC | 1053 |

(2) INFORMATION FOR SEQ ID NO:25525277_c3_4.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1053 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|--|------|
| ATGGCTGATA TTTTAAGCCA AGAAGAAATT GATGCGCTTT TAGAAGTCGT TGATGAGAAT | 60 |
| GTGGATATTC AAAATGTCCA AAAAAAAGAT ATTATCCCCC AACGCAGCGT AACCCCTCTAT | 120 |
| GATTTCAAGC GCCCTAATCG TGTGAGTAAG GAGCAATTGC GCTCTTTTAG GAGCATCCAT | 180 |
| GATAAAATGG CTAGGAATCT TTCCAGTCAA GTCTCTTCTA TCATGCGTTC TATTGTAGAA | 240 |
| ATCCAGCTTC ATAGCGTGGA TCAAATGACT TATGGCGAAT TTTTGATGAG TTTGCCTAGC | 300 |
| CCTACGAGTT TTAATGTCTT TTCCATGAAG CCTATGGGGG GAACGGGGGT TTTAGAGATT | 360 |
| AATCCTAGCA TCGCTTTCCC TATGATTGAC AGACTATTAG GGGGTAAGGG GAGCGCGTAT | 420 |
| GATCAAAACA GGGAGTTTAG CGATATTGAA TTGAATTTAT TGGATACGAT TTTACGCCAG | 480 |
| GTGATGCAAA TTTTAAAAGA AGTGTGGTCG CCTGTGGTGG AGATGTATCC TACCATTGAC | 540 |
| GCTAAAGAAT CCAGCGCGAA TGTGGTCCAA ATCGTCGCTC AAAATGAAAT TTCTATCATG | 600 |
| GTGGTTTTAG AGATTATCAT TGGGCATAGC CGTGGGATGA TGAATATTTG TTACCCGGTG | 660 |
| ATTTCCATTG AGAGCATTCT TTCTAAAATG GGGAGTAGGG ATTTTCATGCT TTCAGAAACG | 720 |
| AACTCCAAAA AGAGCCGTAA TAAGGAATTG CAAGCACTAT TGAGCGGGGT GAGCGTGGAT | 780 |
| ATGATGGTGT TTTTGGGCGC GGTGGAATTG AGTTTGAAAG AAATGTTGGA TTTAGATGTG | 840 |
| GGGGATACTA TCCGGTTGAA TAAAGTCGCT AACGATGAAG TGAGCGTGTA TGTACATAAG | 900 |
| AAAAAGCGTT ATTTAGCGAG CGTGGGGTTT CAAGGGTATA GGAAAACCAT TCAAATTAAA | 960 |
| GAAGTGGTTT ATAGCGAAAA AGAACGCACT AAAGAAATTT TAGAAWTGCT WGAAGAACAG | 1020 |
| CGCAGGAGGC AAAGTTGGGC GRTGTTATGG AGC | 1053 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 570 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|--|-----|
| ATGCCCACGA TGTTAGCGGT TGGTTTTTGG GTGTTGTTTT TTTTATCCAC GAGCAATGCG | 60 |
| GTGAATTTAA CCGACGGGTT AGACGGATTA GCGAGTGTGC CTAGCATTTT CACCCCTCTTA | 120 |
| AGCCTTTCTA TCTTTGTGTA TGTGGCAGGG AATGCGGAAT TTTCTAAATA CTTGCTCTAT | 180 |
| CTTAAAGTCA TAGATGTGGG GGAATTGTTT GTGATTTTCGC TAGCATTAGT GGGATCGCTC | 240 |
| TTTGGCTTTT TGTGGTATAA CTGCAACCCG GCAAGCGTGT TTATGGGCGA TAGCGGGAGT | 300 |
| TTGGCAATAG GAGGGTTTAT CGCTTATAAC GCTATTGTTT CGCATAATGA AATCTTGCTC | 360 |
| TTTTTAATGG GGTCTATTTT TGTAATAGAA ACTCTGTCTG TGATCTTGCA AGTAGGGAGC | 420 |
| TATAAAACCC GTAAAAAACG CCTTTTTTTT ATGGCACCCA TCCATCATCA TTTTGAACAA | 480 |
| AAGGGTTGGG CAGAAAATAA GGTGATCGTG CGTTTTTGGA TCATTTCTAT GCTGAGTAAT | 540 |
| TTAGTCGCTC TTTTGAGCTT GAAGGTGTGT | 570 |

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1467 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | |
|------------|-------------|-------------|------------|------------|------------|------|
| GTGCGTTTTG | AAAATTTTCAT | CAACCGCCTA | GCCTTTTACA | TGGCCACAGG | GAGCGGTAAA | 60 |
| ACGATCGTCA | TTATCAAAC | GGTAGAGCTT | TTAAGCGTGG | CTATGGGAAT | GGGTTTGATC | 120 |
| CCTAAGAAAA | ATATCATGTT | TTTtagCGCG | AACGAGCATT | TAATCAAGCA | ATTTGAAAAA | 180 |
| GAAATTGAAA | AATACAACCG | CAATAAGGAC | TATTCCAAAC | AAATTGATTT | CAAAAACCTT | 240 |
| AAAAGCGTTA | AGAATAAGGA | TTTTTATCGT | GCTCCAAAAG | ATTCTTTAAT | GAAAGAAATC | 300 |
| GCTCTTTTTT | ATTACGCGC | AGATTTAATG | AGCGATGAAG | AAAGCAAGGA | AAACCTTTTA | 360 |
| AATTATAAGG | ATTGTTGGGA | TAATGGGGAA | AATTATGTGA | TTTtagATGA | AGCGCATAAG | 420 |
| GGGAATAAGA | CTGAAAGCAA | AAGACAGGCG | ATTTTTAGCC | TGCTGTCTTT | AAAAGGGTTT | 480 |
| TTATTCAATT | TCAGCGCCAC | TTTCACTGAA | GAAAGCGATC | TCATCACTGC | GGTGTATAAT | 540 |
| TTGAGCGTGG | GCGAGTGGGT | GAAACTTGGC | TATGGTAAAG | AGTCTGTTTT | ATTGAAGAAA | 600 |
| AACAACCTTA | ACGCTTTTAA | GGAATTGAAA | GATTTAAACG | ACAGGGAAAA | AGAAATCGCT | 660 |
| CTTTTAAAGG | CGTTATTGCT | TTTAGGCATG | CAAAAACGCT | ATAAAGTAGA | AGGCTATTTT | 720 |
| CATGACCCTT | TAATGCTCGT | GTTCAACGCAT | TCTGTGAACA | TGGAAAACAG | CGATGCGRAA | 780 |
| ATCTTTTTTA | AAACTTTAGC | GCGCGTGATT | GAAAATGATG | ATGAGAGCGA | TTTTTCAAAA | 840 |
| GCTAAAGACG | ATTTATTAGA | GGAATTAAAG | AATCCGGAAT | TCCTTTTTAG | CGATGGCAAA | 900 |
| GATAAAGAAA | AAGACTATAA | AATTGAGGTC | TTTAAAGAGA | GTTTAAAGGG | CATGGATTTT | 960 |
| AAAGGCTTAA | AAGAAGCAGT | TTTTTATGCC | AGTAATGGGC | ATATTGAAGT | CATCATTAAC | 1020 |
| CCTAAAAACA | ACCAAGAAAT | CGCTTTTCAAG | CTCAACACGA | GCGATAAAGT | CTTTTGCCTG | 1080 |
| ATTAGAATAG | GCGATATTAC | AGAATGGATC | CGTGAAAAAT | TAAAGAGCGT | GAAGGTGGTG | 1140 |
| AGTAAGAATT | TGAGCTTCAA | AGAAGAGAGC | TATTTcAGCC | AGATTGATAA | GAGCAGTATC | 1200 |
| AATATCTTAG | TGGGGTCTCG | TGCTTTTGAC | ACTGGGTGGG | ATAGCACAAG | GCCTAGCGTG | 1260 |

| | |
|---|------|
| ATTTTATTTT TAAATATAGG GCTTGATGAT GACGCTAAAA AGCTGGTGAA ACAATCTTTT | 1320 |
| GGCAGGGGCG TAAGGATTGA AAGCGTCAAA AACCAACGCC AAAGGTTAGC GTATTTAGAG | 1380 |
| ATAGATGAAG CCATTAAAGA ACAAGCTGAA ACCAAACGCT GCAATGCTGG AAATGCTTTT | 1440 |
| TGTGATACCT ACCAACCATG CAAGCCT | 1467 |

(2) INFORMATION FOR SEQ ID NO:25995917_c1_15.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 639 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|--|-----|
| GTGTTTAAAA ATTCCCTCTT TGGTATATCA ATCTCCATGC TTATCACTTG GGTTTTAACC | 60 |
| GCTTGTATTT TGATTTTTTAT CCTTTTTGTC CCGAATTTTA CCCTTACGCA TCCCAATTTT | 120 |
| CATTTCACTC CGTTTGAAAA AACCTATTTT CAAATTCTAG GACTTGTTGG TATTGTAAGT | 180 |
| TCTATTATTT TCACCGGGTT TTTGGCTGAT AAAATCAAAC CGCACAAAGT TTGCATGGCT | 240 |
| TTTAGCSCGA CCTTTGGGTT TTTTGGCTTT TTATTCTTTA AGGAATTTTA TTCTAACGCG | 300 |
| CCAAGTTTAG TCAATACTAT AATTTTATAC TTTTLAGCTT GCTTTTGCGC GGGCATTATG | 360 |
| AATTTTGGCC CCATTTTCAT GAGCGATGTG TTTAGCGCTA RAATCCGTTT TAGCGGGATT | 420 |
| TCCTTTGCTT ATAACATAGC CTATGCTATA ACCGCTGGCT TTACCCCTCA ACTTTCAAGC | 480 |
| TGGTTAAACG CAAAAGCTAT AGCAGTGCCT GAAAGTTTGC AAAGTTATGG TTTAAGCTTT | 540 |
| TATATCCTTA TAGTTTCTTT AATTGCTTTT ATTACATCGC TTTTAATGGC GCCAATTTAT | 600 |
| CACAAATCTA ATACCCAACA CGAAGTGTCG CCCACGGCA | 639 |

(2) INFORMATION FOR SEQ ID NO:26054702_f1_1.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 936 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGAAAAGCG ATAAACCCTT TTTAGAACGC TATTTTTATG ACCCCACTCT TTTGCAAAAG | 60 |
| GGGTTGATTT TCGCGCTCTA TCCTTTTTCT TTAATCTATC AATGTATTGC CACAATTAAA | 120 |
| CGAAAAACCG CTAAAAAGCA TGATTTTAAA ATCCCCATTA TCAGCATAGG CAACTTGATC | 180 |
| GCTGGGGGAA GCGGTAAAAC GCCCTTCATT TTAGAAATCG CTCCAAGATA CCAAGAAGTG | 240 |
| GCGGTTGTTT CTAGAGGGTA TCAACGGGAT TCTAAAGGTT TAGTGGTGGT GAGCGTTAAA | 300 |
| GGAAACATTT TAGTTCCTCA AAAAACAGCG GGCGATGAAG CCTATCTTTT AGCCTTAAAT | 360 |
| CTAAAACAAG CGAGCGTGAT TGTGAGCGAA AAAAGGGAGC TAGGCGTTTT AAAAGCCCTT | 420 |
| GAATTAGGAT CAAAGATCGT GTTTTTAGAC GATGGTTTTA GGTTTAATTT CAACCAATTC | 480 |
| AATGCGCTTT TAAAACCCAA AGTCCCCCCC TACTACCCTT TTTGTTTGCC TAGCGGGTTG | 540 |
| TATAGAGAAA ATATTAAAAG CTATAAAGAA GCCCATTTAG TCATTACAGA AGATAAGGAT | 600 |
| TATCAAAGAA TCACCTCTAT CACTAACCCC ACCAAACGCA TGCTTTTAGT AACGGCTATC | 660 |
| GCTAACCTTA GCAGGCTTGA TGC GTTTTTTA CCCAAAGAAG TGGTTAAAAA ATTGTATTTT | 720 |
| AGAGACCATG CCCCTTTTGA TTTGAAGCTT TTAGAAAAAG AGTTTTATCA AAATAACGCC | 780 |
| ACCTCCTTAT TGGTTACTTC AAAAGATCTC GTCAAATTAC AAGATTGCAA ATTGCCTTTA | 840 |
| AGCGTATTGG ATTTAAAAC T AGAAATTTGC CCTAAAGTTT TAGAGGAGAT TGATCGTTAT | 900 |
| ATCCTTTCTT ATCCTTGTA TATAAAAGAA CATCTA | 936 |

(2) INFORMATION FOR SEQ ID NO:260941_c1_20.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | |
|--|-----|
| ATGTCTTTAG GGGCAGTGAT CAGGCTTATT TTTTGTTATA AGTTAGAGGG GGTAATATTA | 60 |
| GATTTAAAGC GCATCAATTT CAAATCCTAT TACCCCAATA ATAAAAATGC ATTATTTATC | 120 |
| AACAATAAGA AAAATCCATT ATCTAGTRCT TCAAAGTTCA TATTGCTT | 168 |

(2) INFORMATION FOR SEQ ID NO:26197187_f1_2.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 684 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: cell division and sporulation protein

| | |
|---|-----|
| ATGCTAGAAA CCACTATTGA TTTTCTCTCGT TACAGCAGCG TGAAAATCGG TCGCCTTTA | 60 |
| AAAGTGAGCG TTTTAGAAAA CGATAATGAA ATCTCTCAAG AACACCAGAT CATAGGATTA | 120 |
| GCGAACAACC TTTTAATCGC TCCTGACGTG AAAAATCTCG CTTTATTAGG AAAAACTAC | 180 |
| GATTATATTT GCGATAAGGG TGAGTGGGTG GAGGTAGGGG GAGCGGCCAA TCGTCTAAA | 240 |
| ATTTTAAATT ATTTTAGGGC GAATGATTGA GAGGGTTTAG AGTTTTTAGG GCAATTGCCT | 300 |
| GGCACTTTAG GGGCGTTAGT TAAAATGAAT GCTGGCATGA AAGAATTTGA AATAAAAAAT | 360 |
| GTTTTAGAAA GCGCTTGCGT TAATGGCGAA TGGCTAGAAA AAGAAGCTTT GGGGCTAGAT | 420 |
| TATCGCAGCA GCGGGTTTAA TGGCGTTGTT TTGAGGGCTA GGTTTAAAAA GACGCATGGT | 480 |
| TTTAGAGAAG GGGTTTTTAA AGCGTGTAAG AGCATGCGCA AAAGCCACCC CAAATTGCCT | 540 |
| AATTTTGGGA GCTGTTTCAA AAACCCGCCT AACGATTATG CGGGCAGGCT TTTAGAGGGC | 600 |
| GTGGGCTTAA GGGGTTATTG TCTAAAAGAG TGGGCTTTGC CAAAGAACAT GCGAATTTTT | 660 |
| GGTGAATTTG GGGGGCGCAG AATT | 684 |

(2) INFORMATION FOR SEQ ID NO:26261040_f2_2.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: chemotaxis protein cheY

| | |
|---|-----|
| ATGCTCAAAA ATGGCGATAA GATTCCGGAC GCTATTTTAG TGGATATTGA GATGCCTAAA | 60 |
| ATGGATGGCT ACACTTTCGC CTCTGAAGTG CGTAAATACA ATAAATTCAA AAACCTGCCC | 120 |
| TTGATCGCCG TTACCAGTCG GGTAATAAA ACGGACAGAA TGC GCGGCGT TGAATCCGGC | 180 |
| ATGACTGAAT ACATCACCAA ACCTTATAGC GGTGAATATT TAACCACCGT AGTGAAGCGC | 240 |
| AGCATTAAAT TAGAAGGAGA CCAATCG | 267 |

(2) INFORMATION FOR SEQ ID NO:26301059_c2_3.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| GTGTTTGAGC CGGTTATCGC TTACAAGCTT TTCCATTCTT TTGTGATTTT AGGGTGCGCG | 60 |
| ATTGAAACTT TAACGACTAA ATGCGTGGAA GGCATCACGG CTAATGAAAA GATTTGCCAC | 120 |
| GATTATGTTT TTAACAGCAT TGGCATTGTT ACCGCGCTCA ACCCTCATAT CGGCTATGAA | 180 |
| AAATCCGCTA TGATCGCCAA AGAAGCCTTA AAAAGCGATC GCTCTATCTA TGATATCGCT | 240 |
| TTAGAAAAGA AAATCTTAAC CAAAGAGCAA CTGGACGATA TTTTCAAGCC AGAAAACATG | 300 |
| CTAAGYYCTC ACGCTTTCAA AAAGCATAAA GAC | 333 |

(2) INFORMATION FOR SEQ ID NO:26306340_f2_3.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGTTGCGTT TATTAGCCCA AAAAAGCGCT ATTAAACTCA TTCTTATCCC CCCAAGCGCG | 60 |
| AACGCTTTAG GCATCGCTTC TATTTGCGAA TTGAGCGAAG AAGTTTTTGA ACATGAAAAA | 120 |
| ATCGTAGGCA TTCGCGCTCA AGGGGATTTC ACTATCAATA GCGACGATAG GGGTTTTTGG | 180 |
| GAAAGACGCT GTCAG | 195 |

(2) INFORMATION FOR SEQ ID NO:26351567_f1_5.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 804 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|--|-----|
| ATGAAAAAAC TTCTTTTACT CTTAGAGCAT AAGATCGTAA AAATTGGCTT AATTATTGTG | 60 |
| ATTGTGTTAG TGGGTTTTTT TCTTTTTTAT GAACAAGAAA TCAAAGAAAA AGCTGTTAAT | 120 |
| GTTTCTCAAG GTAAATTCCC CACTTCATCT TATTTGTTTC AAGCTTACGA AGGCATTAAG | 180 |
| AATAAAATAG ATACTATCAA TCAAGTGAAG CCAAACGATG AACTTAAAAG CGTTAATGAG | 240 |
| AATATAGAAA AAACACAAAA AGATTTAGAT GATTTTAAATG CGCTAGTGCA AAAGTTACCA | 300 |
| AATTTGCCTA AGGACTTTAA TAAAACACTT ATTAAACCAC AAAGTCCATT TTTCAACTAC | 360 |
| AATACCGCTA ACGAAGATGA AAAAAACCGC CTGGTGATTT TAGCGTCTCG TATTAGCAGC | 420 |
| CAAAAAGAAA CGCAACCTCC CATTTCTATA AAAAATAGCG TTTCTCACAT AAAATCCAAA | 480 |
| GAAAAACGAG AACTTGAAAA AGAATGGGCA AAACCTAGTG TTTCTTTTGG TTCTTTTTTCC | 540 |
| TTGCTTTCCA GTTCTTCTTC TTTTCTTCT TTTGAAGTTT CTTTTTTATC AAGGGGAATA | 600 |
| GGATTGGATT GTGAGAAGCT CAAATCCTTT TTAAAAGCTT TTTCAAGTTC GCTATTTTCC | 660 |
| TTATTATCTT CATTGTTTTG CCATCCACTT TCTCTTTTTT GCTCTCTAAT AGGATTAATC | 720 |
| TTTGTGTTTT CTAAGTTTTT TAGAGAGCTA GTGAATGCGT CTAACAATTC GCTTGAGTTT | 780 |
| TCATCATTGT CAAGGCTAGG ATCA | 804 |

(2) INFORMATION FOR SEQ ID NO:26380318_f3_8.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: FLAGELLAR MOTOR SWITCH PROTEIN F

| | |
|--|-----|
| GTGATGGACA AACTCACTAA AAGCTTGCAA ACGCAAAAAA ACTTCGCTTA TTTAGGCAAA | 60 |
| ATCAAGCCCC AACAACTCGC TGATTTTCATC ATTAACGAAC ACCCTCAAAC CATCGCCTTG | 120 |
| ATTTTGGCCC ACATGGAARC CCCTAATGCG GCTGAAACTT TGAGCTATTT CCCTGATGAA | 180 |
| ATGAAAGCCG AGATTTCCAT TAGAATGGCG AATTTTtaggc GAAATATCGC CCCAAGTGGT | 240 |

(2) INFORMATION FOR SEQ ID NO:26423583_f2_3.nt:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 615 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | |
|--|-----|
| ATGCGGTATT TTAGAAGCGC TTTTTTATTA TTTTTCATGA CGCTTTTTTTT TGTTCCTTGC | 60 |
| TCTAAGCACC CTTTTTCTAA GCAAACCCCT AAGACTAAGG AGCGGATCCG ACAAGAAGAA | 120 |
| GCCAATAAAA AAAGAGAAGA GACTTTGAAT GCCTTGCGCC AATTCAGACT CATTTACATT | 180 |
| AACACGCCGG TTTTTCGCTT TTATGATTAC GGCACGATCA AAACCGATAA AGACCACAAT | 240 |
| ACTGAAGTAA CCCTTTATAA GCTCAGCCAA AAAGTGGGCG ATATTTACAT GACTAAACGG | 300 |
| AGCATTTGTT TTAGCCAAAA ATGTTTCGGCC AAATGGATTG CTGCAAGGGA TTTGTTTGGC | 360 |
| AAGGTGAGCT ATGGGGATTT GTTTGATGAT ATTGTTTTAG GGAGGGATAT TTTTAAAGGT | 420 |
| TTAGGGAAAC GCCACCTAAC CCCTGAATAT GTGATCCAAA GGTTTCAAAA AAGCGGGGAA | 480 |
| ATTATCCTTT ATGAAAGAAA AAATGGCCTG ATTTCTTTCC AAAACTTGAC TCAAAAAATT | 540 |
| GCTATTAGGA TTGAACCCTA TGAGCCTTCT TTGCAAGATT TAGAAGACAA TGAAAACGCT | 600 |
| GATAGCGAGC TTCAA | 615 |

(2) INFORMATION FOR SEQ ID NO:26588588_f1_1.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: flagellar hook polypeptide

| | |
|---|-----|
| ATGCGCATTG AAGAAAATGG CGTGATTCT CTAGCCTTTA GTAACGGGGT GGTAGAGCCG | 60 |
| GTCGCTCGCA TCGGTATTTW AGCTTTCCT AACGATCAAG GCTTAAGGAA AATCGGCGGT | 120 |
| AACCTCTATG AAATGCAAGA AGGCACCATT AATGGCGAAA ACAGACCCCT AAGSGGTAAC | 180 |
| CCCATTTTAG GGTGGGACGA AGAGGGCAAG CTCAAGTTTG GGAAAATCAG GCACAAATAT | 240 |
| TTAGAAACGA GCAACGTGAA TGCCGGGAAC GCCCTAACCA ATCTCATTTT AATGCAAAGA | 300 |
| GGCTATTCTA TGAACGCTAG AGCCTTTGGC GCGGGCGATG ACATGATCAA AGAAGCCATT | 360 |
| AGCTTGAAAA AA | 372 |

(2) INFORMATION FOR SEQ ID NO:26614041_f3_3.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*(xi) SEQUENCE DESCRIPTION: vacuolating cytotoxin - *Helicobacter pylori*

| | |
|---|-----|
| GTGGAAGCGC GTTATTATTA TGGGGACACT TCATACTTTT ATTTGCATGT GGGAGTTTTA | 60 |
| CAAGAGTTCG CTCACCTTGG ATCGAATGAT GTGGCGTCTT TAAACACCTT TAAAATCAAT | 120 |
| GCCGCTCGCA GTCCTTTAAG CACCTATGCA AGAGCGATGA TGGGTGGGGA ATTGCAATTG | 180 |
| GCTAAAGAAG TGTTTTTGAA TTTGGGCGTG GTTTATTTGC ACAATTTGAT TTCCAACGCA | 240 |
| AGCCATTTTCG CTTCCAATTT AGGAATGAGG TATAGTTTC | 279 |

(2) INFORMATION FOR SEQ ID NO:272058_c3_26.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 642 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| GTGGAGGAGC TAGCTAAATT GATCAACAAT AATAATAACA ATAAAAAACT GAGAGGCTTT | 60 |
| TTTTTGAAG TTCTCTTAAG TCTCGTTGTT TTCAGTTCGT ATGGGTCAGC AAATGACGAT | 120 |
| AAAGAAGCCA AAAAAGAAGC GCTAGAAAAA GAAAAAACA CTCCAATGG GCTTGTTTAT | 180 |
| ACGAATTTAG ATTTTGATAG TTTTAAAGCG ACTATCAAAA ATTTGAAAGA CAAGAAAGTA | 240 |
| ACTTTCAAAG AAGTCAATCC CGATATTATC AAAGATGAAG TTTTGGACTT CGTGATTGTC | 300 |
| AATAGAGTCC TTAAAAAAT AAAGGATTG AAGCATTACG ATCCAGTTAT TGAAAAAATC | 360 |
| TTTGATGAAA AGGGTAAAGA AATGGGATTG AATGTAGAAT TACAGATCAA TCCTGAAGTG | 420 |
| AAAGACTTTT TTACTTTCAA AAGCATCAGC ACGACCAACA AACAACGCTG CTTTCTATCA | 480 |
| TTGCACGGAG AAACAAGAGA AATTTTATGC GATGATAAGC TATATAATGT TTTATTGGCC | 540 |
| GTATTCAATT CTTATGATCC TAATGATCTT TTGAAACACA TTAGCACCAT AGAGTCTCTC | 600 |
| AAAAAAATCT TTTATACGAT TACATGTGAA GCGGTATATC TA | 642 |

(2) INFORMATION FOR SEQ ID NO:2738378_f3_6.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| GTGGGGGGCA TTGTGGCAAA CATGAACGAT CTTTCAACTT ACATGGTTGA GAATTTACTC | 60 |
| ATGGGTTTGT ATCTTTTTTC TAGCGCTTTA GATTGCGGCG TGAAAAAGC CATTAAATCTA | 120 |
| GCGAGCTCTT GCGCTTATCC TAAATACGCC CTAACCCTT TAAAAGAGAG CGATTTATTG | 180 |
| AACGGCTCTT TAGAACCAAC GAATGAAGGC TACGCTTTGC CAAACTCTCT GTRR | 234 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 531 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|--|-----|
| ATGAAGAAAA GAAAACATGT ATCCAAGAAA GTGTTTAATG TCATTATCTT GTTTGTGGCA | 60 |
| GTATTCACTC TTTTAGTCGT CATTCACAAA ACCCTTTCAA ACGGCATTCA CATAAAAAT | 120 |
| TTAAAAATTG GAAAAC TTGG CATTTCTGAA TTATACTTAA AACTCAATAA CAAGCTTTCT | 180 |
| TTGGAAGTTG AGCGGGTTGA TCTCTCTTCT TTCTTCCATC AAAAACCCAC TAAAAAGCGT | 240 |
| TTAGAAGTTT CTGATTTGAT TAAAAATATC CGTTATGGCA TTTGGGCGGT GTCTTATTTT | 300 |
| GAAAAACTTA AAGTCAAAGA AATCATTTTA GACGATAAAA ATAAAGCCAA TATCTTTTTT | 360 |
| GATGGGAATA AATACGAGTT WAGAATTTC AGGAATCAAA GGGGAATTTT CCCTAGAAGA | 420 |
| CGATTAAAAA TATCAAGCTT AAAATCATCA ATTTGCTTTT TAAAGATGTT AAAGTCCAAG | 480 |
| TGGATGGCAA CGCCCACTAT TCRCCCAAAG CCAGGAAAAT GCGGTTCAAT T | 531 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 774 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| GTGTCATGTT GGGGAGCGTC AAAAAAGCGG TTTTtagGGT TTTGTGTTTG GGGGCGTTGT | 60 |
| GTTTATGCGG GGGGGTTAAT GGCAGAGCAA GATCCTAAAG AGCTTATATT TTCAGGTATA | 120 |
| ACTATTTACA CGGATAAAAA TTTCACTAGA GCTAAGAAAT ATTTTGAAAA AGCTTGCAAA | 180 |
| TCAAACGATG CTGATGGCTG TGCAATCTTA AGAGAGGTTT ATTCTAGTGG TAAAGCCATA | 240 |
| GCGAGAGAAA ACGCAAGAGA GAGCATTGAA AAAGCTCTTG AACACACCGC TACTGCTAAA | 300 |
| GTTTGTAAT TAAACGATGC TGAAAAATGC AAGGACTTAG CAGAGTTTTA TTTTAATGTA | 360 |
| AACGATCTTA AAAATGCTTT AGAATATTAC TCTAAATCTT GTAAGTTAAA TAATGTTGAA | 420 |
| GGGTGTATGC TGTCAGCAAC TTTTtATAAC GATATGATAA AGGGTTTGAA AAAAGATAAA | 480 |
| AAAGATCTAG AATATTATTC TAAAGCTTGC GAGTTAAATA ACGGTGGAGG GTGTTCTAAA | 540 |
| TTAGGAGGGG ATTATTTTTT TGGTGAAGGC GTAACAAAAG ATTTCAAAAA AGCTTTTGAA | 600 |
| TATTCTGCCA AAGCTTGTGA GTTGAACGAT GCTAAAGGGT GTTACGCTCT AGCAGCGTTT | 660 |
| TATAATGAGG GTAAAGGCGT GGCAAAGGAT GAAAAGCAAA CGACAGAAAA CCTTGAAAAG | 720 |
| AGTTGCAAGC TAGGATTAAA AGAAGCATGC GATATTCTCA AAGAACAAAA ACAA | 774 |

(2) INFORMATION FOR SEQ ID NO:2855006_f2_4.nt:

240

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| GTGGCTCTCA CTTTGGGGGC TAGAGGGGGG GTGTATTTGT GTGGGGGGAT TATCCCACGA | 60 |
| TTCATTGATT ATTTTAAAC TTCGCCCTTT AGAGCGCGTT TTGAAACGAA AGGGCGCATG | 120 |
| GGAGCGTTTC TCGCTTCCAT CCCTGTGCAT GTCGTGATGA AAAAACTCC CGGACTTGAT | 180 |
| GGGGCGGGCA TTGCGTTAGA AAATTATTTA CTGCATGATA GAATA | 225 |

(2) INFORMATION FOR SEQ ID NO:289077_f2_24.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1263 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

241

| | |
|--|------|
| ATGAAAGGTT TAACAATGAA AAAATTAGTT TTTAGCATGC TTTTATGTTG TAAAAGCGTG | 60 |
| TTTGCAGAGG GGGAAACTCC TTTGATTGTC AATGACCCAG AAACCCATGT AAGTCAAGCC | 120 |
| ACTATCATAG GCAAAATGGT AGATAGTATC AAAAGATACG AAGAGATTAT TTCTAAGGCT | 180 |
| CAAGCTCAAG TCAATCAGTT ACAAAAAGTC AATAACATGA TAAATACGAC TAATTCTTTG | 240 |
| ATTAGTAGTA GTGCTATCAC TTTAGCCAAT CCTATGCAAG TTTTACAAAA CGCTCAGTAT | 300 |
| CAAATAGAGA GCATTAGATA CAACTATGAG AATTTAAAGC AAAGCATAGA AAATTGGAAC | 360 |
| GCACAAAATT TGTTAAGAAA CAAATACTTA CAGCAACAAT GCCCTTGGCT TAATGTCAAT | 420 |
| GCTCTTACTA ACAATAAGAT TGTCAATCTT AAAGATCTCA ATAACCTAAT CACCAAAAAT | 480 |
| GGCGAACAAA CCCAAACCGC AAGAGATGTG CAAAATCTCA TTCAGTCCAT TAGTGGCAGT | 540 |
| GGCTATGGAA ACATGCAATC ACTTGCTGGG GAATTGAGTG GTAGAGCGTG GGGGGAAATG | 600 |
| TTGTGTAAAA TGGTAAACGA TAGTAATTAT GAAAGCGAGC AAGCTCTTTT AGCAACAGGC | 660 |
| AATAACCCAG AAGAGCAAAA ACGAAGATTT TTGCTTAGAG TAAAGAAAAA GGTTAATGAT | 720 |
| AATAAGCAGT TAAAAGATAA ACTTGACCCA TTTCTAAAAA GACTTGATGT CCTACAAACT | 780 |
| GAGTTTGGTG TAACTGACCC TACAGCTAAC CATAATAAGC AAGGGATACA TTATTGCACA | 840 |
| GAAAATAAAG AGACAGGTAA ATGCGACCCT ATTA AAAATG TATTTAGGAC AACTCGCTTA | 900 |
| GATAACGAAT TAGAACAAGA AATCCAAACG CTCACACTTG ATTTAATCAA AGCCTCCAAT | 960 |
| AAAGACGCTC AAAGCCAAGC CTACGCAAAT TTCAATCAAA GGATTAAATT ACTTACTCTA | 1020 |
| AAATATTTTAA AAGAAATTAC CAATCAAATG CTCTTTTAA ATCAAACAAT GGCAATGCAA | 1080 |
| AGCGAGATTA TGACAGATGA TTATTTTAGG CAAAATAATG ATGGCTTTGG GGAAAAAGAA | 1140 |
| AACCATATAG ACGAACAATT AACGCAAAAA AGAATAAACG AAAGAGAAAG AGCTAGAATA | 1200 |
| TACTTTTCAA ACCCTAATGT TAAATTTGAC CAATTTGGCT TTCCCATTTT TAGTATATGG | 1260 |

GAT

1263

242

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGAGCGTGA ATTTATTGGA ATTGTTAAAA CTCGCTGTGC CTTTAGCGGT TATTTTGAGC | 60 |
| GTTCAAGTGG CGGTTATGAT CCTTTATGTG GTGCTTGTA CTTTAGGGT ATGCGGGAAG | 120 |
| GATTATGATG CGGCGGTGTT GTGCGCGGGG CATTGCGGTT TTGGGCTTGG AGCGACCCCA | 180 |
| ACGGCTATGG TGAATATGCA AACCATCACC AACCACTATG GGCCATCGCA TGTGGCGTTT | 240 |
| ATCGTCGTGC CTTTAGTGGG AGCGTTTTTT GTTGATATTA TTAACGCTTT AGCGATTAAA | 300 |
| GGCTTTTTGC TTTTGCCTTT TTTCCCTAGT | 330 |

(2) INFORMATION FOR SEQ ID NO:2915903_f1_2.nt:

244

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 336 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | |
|--|-----|
| ATGCAACTAA GCCCCTTACA AAGCGCGCTG TTATATTTCC GTTACTTTAT TTATCCGGAA | 60 |
| AAAAAAACAA GGAGCTTTGA TTTAAGCGAT TTAATTTTTTA TTGTCATGGT TTTTTTAGTC | 120 |
| CTAGCTTTGG GGCTGTTGAT GAGCGAAGAA ATTTCTATCA GCTACAATGA AGCGAAAGAC | 180 |
| TTTTTTTATA GCGATGCGTG GTTTGTCAAA ATCGCTCAAA AAAGCGTAGC CATTTTAAGG | 240 |
| CCAAAACGAT TTGGCTTTAA GATTGCCTTT TTTGATCGCT CACGTCATCA ACATGTTTTT | 300 |
| ATTCTACCTC ATAGGGCGAA AGATTTTAAA AAAGCC | 336 |

(2) INFORMATION FOR SEQ ID NO:29302003_f1_1.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

GTGTATGCGC TCATGGTGGC GTTTTTTGCT TACATGAGTT ATTGCTTGGG GTATCAATTC 60
TCCAAATTCG TTTCTAAAAA CAACATTTC TCGCTCTCAT CGCTTTTATC AAGCTGTGTG 120
CGCGTGGTCT CTGTGCTAAT CTTGTCGCTC AGTAGCCTAG AGTTGCGTTA CTTCTCACCC 180
CTAACTATCA TAACCATGCA TTTTGCCCTA ACGCTTATCA TCCTCTTTTT CTTTTTGTAT 240
AAGGCTAAGC CGTTTGATGA G 261

(2) INFORMATION FOR SEQ. ID NO:29386577_f3_10.nt:

246

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1257 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|--|------|
| ATGAGGTCTT GGATGAAGAA AAAATACTTC ACGCTTTTAT TGCAAAGTAG TGTGGTATTA | 60 |
| GCGGTTTTTA TAGGGTGTTT TTCTACCAGG AATCATACTT TTCAGCCCT TAGTAATCAA | 120 |
| GAAAATACAG ACGATAAGCT CCCAGTGGTC CATTCCATTA AAACGATTAA CGATGTGAGT | 180 |
| TCAGTGGGCT TTGAATGGTC TAAAGTCGCT GACACTTATG ACATTGACGG GTTTGTTTTG | 240 |
| TATCGTTTGA AAAAAGACTC CAAGCTTAAA AGAATCGCCA CCATTAAAAA CCCTTATGCG | 300 |
| ACCCACTATT ATGATGAGGG GTTAGAAACA GAGAGTTCCT ACACTTACCA ATTAGCCACC | 360 |
| TACAAGGGCG ATAAAATTTT CAAACTTTCA GAACCCATTT TAGTAAAAAC CTCCTTTATC | 420 |
| AATCCTGTAG AAAGCGTGTT TGCAAGCCTT GAATACCCTA AAAGCGTGAA AGTCTTTTGG | 480 |
| AGCCCGCACC CAAATCCCAG CGTTTCTAAA TACATCATTC AAAGGCAGAA TAAAGACGGC | 540 |
| AAATTTTTTA ATGTGGGGGC TGTA AAAAAC CGCTTATTCG TGGAGTTTTT TGATAAAGAT | 600 |
| TTAGAAGATG GGCAAAAATA CCGCTACCAA ATCATCGCCG AAAATTTTCAT GGGGGATAAA | 660 |
| TCCAGGCCTA GCGTGATAGT GGAGGGGAAA ACCAAAGACT TGCCCAAAGA AATCGCTAAT | 720 |
| GTTAGAGTGA GTCAAAACCT CACACGACAA ATTGAATTGA GTTGGGATAA ATCCCAGAA | 780 |
| GAAGATGTGA TAGCTTATCG CATTACGCT TCCAATAACC GCAACGATAA ATACAAATTC | 840 |
| ATCGCTCAA CCACCAACAC TTCCTATGTG GATAAGATAG AAAAAGACAA TCTCACTCGT | 900 |
| TATTATAAAG TCGTCGCCGT AGATAAAACG CATCTTGAAG GGGCGTTACC CAAAGAGCCT | 960 |
| GCCATGGGTG AGACCTCTGA TAGGCCTGAA GCCCCTATCA TCACTAAAGG GACTATTCAA | 1020 |
| GACTCTTCGG CCTTGATCCA ATGGGAAAAC AACCCAAGCC CTAAAATAGC CACTTATGCG | 1080 |
| GTGTATCGTT TTGAAGCCAA CTCCAAAACC CCTTTGCGTT TTGGGAATAT CACACAAAAC | 1140 |
| CAGTTCGTGG ATAAGGACAT GAAAGTGGGC GTGGCTTATC GCTATCAGGT GGTGAGCGTG | 1200 |
| GATAAAGATG GTTTAGAGTC GCACCCAAGC AAAGAAGTGC GTTTGTTTTT AGAGCGC | 1257 |

(2) INFORMATION FOR SEQ ID NO:29458178_c3_41.nt:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 378 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGCTTCCTA CTAAAACACG CATTAGAGAT CCGAACAAGC AAGAACTTAC ACAACCAAAA | 60 |
| ATAAAAGGAT TGAGTATGGG AAAAATTTTA GCTTCTTTGT TGGGTGGCGG AACAAATCTT | 120 |
| TTTACAGGTT TATCCAGTGA TTTGTTTTCT ATGATATTAA ATTTTTTGTT CTCCTGATG | 180 |
| TTAATGATGG GACTTAATGA AGCATTAGGG AAAAAATTTA ACTTGCCTAT GGACAATATC | 240 |
| AAGAATTTTA TGGCAGAAGT GCTGAAGAAT GGATTCGATA GTATCAAAAA CATGGGATCT | 300 |
| GCTTTGGTTG GTAATGGTTT TGGTAGCAGC AAATCAGACA AAACCACTAA TAAAATGAGT | 360 |
| GTCCCACAAG TAAGACTC | 378 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: OXYGEN-INSENSITIVE NAD(P)H NITROREDUCTASE

| | |
|---|-----|
| ATGGCGAACA TGATGATGGC AGCGGCCATG TTAGGGATTG ATTCTTGCCC GATTGAAGGG | 60 |
| TATGATCAAG AAAAAGTGGA GGCTTATTTA GAGGAAAAG GCTATCTAAA CACGGCAGAA | 120 |
| TTTGGCGTGT CGGTAATGGC CAGTTTTGGT TATCGTAACC AAGAGATTAC CCCTAAAACC | 180 |
| CGCTGGAAGA CAGAAGTTAT TTATGAAGTG ATTGAA | 216 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGGCCGGGC TTGTTTTGAT GGTGCTGCTC GCCAGTTATG AAAGCTTTGT TTCTAAATTA | 60 |
| GACAAGGTGG ATGCTAGCGA AATCACTTGG CTAAAACACA CAGATTTTAA CGCTTTAAAA | 120 |
| TTAAAGGTTT CCCTCTCCAT TGTAGCCATT TCGGCGATTT TCTTGCTCAA ACGCTACATG | 180 |
| AGTTTAGAAG ACGTTTTATC CAGTATTCCT AAAGACACGC CCCTATCGCA TAACCCTATT | 240 |
| TTTTGGCAAG TGGTGATCCA TTTGGTGTTT GTGTGTTT CAG CGCTGTTAAC CGCTGTTACC | 300 |
| AATAACATCG CTTTTTCGCA GAAAGAAAGG CAT | 333 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGATTACGA TCGTTATTGC AAAAGCGGGG AATATAGTCA AAGYCGATAT TTTTACGCAC | 60 |
| ATTAGCGATA TTAAAATGGG GCTTATTAAA GGAGGTCAAT GGGGGGTTAT TGGTTTAGGC | 120 |
| AATATCGGTA AAAGAGTCGC CAAGCTCGCT CAAGCTTTCG GGGCAAAGGT GGTGTATTTT | 180 |
| TCCCCTAAAG ATAAAAAAGA AGAATACGAG CGCTTGAGTT TAGAGGAATT GCTTAAAACA | 240 |
| AGCGGTATTA TCAGCATTCA TGCCCCCTTA AATGAAAGCA CGCGCGATTT AATCGCTCTG | 300 |
| AAAGAATTGC AAAGCTTAAA AGATGGGGCG ATTTTAATCA ATGTGGGGCG TGGGGGCATT | 360 |
| GTGAATGAAA AGGRTTTGGC TTRRTTTTA GAAACCACAG ATTTGTATTA CGCGAGCGAT | 420 |
| GTGTTT | 426 |

(2) INFORMATION FOR SEQ ID NO:29843937_f2_4.nt:

251

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 189 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: vacuolating cytotoxin of *Hpylori*

| | |
|---|-----|
| GTGAATTTC ACGCTAAAA TATTTCAATT GATAATTTGG TAGAAATCAA TAATCGTGTG | 60 |
| GGTTCTGGAG CCGGGAGAAA AGCCAGCTCT ACGGTTTTGA CTTTGCAAGC TTCAGAAGGG | 120 |
| ATCACTAGYA GTAAAAATGC GGAAATTTCT CTTTATGATG GCGCCACGYC AATTTGGCTT | 180 |
| CAAACAGMG | 189 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 930 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | |
|--|-----|
| ATGCGAACGC TCATTCTGTC GCTTCTAAAA CATGCGATTT TAATGGGCAT GCTTTTAAAA | 60 |
| GAATGCCAAG AAAAGTTAAA GCGTTCTTTA AATTTGAGTG CTAATCATTG CGTCTTGAGC | 120 |
| BCGGGGTATG GGGCGAGTTC AGCGATTAAG AAATTTCAAG AAATTTTAGG GGTGTGTATC | 180 |
| CTTTCAAAAA CGAAGAAAAA TTTAGAGCCG TATTTGAAAG ATATGGCTTT AAAGCGTGTG | 240 |
| ATTGTAGGGC CTTATGAGCA TCATTCTAAT GAAGTTAGCT GCGGTGAAGG CTTGTGTGAA | 300 |
| GTGGTGCGTA TCCCTTTAAA TGAACATGGT TTATTGGATT TAGAAATTTT AGAGCAAAC | 360 |
| TTAAAAAAA CCCCTAACAG CTTGGTTTCT GTGAGCGCGG CTTCTAATGT AACGGGAATT | 420 |
| CTTACGCCTT TAAAAGAAGT TTCATCATTG TGTAAGGAAT ATAGGGCTAT TTTAGCTTTG | 480 |
| GAATTTAGCGA ATTTTAGCGC GCATGCTAAC CCTAAAGATT GCGAATACCA AACCGGTTTT | 540 |
| TATGCGCCTC ATAAGCTTTT AGGGGGCGTT GGAGGGTGCG GTCTTTTAGG CATTTCTAAA | 600 |
| GAATTTGATTG ACACGCAAAT YCCTYCGAGT TTTAGCGCAG GGGGCGTGAT TAAATACGCT | 660 |
| AATCGCACAC GGCATGAATT TATTGATGAA TTGCCTTTAA GAGAAGAATT TGGCACGCCA | 720 |
| GAATTGTTGC AATTTTACAG GAGCGCTCTA GCGTATCAAT TAAGAGATGA ATGCGGTTTG | 780 |
| GAATTTTATCC ATAAGAAAGA AAACAACCTT TTAAGGGTGC TTGTGTATGG CTTAAAAGAC | 840 |
| TTGCCCGCTA TTAATATTTA TGGGAATTTA ACGGCGAGTC GTGTGGGGGT AGTGRCTTTT | 900 |
| AATATTGGAG GGATTTTCRC CTATGATTTA | 930 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 564 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|--|-----|
| GTGGCATGCA ACACCGCGAG CGCTCTGGCT TTAGAAGAGA TGCAAAAGTA TTCTAAAATC | 60 |
| CCTATTGTGG GCGTGATTGA GCCAAGCATT TTAGCGATCA AGCGGCAAGT GGAAGATAAA | 120 |
| AACGCCCCTA TTTTAGTGCT AGGGACAAAA GCGACGATTC AATCCAACGC CTATGACAAC | 180 |
| GCCCTGAAAC AACAAGGCTA TTTGAACATT TCGCATTTAG CTACTTCTCT TTTTGTGCCT | 240 |
| TTGATTGAAG AAAGTATTTT AGAGGGCGAA TTGTTAGAAA CTTGCATGCA TTATTATTTC | 300 |
| ACTCCCTTAG AGATTTTACC CGAAGTGATC ATTTTAGGTT GCACGCATTT TCCCTTAATC | 360 |
| GCTCAAAAAA TTGAGGGCTA TTTCATGGGG CATTTTGCcc TtCCAACGCC CCCCCTACTC | 420 |
| ATCCATTTCGG GCGATGCTAT TGTAGAATAT TTGCAACAAA AATACGCCCT TAAAAACAAT | 480 |
| GCATGCACAT TCCCTAAAGT GGAATTTTCAT GCGAGCGGCG ATGTGATCTG GCTAGAAAGA | 540 |
| CAAGCTAAAG AATGGCTCAA ATTG | 564 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| GTGTTGTGGG TGCTATATTT TTAAACCACT TTATTTATTT GCTCTTTGAT TGTTTTGTGG | 60 |
| TCTAAAAAAT CCATGCTCTT TGTGGATAAC GCTAATAAAA TCCAAGGCTT CCATCATGCA | 120 |
| AGAACCCAC GAGCCGGGGG GCTTGGGATC TTTCTTTCTT TTGCGTTGGC TTGTTATCTT | 180 |
| GAACCTTTTG AGATGCCTTT TAAGGGGCCT TTTGTTTTCT TAGGGCTATC GCTAGTGTTT | 240 |
| TTGAGCGGTT TTTTAGAAGA CATTAACCTT TCATTAAGCC CCAAATACG CCTTATTTTG | 300 |
| CAAGCTGTAG GGGTCGTTTG CATCATTTCA TCAACGCCTT TAGTGGTGAG CGATTTTTCG | 360 |
| CCCCTTTTTA GCTTGCCTTA TTTCATCGCT TTTTATTCG CTATTTTSTA TGCTGGTGGG | 420 |
| TATCAG | 426 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGGCGTGTA AATTTTGCCC TAAGATCAGA AAAACAGATT GGATTTTAT TTTAATCGCC | 60 |
| GCTTTAGGCT TTTATTCAGT TAATAAGCTA GGGTATGCGC CCAAATTCAA TACCCCACT | 120 |
| CCAAAATCTT CACGCCCTCT TTCACGCCCT ATTGAAAAGC CTAACAATAT GACTGAAGAA | 180 |
| GAAAGGAAAA AGCGTTTTAT AGAGTTGCAA AAAGCATGCT TACTTCATAA AGACAAAAG | 240 |
| GCATGCGAAG AGGTTTTT | 258 |

(2) INFORMATION FOR SEQ ID NO:30662792_c2_6.nt:

256

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: PREPROTEIN TRANSLOCASE SECA SUBUNIT

| | |
|---|-----|
| GTGGATTCCA TTTTAATTGA TGAAGCGAGA SCTCCTTTAA TCATTTTCAGG GCCTGTGGAT | 60 |
| AGGCGCATGG AAAATTACAA CAAGGCTGAT GAAGTCGCTA AAAGCATGCA AGTGGAAGTG | 120 |
| GATTTTCACCA TAGACGAAAA AAACCGCGCG ATTTTAAATCA CTGAAGAGGG GATTAAAAAA | 180 |
| GCCGAAAATC TCTTTGGCGT GGATAATTTA TACAAAATTG AAAACGCCGC CCTATCGCAC | 240 |
| CATTTAGACC AAGCCTTGAA AGCGAATTAC CTCTTTTTTTA TTGRTAAAGA TTATATTGTA | 300 |
| GCCAATAATG AAGTGGTGAT TGTAGATRRR TTTACCGRCC GTTTGYYTGA AGGGGAGGCG | 360 |
| CTT | 363 |

(2) INFORMATION FOR SEQ ID NO:30703183_f3_5.nt:

257

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGACGATCA CCACCCTATC TTTTTTATTC ACAACGCCAG AAGTGTTTGT CAATCAGGAT | 60 |
| TTCCCATGGC TTTCTGGGGC TGGAAGGCTA GTGGTTAAAG ACTTGCGGTT ATTTGCTGGA | 120 |
| GGCTTGTTTG TGGCCGGATT TGATCGAAAC GCTATTTGGA GGGTAAAGGG TTTTGCT | 177 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| GTGTTTTCTG GCAATAAAAG GGCTATAAAT TATCGCACGA TTGTCAGCGC CTTTGTGATT | 60 |
| CAAGTGGCTT TAGGGGCGTT GGCTTTATAT GTGCCTTTGG GCAGAGAAAT ACTGCAGGGT | 120 |
| TTAGCTAGCG GCATACAAAG CGTGATTGGT TACGGCTATG AGGGGGTACG CTTTTTATTT | 180 |
| GGCAATCTCG CTCCAAACGC TAAGGGCGAT CAAGGGATAG GAGGCTTTAT CTTTGCGATC | 240 |
| AACGTTTTAG CGATCATTAT CTTTTTTGCT AGCTTGATTT CACTTCTATA TTATTTAAAA | 300 |
| ATCATGCCTT TAGTAATCAA CCTCATCGGS GGGGCGTTGC AAAAATGCTT AGGCACTTCT | 360 |
| AAAGCAGAAA GCATGAGCGC AGCGGCTAAT AYTYYTGTGG CGCACACCGA AGACRCCCTT | 420 |
| AGTCAT | 426 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|--|-----|
| ATGCTGGTGG GTATCAGTAA CGCTATTAAT ATCATTGACG GGTTTAACGG GCTTGCATCT | 60 |
| GGGATTTGCG CGATCGCGCT TTTAGTCATT CATTATATAG ACCSTAGCAG TTTGTCTTGT | 120 |
| TTGCTCGCTT ACATGGTGCT TGGGGTTTAT GGTGTTAAAW TTCCCTTCAG GAAAGATTTT | 180 |
| TTAGGWCGAT CGGGGGGGCG TATTTTTTTGG GTTTGGTGWR CGGRATTTCT CTCTTGCATT | 240 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: invasion protein A

| | |
|---|-----|
| ATGCTACATA AAAAATATCG TCCTAATGTT GCGGCCATTA TCATGTCGCC AGACTACCCT | 60 |
| AACACATGCG AAGTTTTTAT CGCTGAGCGC ATAGACATTG AAGGGGCGTG GCAGTTCCCC | 120 |
| CAAGGAGGCA TTGATGAGGG AGAGACCCCT TTAGAAGCAC TCTATAGAGA ATTACTAGAA | 180 |
| GAAATTGGCA CGAATGAAAT AGAGATTTTG GCGCAATACC CTAGA | 225 |

(2) INFORMATION FOR SEQ ID NO:3166040_f3_7.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| GTGATGCTAA TGGCAATTTT TACCCCTTAT ATTCTTATTT TGAAAATGAT GAAAAAGTCT | 60 |
| ATGAGTTTAT TCGCCAATAT GGGGTTGGAG CAAATTTTTT GCAACAGAGA CATTAAAGAT | 120 |
| TTAAATGATT TTGTTTTTGG TATAGAAGTG GGGCTTGATA GCAATGCGAG AAAAAATCGT | 180 |
| AGCAGAAAGG CTATGGAAAA TCATCTTATC GGTCTTTTTG TCCAAGCTCA ATTAAATTTT | 240 |
| AAAGAACAAG TAGATATTAG AGAATTTGAG GATTTACGCC AGGCTTTTGG AAATGATACT | 300 |
| AAAAAATTTG ATTTTGTTAT TTTTAGCAAA GAGAAACTT ATTTTCATAG AAGC | 354 |

(2) INFORMATION FOR SEQ ID NO:31681556_f1_3.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 627 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGATCCGTC TAGCCGCGTT TTTTTTAGCT CTCGCTTGCG CGATTACGCC AAAAAGCCGC | 60 |
| CTTCTTTTAA AAAATGTCTT GCTCAACCCC ACTCGCATAG AAGCTTTTGA GGTTTTGAAA | 120 |
| AAAATGGGCG CTCATATAGA ATATGTTATC CAATCCAAAG ATTTAGAAGT TATTGGCGAT | 180 |
| ATTTACATAG AGCATGCCCC TTATAAAGCG ATCAGTATTG ATCAGAATAT CGCCAGCCTT | 240 |
| ATTGATGAAA TCCCCGCTTT AAGCATCGCT ATGCTTTTTG CAAAAGGCAA AAGCATGGTG | 300 |
| AGAAACGCTA AAGATTTACG AGCCAAAGAA AGCGATAGGA TTAAAGCGGT TGTTTCTAAT | 360 |
| TTCAAAGCTT TAGGGATTGA GTGCGAAGAA TTTGAAGACG GGTTTTATAT AGAGGGATTA | 420 |
| GGAGATGCGA GTCAATTAAA GCAGCATTTT TCTAAGATTA AACCCCCTAT TATCAAGAGT | 480 |
| TTCAATGATC ACAGGATTGC GATGAGTTTC GCTGTTTTAA CTTTAGCGTT GCCTTTAGAA | 540 |
| ATTGATAATT TAGAATGCGC GAACATTTCT TTCCCAACCT TTCAGCTTTG GCTCAATCTA | 600 |
| TTCAAAAAAA GGAGTCTCAA TGGAAAT | 627 |

(2) INFORMATION FOR SEQ ID NO:3203142_c1_5.nt:

263

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: PROBABLE COPPER-TRANSPORTING ATPASE

| | |
|---|-----|
| GTGGGGAGTT TGAAATTTTT AAACGCTATG GGGGTTGATT TAAAGGTTAA AGAGAGCGCT | 60 |
| AATATCATGG TAGGCTTTGC GAAAAATAAG ACCTTATGCG CGTTATTCAT TTTAGAAGAG | 120 |
| CGTTTGAAAG CTAACGCTAA AGAAGTCATT CAGGCTTTAC AAAATCAAGG CTTGGAATTA | 180 |
| GAAATTTTAA GCGGGGATAA TGAAAGCTCG GTTAAGGAGT GCGCG | 225 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|--|-----|
| ATGGAGGCTT TAAACGCTTT GAACGCGCAA AGTGATGAGC AAATTTTATG CGAGGGTTAT | 60 |
| TTTGTGTTGT TGCAAATCTT AGAGCCTATG ATCCCGCACA CGGCATGGGA ATTGAGCGAG | 120 |
| AGGCTTTTTTA AAAGAGAGAA TTTCAAGCCT ATAGAAGTAG ATGAAAGCGC TTTGATAGAA | 180 |
| GACTTTATGA CTTTAGGGCT TACCATTAAT GGCAAAAGGC GCGCGGAATT GAAAGTCAAT | 240 |
| ATTAACGCTA GCAAAGAAGA GATTATTATT TTGGCTAAAA AAGAATTAGA GAAATATTTA | 300 |
| GAAAACGCGA GCGTTAAAAA AGAAATTTAT GTGCCTAATA AACTTGTTAA TTTTGTTACC | 360 |
| GCA | 363 |

(2) INFORMATION FOR SEQ ID NO:32144532_f1_2.nt:

265

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGAAAGAAA GTATTAAATA CTTGCTAGAA AGCGTGGGGC TAGTGCTTTT AATGAGCGTG | 60 |
| AATCCGGGCT TTGGCGGGCA GAAGTTTTTA GATCTAGTGC TAGAAAAGTG CTTGAAAGTT | 120 |
| AAAGAACTGA TCAAACGCTA CAACCCTAGC TGTCTTTTAG AAGTGGATGG GGGCGTGAAT | 180 |
| GATAAAAATA TCTTTGAACT CCAACAAGCG GGCGTGGATG TGGTGGTTTC AGGGAGTTAT | 240 |
| ATTTTTGAAT CCAAAGATYG TAAGCTGGCT ATTGAAGGCT TACAGAATGT CAGACAACCT | 300 |
| CTTGCA | 306 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 393 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| GTGCATGACG GCGTGCTTGG GTGGGTAGGC TTCACTTTGA TTGCGAGCAT GTATCACATG | 60 |
| ACCCCTAGGC TTTTCAAAAG AGAGATCTAT TCAGGAAGAC TTGTGGATTT CCAATTTTGG | 120 |
| ATCATGACTT TAGGGATTGT GCTTTACTTT TCGTCCATGT GGATTGCAGG GATCACGCAA | 180 |
| GGGATGATGT GGAGGGATGT GGATCAATAC GGGAATCTCA CTTACCAATT CATTGACACG | 240 |
| GTTAAGGCGC TAATCCCTTA TTACAATATT AGAGGCGTTG GGGGTCTTAT GTATTTTATT | 300 |
| GGATTTATTA TTTTGTCTTA CAATATCTTT ATGACAATCA CGGCAGGCAA AAAATTAGAG | 360 |
| CGTGAGCCCA ATTACGCCAC SCCTATGGCA RRA | 393 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1323 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|------|
| ATGATAACGC | TCTTTAGTTT | TGGAGCGTTC | GCTTACTATT | TCGTGTCTTC | TCAAATCAGT | 60 |
| CACGAAAAC | ATCAAAACGA | AATGCGCCAT | TACCAGTTTG | TTACCACTAT | CAATGAAATT | 120 |
| TTAAATAAC | ACTCTGATTA | TAGAGCCATA | GAAGATTACC | TCTATAAAAT | TGGCTTTAGA | 180 |
| GAAACCACAA | TAGAAAATTT | AGAAAAGGTT | TTAGCCAAAA | GACGCCACCA | GTTGCACCAC | 240 |
| AGAAATATTT | GGTATGCTGA | AGTGTTTAAA | TTCAGCGATA | TGGTTTTTAT | CCTTTTAAAA | 300 |
| AAGGATGAGC | ATTTTGTGCT | TTATAAAGAT | TTGCATTCGG | TTTCTTATAG | GAATTATTTT | 360 |
| TTAGCCATTA | CGGTGGGTTT | ATTATTGATT | TTATTCCTCT | TTTTATTTGT | TTTGCAGAGT | 420 |
| TTATTGCCTT | TAAGAGAGTT | AAGATCTCAA | GTGAAACGCT | TCGCTCAAGG | GGATAAAAGC | 480 |
| GTGAGTTGTA | AAAGCAAGCA | AAAAGATGAA | ATAGGGGATT | TGGCTAACGA | ATTTGACAAT | 540 |
| TGCATCCAAA | AAATCAATGC | GATGAATGAA | TCTCGGGTTT | TATTTTTGCG | CTCTATCATG | 600 |
| CATGAATTAC | GCACCCCTAT | CACTAAGGGC | AAGATACTAA | GCTCTATGCT | CAAAGAAGAG | 660 |
| CTGTCTTGCA | AACGCTTTTC | ATCTATATTT | GATCACTTGA | ACATGTTGAT | TGAGCAATTT | 720 |
| GCCCGCATTG | AGCAGCTCGC | TTCCAAAAAT | TATGGGAGCA | ATAAAGAAAA | ATTTTTAATG | 780 |
| AGCGATTTGA | TAGATAAGAT | TGAAAAAATG | CTTTTAATTG | ATGAAGATAA | AAAAAGCCCT | 840 |
| ATCCATGTAT | CCTCTTCAAA | TTACATCATT | GAAGCGGATT | TTGAATTGTT | TGCTATAGCG | 900 |
| TTAAAAAACA | TGATAGACAA | TGCGATCAAA | TACAGCGATG | ACAAACAGGT | GTTTTTGGAT | 960 |
| TTCATAGGGA | ATAATTTAGT | GGTGTCCAAT | AAAAGCAAAC | CTTTAAAAGA | AGATTTTGAA | 1020 |
| AAGTATTTGC | AACCCTACTT | TAAATCTTCT | AACCCAGCC | AAGCCCATGG | GTTTGGGTTA | 1080 |
| GGCATGTATA | TCATTAAAAA | CGCTTTAGAG | GCTATGGGAT | TGAATTTGAG | CTATCATTAT | 1140 |
| AGCAATGGAA | GAATCTGTTT | CACTATCCAT | GATTGCGTTT | TTAATAGTTT | TTACGATTTA | 1200 |
| GAAGCGGATA | ATGAAGAGCT | ACCCCCCCCC | GAAAATTTGA | GAGAGGTGAA | GGGAATGAAG | 1260 |

GGAACAGAAA AAGCCAATTG TGGGGTTAAA GAAAAACAAA AAGAGAGAAC ATGTTCAAAC

1320

268

GAT

1323

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| GTGCTTCTCC TTTCTCGTAT GGGTATCGCT TTTGCCCCACT CTATTTTTTTG GTCCATCACG | 60 |
| GCTTCTTTAG TCATTCGTGT CGCGCCAAGA AACAAAAAAC AACAGGCCTT AGGGCTGTTA | 120 |
| GCGTTAGGGA GTTCGTTAGC GATGATTTTA GGGTTGCCGC TTGGGAGGAT CATTGGGCAA | 180 |
| ATTTTGGATT GGCATCCAC TTTTGGCGTG ATTGGGGGCG TTGCGACTCT TATAATGCTG | 240 |
| CTTATGTGGA AATTGCTCCC GCATCTACCG AGTAGAAACG CCGGCACGCT CGCAAGTGTT | 300 |
| CCTATATTAA TGAAACGCCC GCTTTTAGTG GGGATTTATT TGCYTGTGAA TCATGGTTAT | 360 |
| TTCTGGGCAT TTCACCACTT A | 381 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | | | | | | |
|-----------|-----------|-----------|-----------|-----------|-----------|-----|
| ATGCGCATT | TCATAAGGT | ACTTTCATT | AAAATGAAC | CTTTTTTAA | ACTCGCGCT | 60 |
| GCTTCTTTG | TGGGGGGG | TTGGTATG | TTCAATGG | AAGGCTCT | GATTGTCG | 120 |
| ATAGGGATT | TTGTGTTG | CTTGTTTG | TTTTTTAT | CCCCTGTG | TTCCAAGAC | 180 |
| CCAGAAAAC | GAGAAGAAT | CATAGAAC | CTTAAAAAA | ACCATGAG | GAAAATGAT | 240 |
| TTACAAGAC | AGCAAAAAG | AGAGCAAAT | CGCCTCTAT | AAGCCAAAA | AGAGCGAG | 300 |
| AGCAGGCAA | AACAAGAC | TAAAGAAC | ATGAAAAAA | ACTCA | | 345 |

(2) INFORMATION FOR SEQ ID NO:32595137_f1_1.nt:

271

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| GTGCGATCTT GCAAACAGAT TTTTGATAAG GGTTTAAAGC CCTATTATAA ACATTCTGTT | 60 |
| TGCTTAAAGC CTTTTTTTAG GTTTTGTTTT CTCAAAATTC ATGCTTATCA ACAGCGTTAT | 120 |
| AGAGCGTTTG CTCTAACGCT CTTTCTTGT AAGTTTTTTA ACGCTTGTA GATTTTTATT | 180 |
| CCCATAATTG ATTTTAAAT CGTTTTTATC CCTATTCTAA AACACCAAGC CAAGCTAAAA | 240 |
| AGAGTCTCTA ATGCCTAT | 258 |

(2) INFORMATION FOR SEQ ID NO:32600912_c1_5.nt:

272

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGTGTGGAA TGGGGTTTAT TGGCTTCAAA ACAAACTTA CTCAAACAAA GGCATTTATT | 60 |
| ATATTGATCC CAATCTTTCA GGACAGAGCG GTCAAAGCGG CAACACGCTC AGCACCTATA | 120 |
| CAGCTAATTT GT | 132 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1680 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|--|------|
| ATGGGGAATT TTAATAGCTA TGGCGATTTG GTGTTTAACC TCAGTCATTC AGTTAGTCAT | 60 |
| GCTATTATCA ATACTCAAGG CACAGCGACG ATCATGGCCA ATAATAACCC TTTGATCCAA | 120 |
| TTCAACGCTT CTTCAAAAGA AGTGGGTACT TACACGCTGA TTGATAGCGC TAAAGCCATT | 180 |
| TATTACGGGT ATAACAACCA AATCACAGGA GGCAGTAGCC TGGATAATTA CCTTAAGCTT | 240 |
| TATGCGCTCA TTGATATTAA TGGCAAGCAC ATGGTGATGA CTGACAACGG CTTAACCTAT | 300 |
| AACGGGCAAG CCGTGAGCGT TAAAGATGGC GGTTTAGTTG TAGGCTTTAA GGA CTCTCAA | 360 |
| AATCAATACA TTTACACTTC CATTCTTTAT AATAAAGTGA AAATCGCTGT TTCTAATGAT | 420 |
| CCTATCAATA ACCCACAAGC CCCCACTTTA AAACAATATA TCGCTCAAAT TCAGGGCGTT | 480 |
| CAAAGCGTGG ATAGCATCRA TCAAGCTGGG GGAAATCAAG CGATTAATTG GCTCAATAAA | 540 |
| ATCTTTGAAA CTAAAGGAAG CCCTTTATTC GCTCCCTATT ATCTAGAGAG CCACTCCACA | 600 |
| AAAGATTTAA CCACGATCGC TGGAGATATT GCTAACACTT TAGAAGTCAT CGCTAACCTT | 660 |
| AATTTTAAAA ATGACGCCAC TAATATTTTA CAGATCAACA CCTACACGCA GCAAATGAGT | 720 |
| CGTTTAGCCA AGCTCTCTGA CACTTCAACT TTCGCCC GTT CTGATTCTT AGAACGCTTA | 780 |
| GAAGCCCTTA AAAACAAGCG ATTCGCTGAT GCGATCCCTA ACGCTATGGA TGTGATTTTA | 840 |
| AAATACTCTC AAAGGAATAG AGTTAAAAAT AATGTGTGGG CGACAGGAGT TGGAGGGGCT | 900 |
| AGTTTCATTA GTGGAGGTAC TGRAACTTTA TATGGTATCA ATGWAGGGTA TGATAGGTTT | 960 |
| ATTAAGGGCG TGATTGTGGG AGGTTATGCC GCTTATGGGT ATAGCGGGTT CCATGCAAAC | 1020 |
| ATCACTCAAT CAGGCTCTAG CAATGTCAAT GTGGGCGTTT ATAGCCGAGC GTTTATCAAA | 1080 |
| AGAAGCGAGC TAACCATGAG CTTGAATGAG ACTTGGGGAT ACAATAAAAC TTTCATCAAC | 1140 |
| TCCTATGACC CCCTACTCTC AATCATCAAT CAGTCTTACA GATACGACAC TTGGACGACT | 1200 |
| GACGCTAAAA TCAATTATGG CTATGATTTT ATGTTTAAAG ATAAAAGCGT TATTTTTAAA | 1260 |

| | | | | | | |
|------------|------------|------------|------------|------------|------------|------|
| CCCCAAGTAG | GCTTAAGCTA | TTATTACATT | GGTTTGTCTG | GTTTAAGGGG | CATTATGGAT | 1320 |
| GATCCTATTT | ACAACCAATT | CAGAGCCAAT | GCTGACCCTA | ATAAAAAATC | CGTTCTAACG | 1380 |
| ATCAATTTTG | CCCTAGAAAG | TCGGCATTAT | TTCAATAAAA | ACTCTTATTA | TTTTGTGATT | 1440 |
| GCGGATGTGG | GCAGAGACTT | ATTCATTAAT | TCTATGGGGG | ATAAAATGGT | GCGTTTCATC | 1500 |
| GGTAATAACA | CCCTAAGCTA | TAGAGATGGT | GGCAGATACA | AACTTTTGC | TAGCATTATC | 1560 |
| ACAGGCGGGG | AGATAAGATT | GTTCAAAACC | TTTTATGTGA | ATGCGGGCAT | AGGGGCTAGG | 1620 |
| TTTGGGCTTG | ATTATAAAGA | TATTAATATT | ACCGGAAATA | TTGGTATGCW | SYATRCTTTT | 1680 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 423 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | | | |
|-----------------------|-----------------------|------------------------|-----|
| ATGGAGTCGA ATCAWTCAC | CCCCATGGCA TTAATATCAT | GCTCACCTAA CGCTAAAGGG | 60 |
| GCGGACATTA AAGGCTATAA | CGGCTTAGTG GGGGAATTGA | TTGAAAGGAA TTTCCAACGC | 120 |
| TATGGCGTGC CGTTACTGCT | TTCTACGCTC ACTAACGGCC | TATTGATTGG GATCACTTCG | 180 |
| GCTTTAAACA ACAGAGGCAA | TAAAGAAGAG GTGACTAATT | TCTTTGGGGA TTATCTTTTA | 240 |
| TTGCAATTGA TGAGGCAAAG | CGGCATGGGG ATCAATCAAG | TGGTCAATCA AATTTTAAGA | 300 |
| GACAAGAGCA AGATCGCCCC | CATTGTGGTG ATTAGAGAGG | GGAGTAGGGT CTTCATTTTCG | 360 |
| CCCAATACTG ACATCTTCTT | CCCTATACCC AGAGAGAATG | AAGTCATCGC TGAGTTTTTG | 420 |
| AAG | | | 423 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: PHOSPHATIDYLSERINE DECARBOXYLASE

| | |
|---|-----|
| GTGAATTTTT ACCTTTCGCC CAAAGATTAC CACCACTACC ACGCCCCTTG CGATTTAGAA | 60 |
| ATTTTAGAGG CTCGTTATTT TGCGGGGAAA TTACTACCAG TCAATAAGCC CTCATTACAC | 120 |
| AAAAAACAAA ATCTGTTTGT GGGCAATGAA AGG | 153 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 699 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: PROBABLE ABC TRANSPORTER

| | |
|---|-----|
| ATGGATATTT TAAAAGCAGA GCATTTAAAC AAACAGATTA AAAAAACCAA AATCGTTTCA | 60 |
| GATGTTTCTT TAGAAGTGAA AAGCGGCGAA GTGGTGGGGC TTTTAGGGCC TAATGGGGCG | 120 |
| GGTAAAACCA CCACCTTTTA CATGATATGC GGGCTTTTAG AGCCTAGTGG GGGGAGCGTT | 180 |
| TATTTAAACG ATGTGGATTT AGCTAAATAC CCCTTACACA AGCGTTCTAA CTTGGGCATA | 240 |
| GGCTACTTGC CCAAGAATC CAGTATTTTT AAAGAATTGA GCGTGGAAGA GAATTTGGCC | 300 |
| CTAGCAGGGG AGAGCACTTT TAAAACTCT AAAGAGAGCG AAGAAAAAAT GGAAAGCTTG | 360 |
| CTTGATGCTT TTAATATCCA AGCCATAAGA GAGCGCAAGG GCATGAGCTT GAGTGGGGGA | 420 |
| GAAAGAAGGC GCGTAGAAAT CGCTAGGGCT TTAATGAAAA ACCCTAAATT CGTGCTGTTA | 480 |
| GATGAGCCTT TTGCGGGCGT GGATCCGATT GCGGTGATTG ACATTCAAAG AATCATTGAA | 540 |
| AGCTTGATTG GATTAAACAT TGGCGTGTTG ATTACTGATC ACAATGTGCG AGAGACCTTG | 600 |
| AGCGTGTGCC ATAGGGCGTA TGTGATCAAA AGCGGCACGC TTTTAGCGGC GGAACGCTA | 660 |
| ATGAAATTTA TGAAAACGCT TTGGTGCGTA AGTATTATT | 699 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 474 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: HYPOTHETICAL ABC TRANSPORTER

| | |
|--|-----|
| ATGAAAGAAA TCGTTACAAT AGAGAATGTG TCTTTTAACT ACCACAATCG CGCTATTTTTT | 60 |
| AAGGATTTTA ATTTAAGCAT TCAAGAAGGG GATTTTTTTAT GCGTTTTAGG GGAGAGCGGG | 120 |
| AGCGGTAAAA GCACGCTTTT AGGCTTGATT TTAGGGCTTT TAAAACCCAG TCTGGGGAGC | 180 |
| GTTAAAATCT TTAATGAGAC CCTTTCAAAC AACGCTTTTT TACGCCAAA AATAGGCTAT | 240 |
| ATCGCTCAGG GCAATTCCTT ATTCCCTCAT TTAAACGCCT TACAAAACAT GACTTTTTTGC | 300 |
| CTTAATTTAC AAGGCATAAA CAAACAAGCC GCTCAAAAAG AAGCCAAAGC CTTAGCGTTA | 360 |
| AAAATGGGGT TAGACGAGAG CCTTATGGAT AAATTCCCTA ATGAATTGAG TGGGGGGCAA | 420 |
| GCCAAAGAGT GGGCATTATT AGGGGGATTA TCCACAGGCC AGAACTCATT TTAT | 474 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 573 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGATTTTCC CCGAGCGCTT TCAAAACGCC TTTTtagggT TAAGCGAATT GTTTTACTAC | 60 |
| GCTTCCAGCT TGAGTTTTTA TACGATTTTG TCTTTATCGC CTATTTTGTT GTTCGTGTTC | 120 |
| AGTCTTTTTG TGTCTCATTA CTTGCAAGCG CACAGCGGTG AAATGGAAGC CTTGATTTTC | 180 |
| CCTAACGCTC CTAAACTCAT TGGCGCGATT AAGGATTTTT TAGAAAATTT TAAAAAACA | 240 |
| GACATGACCT TAGGCACGCT TGAAGAGGTG TCTATTGTGG TGGCGTTGGT GCTTTTTTGT | 300 |
| GAAAACTACC GCTCCATCGC GTCAAAAATT TTTGACGCAA AGCCCAGAGA TTATGCGCAT | 360 |
| TTTAAGGGTA AAGAAATCTT TTTATTTTGG GGGTTTGGCA CGACTTTAGT GTTTTTATTC | 420 |
| GCTTTGCCTT TGGTGGTGTT TTTTGATATT AAGATCCAAG TGTTTTTTGA AGATAAAGAT | 480 |
| TCAAGCTTGT TGCATGTTTT AAGATGGATA GGCACCTACG CGTTTTTTTT GATCCTTTTT | 540 |
| ACCATTCCCA CGAATAAGGT GTTTAAACTA YYA | 573 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 729 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGGTTTTGA TGATTTTCAC AAGCATCTTG AAGATAGCGT TAAAAGTTTT ATCAGAGCGA | 60 |
| AAAAAAAATC GTTATGGTTT TCCTAGAATC TTTGATGTTG CAGACATAGA ACAAGAAGAG | 120 |
| AGGGAAGTCA TTGAATGGCG AGAAAAAAG AAAGCGTCAA AACAAAGCTA TAAACAAAAC | 180 |
| TTTCAAATCA ATAAAATCGC TAACGATTTA AAGCGTGATA AGATAGTGGA TAAAAGAACG | 240 |
| ATTTTAAGCG TGATAGACGC TGATATAGAG CGTGGTTTTA TCCCGCCTAA AGATTTGTTA | 300 |
| AAACAATTAG AAAAAATTAG CGCTTCTCTT TCTAAAGACA TCGTAATAAC GATAAAGCAA | 360 |
| GTAGAAAAAT TAGAGCTTAA CTATGCGCTA ATAGACAATA TCCAACATAA CACGCTTGAT | 420 |
| GACACGCTTG ATTTTACCTT TATTGTTGGG GATTCTTTGA GCGTTCAGTC GCTTTATGTT | 480 |
| ACCTTTAATC TTGTGATTGA TATTGATAGA CCCATGAGCG AGCAGTTTCT CAACCWTATT | 540 |
| GGGAAATTGG GGAGTTTTGA ATCTAGAGAG CAAGCGTTAG AGTGGGTGCG ATTATCGCAA | 600 |
| ACTAAACTGA TCATTGAAAC GCCTAAAGAA GCGTTAAAAA ATGCGGAATT ATCACAAATT | 660 |
| GAAGAAATAT TGACCGGCTG TATTTTTAAT GGCGCTTACC GCCTTCAAAA CGATCTTAAG | 720 |
| AAAGGGCGA | 729 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 708 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|--|-----|
| GTGAGTGAGG TCGCGAGCGT GGGGGGCTTT GTGAAGGATT ATGAAGTAAC GCTTCAAAAC | 60 |
| GATTCTTTGA TCCGTTATAA CTTGAGTTTA GAACAAGTCG CTAACGCGAT TAAAAATTCC | 120 |
| AATAACGATA CCGGTGGGGG CGTTATTTTA GAAAACGGGT TTGAAAAAAT TATAAGATCG | 180 |
| CATGGCTATA TCCAATCTTT AAACGATTTA GAAGAAATTG TGGTTAAAAA AGAAGGGGCT | 240 |
| ATCCCTTTAA AAATCAAAGA TATAGCGAGC GTTAGGCTAG CGCCCAAACC GCGCAGAGGG | 300 |
| GCGGCTAATC TCAACGGCGA TAAGGAAGTG GTGGGCGGGA TTGTTATGGT GCGCTATCAC | 360 |
| GCTGACACTT ATAAGGTGCT TAAAGCCATT AAAGAAAAAA TCGCCACCTT ACAAGCGAGT | 420 |
| AACCCTGATG TGAAAATCAC CAGCGTGTAT GACAGGAGCG AATTGATTGA AAAAGGCATT | 480 |
| GACAATTTGA TTCACACGCT CATAGAAGAA AGCGTCATTG TGCTAGTCAT TATTGCGATT | 540 |
| TTCTTACTGC ATTTCAAGGAG CGCTTTAGTG GTGATTATCA CTCTGCCTTT AAGYGTGTGC | 600 |
| ATCAGTTTCT TGCTCATGSG TTATTTCRAT ATTGAAGCGA GCATCATGAG TTTGGGGGGC | 660 |
| ATTGCAATCG CTATAGGGGC GATGGTGAAT GCGGCGATTG TGATGGTG | 708 |

(2) INFORMATION FOR SEQ ID NO:33476715_c1_10.nt:

282

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 525 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: KERATIN- TYPE II CYTOSKELETAL-intermediate filame

| | |
|--|-----|
| GTGGAAACTT TTCTTAGAAT TTTTGAAAAA GATATTTTTA ACACGCCCTA TAAATTAGAA | 60 |
| GTCATTAACG CTACTGAGGG GGGGGCTAGG ATTAAAGGGA CTAAAGAAAT GCCCTTTAAA | 120 |
| GAAGTGTGCG AAAAAWTAGA CAAATCCAAG CCAAAGCCTC CTATCAATCT TATTTATCCC | 180 |
| ACCCAATCAG AACAGGCTAA AAATTTAAAG ATCGCCAAGA AAAAATGCGA AGAGATCATC | 240 |
| AAATACGCCA ATGAGAAAAA AACGCAAGTT GAAGAAGCGT TTTTAAAGGT GGCAGAGTTT | 300 |
| TTAGAAAAAG TGGAAAAGCT TCATGAAAAA AACAAATTAG AAGAGTTGGA TTTTGAAGAA | 360 |
| TTAGAAAATT TGAGCGCTGA AATTGATAAC GTTAAAGAGC TTTTGTGATGA CAAACGATTC | 420 |
| AATTCGTATT TTATGGATGC GATACAATCT TACATTTTCC ACCAGGAATT GCATATCGCT | 480 |
| GAAATCGTGT GTAAAAAAAC GAGTAATGAA GACGGGATTA AGGGC | 525 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 678 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGAAAACGC CTTGCAACGC CTATTTTCTC AAAACGCCAC CCAAAAACAA AAAAAGAAGA | 60 |
| GTTTATGTTA ATTTAGCGGT GTTCTTTTTT TTATTGCTAG CGAGCGCTTT ATGGCTCATT | 120 |
| CCTAGAAGTG CCATAGAAGR AAAGCCCTTA GTCGTGGCGA CAAAACCTAG CAGCGAGCAG | 180 |
| TATATTTTGG GCGAAATTTT AAGCCTTTTG TTAGAAAAAC ACCATATCCC TATCAAGCGA | 240 |
| GCGTTTGGCA TTGGTGGGGG GACGATGAAT ATCCATCCGG CATTGATTAG GGGCGATTTT | 300 |
| GATTTGTATG TGGAATATAC CGGCACCGCT TGGGTGAACA CGCTCAAAAA CCCTTTGACT | 360 |
| CAAAAAGTGG ATTTTGAAAC GATTAAAAAG CGTTATGAGA AGGAATTTAA TCTTTTGTGG | 420 |
| GTGGGACTTT TGGGCTTTAA TAACACCTAT TCTTTAGCGA TTTCTAAAGA AGACGCTCAA | 480 |
| AAATACGCAA TTGAAACTTT CAGCGATTTA GCCTTTCATA GCCCGAATTT TGATTTTGGA | 540 |
| GCGGAGYTTG ATTTTTTTGA AAGAGAGGAC GCTTTTAAGG GCTTAATCAA AGCTTATCGC | 600 |
| TTTCATTTTA GAAGTTTGCA TGAAATGGAY ATTAATTGTC GTTATAAAAG TTTTGAATCC | 660 |
| CTCATAAGAT YAACGCTT | 678 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 237 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| GTGATGGTTT ATAAACTCCC CAAACACCAG CAAAATAAGG TCATGATTTT AGGCTTGGGC | 60 |
| TTAGCGATGA TCACTCGTAT AGGGCTTTTA GGGAGCTTGT TTTTCATCAG CCATTTGCAA | 120 |
| AAGCCTTTAT TCGCTATAGC GGGCATGAGC TTTTCATGGC GTGATGTGGT GCTGCTTTTA | 180 |
| GGGGGGGCGT TTTTGGCTTT TAAGGCGTTA GTGGAATTAA AAAGAGCAGA TCTATCC | 237 |

(2) INFORMATION FOR SEQ ID NO:33986087_c3_18.nt:

285

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 630 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGTTTGTGG TTTTATAGA AGGTTTGGT TTAGCGATTT CTTTGTGCGC GGCGGTGGGG | 60 |
| GCGCAATCCT TGTTTATTGT GGAAAGGGGG ATGGCTAGGA ATTATGTGTT TTTGATTTC | 120 |
| GCCTTGTGTT TTATGTGCGA TATTGTCTTA ATGAGCATGG GCGTGTTTGG CGTGGGGGCT | 180 |
| TATTTTCGCTA AAAACCTTTA TTTGAGCTTG TTTTGAATT TATTTGGGGC AGTTTTTACC | 240 |
| GGATTTTACG CTTTTTTGGC TTTAAAAACC CTTTTTCAA CCTTTAAAA AAAGCAAGTC | 300 |
| CAAACCCCTA AAAAATTATC CTTAAAAAAG ACCTTATTAT TCACTTTAGG CGTTACCTTA | 360 |
| CTCAATCCTC AAGTGTATTT GGAAATGGTG TTTTAAATTG GCGCGAGCGC TATGTCTTTT | 420 |
| AACCTAGTGC AAAAATTCGT CTTTCTAGCT GGCACCTTAT CGGCTGCCTT TTCTTGGCTT | 480 |
| TTATTGTTAT GCACCATGTC CTTACGCTAT GGCTCTAAAC TTTTGAACAA CCAAAAAATC | 540 |
| TTTATGGGCG TGAATCTCTT TGTAACCGCT ATCATGGGAA CGCTCAGCGT TACTTTATTC | 600 |
| AGGGATTTTT TAGCGTTATT GAGCAAAACC | 630 |

(2) INFORMATION FOR SEQ ID NO:34089087_f3_3.nt:

286

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 888 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|--|-----|
| GTGAAGCCAA AGAGCATGAA AGAGAAGCTA AGAGGCGCTA TGGTGAATAT CTTAAGGATA | 60 |
| AAAATGATTG AAATAAGCGA ATGGTTGCAA AACTAGACG ATGCCTTAGA TAAAGTTGTT | 120 |
| GCTAAAAAAG AGCCAGAGAG TTTTCTCAAG CCGATCATT CACCAATAGA GGACTACCAA | 180 |
| AAGAGTGTCA GGCAAATTCA AGCGCAATTC ACAGACGCGC CGAAGTTCAA TGAAGAGGGT | 240 |
| GCTTACCCTC AATTTTTTAAG CTGTGGTTTA TTGCAAGTTA GGGGCAAAAA TGGTGCTAAC | 300 |
| ATGGAATTTT TATTGCCTAA AGTTTATCCT TTCCCCCCTA AAAGCTTGTA TATAGAGCAT | 360 |
| GAAAAAGACG GGCAGTTTTT GAGAGAAATG CTCATGCGCT TACTCTCCAG CGCGCCTTTA | 420 |
| GTGCAATTGG AAGTGATCTT AATTGATGCG TTGAGCTTGG GGGGCATTTT CAATCTGGCC | 480 |
| AGAAGGCTTT TAGATAAAAA CAATGACTTT ATTTACCAGC AAAGGATTTT GACCGAAAGC | 540 |
| AAGGAAATAG AAGAAGCCCT AAAGCATTTG CATGAATATT TAAAGGTTAA TTTGCAAGAA | 600 |
| AAATTAGCCG GTTTTAGAGA TTTTGTGCAT TATAATGAAA ACGCCAAAGA CTCCTTGCCT | 660 |
| TTAAAAGCGC TTTTTTTAAG CGGGGTGGAT GCTTTGAGTA AAGACGCGCT TTATTATCTA | 720 |
| GAAAAGATCA TGC GTTTTGG CTCTAAAAAT GGGGTTTTGA GCTTTGTCAA TTTGGAGAGC | 780 |
| GAAAAAACA ATCAATCCGC AGAAGATTTG AAACGCTATG CGGAGTTTTT TAAAGACAGG | 840 |
| ACAAGTTTTG AGTGSTTAAA ATACCTTAAT GTAGAAATCA TCAGCGAT | 888 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| GTGCTTATAA GCGTGATGAT AGGCCAAAAT CAAGTCTTAG GCTTTATAGG GACTAATTTC | 60 |
| AAGCAAGAAT TAGTCGTGGA TTTCATTGTC CCAAGCGCTG AAATCAACAT AGGCRRTCAA | 120 |
| GTGYTAACGA GCGGGCTAGA TGGGATTTTT GGAGCGGGGG TGTGTGTGGG TGAAGTTTCA | 180 |
| AGCGTTGAAG ATCATTACAC TTATAAAAGC GCGGTGTTGA AAAACGCTTT TTTAAGCGAA | 240 |
| GCCAAACTTT TAAGGCATGT GTTTTAAAGC GGTGTGAAAA AC | 282 |

(2) INFORMATION FOR SEQ ID NO:34099062_c1_8.nt:

288

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGGAAGCGC AATTACGATT TACGGGTGTT GGAGGGCAAG GCGTGTTGTT AGCGGGAGAG | 60 |
| ATTTTAGCTG AGGCTAAGAT CGTGAGCGGG GGCTATGGCA CTAAGACTTC CACCTACACT | 120 |
| TCGCAAGTGC GTGGAGGTCC CACTAAAGTG GATATTTTGT TAGATAAAGA TGAAATTATT | 180 |
| TTCCCTTATG CTAAAGAGGG CGAGATTGAT TTCATGCTTT CAGTCGCTCA AATCAGCTAC | 240 |
| AACCAGTTT | 249 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 609 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGCAAGCTT GGGTGGATAA GCCGGTATTG TTAGAGCCAG ATAGTAACGC CCAATACGCC | 60 |
| GCTGTCATTG AAATTGATGT GGCAGAAATC ACGGAGCCTA TTTTGGCATG CCCTAATGAC | 120 |
| CCTGATGACG TCGCTACTTT GAGCGAAGTT TTAGCGGATA CGACCGGCAA AAGACCCAC | 180 |
| GCTATTGATG AAGTGTTTAT TGGCTCTTGC ATGACGAATA TTGGGCATTT CAGAGCCTTT | 240 |
| GGTGAAATCG TTAAAAACGC CCCTCCCAGT CAAGCACGCC TTTGGGTAGT GCCACCCAGT | 300 |
| AAAATGGACG AACAAGAGCT TATTAATGAG GGCTATTATG CGATTTTGGG GGCTGCCGGG | 360 |
| GCAAGGACTG AAGTACCAGG CTGTAGCTTG TGCATGGGCA ATCAAGCGAG GGTTAGGGAT | 420 |
| AATGCGGTCG TTTTTTCTAC TTCCACACGG AATTTTGATA ATCGTATGGG TAGAGGGGCT | 480 |
| AAAGTGTATT TGGGCAGTGC GGAGCTTGGG GCGGCGTGCG CTTTACTAGG GAGGATCCCC | 540 |
| ACTAAAGAAG AATACATGAA TTTAGTGAGT GAAAAGCTAG AGAGCCAAAA AGACAAGATC | 600 |
| TATCGCTMC | 609 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 660 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| GTGGGCAATG CCGGGGTGGC TTTAGCGGGT TTGATGAGCG ATGAAATTTA TTTGTGCGCT | 60 |
| TTAGATTGCG CTTATATCAA AGGGTTTAAA AAGCACGCTC AAAATTCCTA TTATGGAGAT | 120 |
| GAAAAAGAGA TTGACACCTC ATCTTTAATC AGCGTAGAGG GTAATGTTGA AGGTTATGAA | 180 |
| ACTTTTAGCG ACTCGCTTTT TTTGCTCTCT AAAGAAAGGA TTGAAGAAGC CCTTCATTAT | 240 |
| TACCAGCCTA AAAAAGTCTA TAATTTAAGC TATGGGGCGA AAATCAAGCA CGCCGTTAGC | 300 |
| CTCAATCACT CTCAAGTGAA ATTGAAACAA ATCAACAAAC AAGACGCTAT CGTTCGCATT | 360 |
| AAAAGCATGT TTAGCCCTAG AAGTAATCAT GCTAAGGATT TAAAAAATTT ACAAAAAAAT | 420 |
| CTGATTTCGTT TTAAAGAGGA TTTTTTCACG CATTTAAACA CGCCTTGTA Aaccaagcaa | 480 |
| GAAGCATTTG AATGGGTGGA TAGCTTGAGT GGATTTTGCC AAACAGCCAG CGCTAAAACC | 540 |
| CCCCTATAG GCATTTTATT TGAAGGGAGT GTCGCCATA TCTTACAAAG CGTTCTAATC | 600 |
| GTTTCATTGC ATCTTAAAGA AAATGAGCTG ACGCTTTTAT CAAATTCTCT CAAAACGCCT | 660 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 744 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGCAAAAAA GTATATTCAA AATAACTCTG TTGTTGGTTT TCCTCTTTTT AAGGAATGCT | 60 |
| GTTGGTTTAG ACGATAAAAA AGCAGCTCCT AAAAGCGTTC AAAATACCCC TAAAAATTTA | 120 |
| CCCCCTATCC AGTTAAGGCT CGATCAAGCC TATGAAGACC TTATCAAAAT GTTAGACAAT | 180 |
| ATGGGAAAAA GCACGCAGTA TGAGTTCCTT AAAATTAAAG AAATCCTAGA ACAAAGCGAA | 240 |
| GAGGAATGGC TAGGAGTCGC CCATGAAGAA TGTGTGGCGT TAGTCATGTT AATAAGCCCT | 300 |
| AAGGCTTCTA TTGAAAACAG CCCGATTTAT AAGAATTGCT ATGAAGCTTA TGTGAAACAA | 360 |
| AGAATCCATG ATTTATATGA TTTTATATA GAGGGCAAAA AAGTGAAAAG AAAAATCAAG | 420 |
| AAAGCCCATG AGCATGAAAT GGCCCTCAAC AAATCCCAAC CCTTAAAAAA GGAACCGCCT | 480 |
| AAAAGCGAGA ATAAAAAGGG CTTAACAAAA CCTAGCTTGA AAGACGCAA GATCCCTAAA | 540 |
| GGGTATTACT TGCAAATTGG GGCTTTTTTA AATTCGCCCA GTAAGGATTT TTTGCAAACG | 600 |
| CTCAAAACTT TCCCTCACCA AATGGAGGAA AAAGACTCCC TCACGCATTA TTTGATTGGC | 660 |
| CCTTATAAAA CCAAAGAAGA AGCCCTAAAA CAGCTTGAAA ATGCGGCTAA AAGCTTTAAA | 720 |
| AATAAGCCTG CGTTGGTAGA GAAG | 744 |

(2) INFORMATION FOR SEQ ID NO:34189716_c3_7.nt:

292

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|--|-----|
| ATGCAAGAAA TCTTAATCCC TTAAAAAGAA AAAAGCTATA AAGTGTTTTT GGGGGAAGTG | 60 |
| CCTGAAATAA AATTGAAACA AAAAGCGCTC ATCATTAGCG ATAGCATCGT GGCCGGGTTG | 120 |
| CATTTGCCCT ATTTGTTAGA GCGCTTGAAC GCCTTAGAAG TCAGAGTGTG CGTGATAGAG | 180 |
| TCCGGGGAAA AATACAAAAA TTTTCATTCA TTAGAGCGGA TTTTAAACAA CGCCTTTGAA | 240 |
| ATGCAATTAA ACCGCCATTC TTTAATGATA GCCCTTGGTG GGGGAGTGAT AAGCGATATG | 300 |
| GTGGGGTTTG CGAGCAGTAT TTATTTTCAGG GGGATTGATT TTATTAATAT TCCCTACGAC | 360 |
| TTTACTCGCT CAAGTGGATG CGAGCGTGGG GGGGAAAACA GGGATCAACA CGCCTTATGG | 420 |
| CAAGAACCTA ATCGGATCGT TCCACCAGCC | 450 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 561 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: UDP-N-ACETYLMURAMYL-TRIPETIDE SYNTHETASE

| | |
|---|-----|
| ATGCGAATAC TTCATTATGG AGGTGAGCTC CCATGCGATT GTCCAAAACG CATCGCTGGG | 60 |
| CTTGATTTTCG CTCTTAAAT TCTCACCAAT ATCACAAGCG ATCATTTAGA TTTCCATCAA | 120 |
| AATATAGAAA ATTACAGGGA CGCTAAAAAC AGCTTTTTTA AAGATGAGGG CTTAAAAGTC | 180 |
| ATCAACAGAG ATGAAACAAA CGCCCTTTTT AACCCCATTA ACGCGCGCAC TTACGCACTG | 240 |
| GATAAAAAAG CGCATTTGAA TGTTCAGCC TTTTCGCTCA ACCCTTCCAT TAGCGCGTCT | 300 |
| TTATGCTACC AACACGATTT AAGAGATCCC AATCTTAAAG AAACCGCCCT GATCCATTCC | 360 |
| CCCCTTTTAG GCGTTACAA CCTTTATAAT ATTTTAGCGG GCGTTTTAGG GGTAAATTG | 420 |
| CTCACTCAAT TGCCTTTAGA AACGATCGCA CCGTTATTGG AAAACTTTTA TGGGGTTAAG | 480 |
| GGGCGTTTGG AAATTGTACA TTCTAAACCT TTAGTGGTCG TGGATTTTGC CCACACAACA | 540 |
| GACGGCATGC AACAAGTTTT T | 561 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 594 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: PREPROTEIN TRANSLOCASE SECA SUBUNIT

| | |
|--|-----|
| GTGAGCATT AAGAAGAGAG CCAAACCTTA GCCGATATTA CTTTCCAAAA TTATTTTCAGG | 60 |
| ATGTTTTTCTA AACTTTTCAGG CATGACAGGC ACGGCTCAAA CCGAAGCCAC AGAATTTTTTA | 120 |
| GAAATCTACA ATTTAGAAGT GGTGTCCATC CCTACTAATC TAGCGATCAA GCGAAAAGAT | 180 |
| TTGAACGATC TGATCTATAA GAGTGAAAAA GAAAAATTTG ACGCTGTGAT CCTTAAAATT | 240 |
| AAAGAATTAC ACGATAAGGG TCAGCCCGTT TTAGTCGGCA CGGCTAGCAT TGAAAAGAGT | 300 |
| GAAACCTTGC ACGCTTTACT CAAAAAAGAG CGCATCCCTC ACACCGTTTT AAACGCCAAG | 360 |
| CAACACACTA AAGAAGCTGA AATCATCAAA GACGCCGGGC TTAAAGGGGC GGTTACGATT | 420 |
| GCGACCAACA TGGCAGGCAG GGGCGTTGAT ATTAAGCTCA CTGATGAAGT TAAAGAACTT | 480 |
| GGGGGGCTGT ATATCATTTG CACTGAAAGG CATGAGAGCC GTAGGATTGA CAATCAATTA | 540 |
| AGGGGGCGAA GCGGGCGTCA AGGCGATCCG GGAGTGAGTC AGTTTTATTT GAGC | 594 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 624 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: putative chemoreceptor

| | |
|---|-----|
| GTGGTGGCTG ATGAGGTGAG AAAGCTCGCT GAAAAAACCC AAAAAGCCAC TAAAGAAATC | 60 |
| GCTGTCGTGG TTAAAAGCAT GCAACAAGAA GCGAACGATA TTCAAACCAA CACCCACGAT | 120 |
| ATTAATTCTA TTGTAGGCTC TATTAAGGGT GATGTGGAAG AGCTTAAATC CACCGTAAAA | 180 |
| AATAACATGA TTGTCGCGCA AGCCGCAAAA TACACCATCT ACAATATCAA TAACCGGGTG | 240 |
| TTTTGCGGTY TGGCTAAACT CGATCATGTG GTCTTTAAAA ACAATCTTTA TGGCATGGTG | 300 |
| CSTTTGGTCT CAATTCCTTT GACATTACCA GCCCATAAGA GTTSCCGTTT AGGCAAATGG | 360 |
| TATTATGAGG GTGCGGGTAA AGAAAACTTT GCTAACACTT CAGGCTATAG AGCTTTAGAA | 420 |
| AGCCACCATG CGAGCGTGCA TGCTGAAGCT AATGATTTGG TTAAAGCCGT TCAAGAAGAT | 480 |
| CACGTCACCG ATTCAAAATA CCTAGAACAT AAAGTGCATT TAATGGAAGA TAGCGCTAAG | 540 |
| CATGTCAAAG AAAATATTGA TAAGATGTTT TATGAAAAAC AAGATGAACT CAATAAAATC | 600 |
| ATTGAAAAAA TTCAAAAAGG CGAA | 624 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 603 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGAATACAT CAAAAAATT AGGTAACCCC TTGCTTTTTT TGCATGATAA TAAAATTTTG | 60 |
| TTGTTTGTCG TAGGGGTGAG CATGGGCGGG TGGGCCACTT CTAAAATCTA TCAATTTGAA | 120 |
| AGCGCTTTAG AGCCGATTCA TTTTAAGTTT GCGCGAAAAC TCTCTTTAAG CCCTTTTTTA | 180 |
| AATTTGAGCC ATTTAGTAAG GAATAAGCCT TTAAACACCA CTGATGGCGG GTTTATGCTA | 240 |
| CCACTCTATC ACGAATTAGC CACCCAATAC CCCTTGTTGT TGAAATTTGA CCAACAAAAT | 300 |
| AACCCAAGAG AGCTTTTAAG GCCTAATACC TTAAACCACC AGCTCCAACC AAGCTTAACC | 360 |
| CCCTTTAAAG ACTGCGCTGT CATGGCGTTT AGAAACCATT CTTTTAAAGA TAGCCTCATG | 420 |
| CTAGAAACCT GTAAAACCCC CACTGATTGG CAAAACCCA TTTCTACAAA TCTTAAAAAC | 480 |
| TTAGATGATT CTTTAAATTT ACTCAATTTA AATGGAATAT TGTATTTGAT CCACAACCCT | 540 |
| AGCGATTTAT CACTGCGTCG TAAAGAACTT TGGCTTTCTA AATTAGAAAA CCYYCAACTC | 600 |
| RTT | 603 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGAGTATTC AACATTTCCG TGTGCCCCTT ATTCCTTTT TTGCGGCATT TTGCCTTCCT | 60 |
| GTTTTTGCTC ACCCAGAAAC GCTGGTGAAA GTAAAAGATG CTGAAGATCA GTTGGGTGCA | 120 |
| CGAGTGGGTT ACATCGAACT GGATCTCAAC AGCGGTAAGA TCCTTGAGAG TTTTCGCCCC | 180 |
| GAAGAACGTT TTCCAATGAT GAGCACTTTT AAAGTTCTGC TATGTGGCGC GGTATTATCC | 240 |
| CGTATTGACG CCGGGCAAGA GCAACTCGGT CGCCGCATAC ACTATTCTCA GAATGACTTG | 300 |
| GTTGAGTACT CACCAGTCAC AGAAAAGCAT CTTACGGATG GCATGACAGT AAGAGAATTA | 360 |
| YGCWGGTGGT GCCATAACCA T | 381 |

(2) INFORMATION FOR SEQ ID NO:34666680_c1_4.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 237 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

298

| | |
|--|-----|
| GTGAACGTGG GCGTGCCTTT TAGCTATCAA GTGAGCGCGA CCTTTCAAAA CTCACGCCTT | 60 |
| TCTAGTTTGC TAGAACTTT AAAAAAGAGT TTTTATAGAAA AGCCCTTAAT TGAGAGCAGC | 120 |
| GCGAATAAAA TCGCGGATAT TTTTCTCTAAA GCGGTGTTGT TTTTAGCCTT TGTGAGCTTT | 180 |
| TTATTGTGGC AATTTGGTTT GGGGGGTAAT TTTGAAAAAS GCTTTAATGG TGTGTAT | 237 |

(2) INFORMATION FOR SEQ ID NO:35156938_c2_14.nt:

299

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: antigen [Entamoeba histolytica]

ATGCTAATGG TTAATGGCTA TCAAATCACG ATGCATAAGG GTTATAAGGT AGGGTTTTTT 60

ACAAGCGGTT ACAACCCTGA TTTCGCTCAA ACCATTCAAA ATAGAAGCTA TTTGATGAGC 120

TCTTATGAGT TATCGTTTTT AAGAAAT 147

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1236 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|------|
| ATGGTGCAAT TTCAAACAC GCTTATAAAA TTCCATGCCC TATCCTTTAA AAACGCAAAT | 60 |
| TTAATTTATA ATGCAAATT AAACAAAACA TGCTATAAAG AAAATTCAAA TACTATCATT | 120 |
| TTAAGGATTA AAATGCTCAC CCAAGAAGAT GTCTTAAACG CGTTAAAAAC GATCATCTAC | 180 |
| CCTAATTTTG AAAAGGATAT TGTCAGCTTT GGTTTTGTTA AAAACATCAC CTTGCATGAC | 240 |
| AACCAATTAG GGCTTTTAAT AGAAATCCCC TCAAGCTCTG AGGAAACGAG TCGGATTTTA | 300 |
| AGGGAAAATA TCTCAAAGC GATGCAAGAA AAAGGCGTGA AAGCTTTGAA TTTGGATATT | 360 |
| AAAACCCCGC CTAAACCGCA AGCTCCAAAG CCCACCACTA AAAATCTGGC TAAAAACATC | 420 |
| AAGCATGTGG TCATGATAAG CTCAGGCAAG GGCGGTGTGG GTAAAAGCAC CACCAGCGTG | 480 |
| AATTTAAGCA TCGCTTTAGC GAATTTAAAC CAAAAAGTGG GGCTACTAGA CGCTGATGTG | 540 |
| TATGGCCCTA ATATCCCTAG AATGATGGGC TTGCAAAACG CTGATGTGAT CATGGATCCT | 600 |
| AGCGGTAAAA AACTCATTC TTTAAAAGCT TTTGGCGTTT CTGTGATGAG CATGGGGCTT | 660 |
| TTGTATGATG AGGGGCAGAG TCTCATTTGG AGAGGACCCA TGCTCATGCG AGCGATTGAG | 720 |
| CAGATGCTAA GCGATATTAT TTGGGGGGAT TTAGACGTGC TGGTGGTGGA TATGCCCCCA | 780 |
| AGGAACAGGC GATGCGCAGC TCACGCAGCC CAAGCCGTGC CACTCAGCGC AGGAATCACC | 840 |
| GTTACTACGC CTCAAATCGT GAGTTTAGAT GACGCTAAAC GGAGTTTGGA CATGTTTAAG | 900 |
| AAACTACACA TTCCTATTGC GGGCATTGTA GAAAATATGG GGAGTTTTGT GTGCGAGCAT | 960 |
| TGCAAGAAAG AGAGCGAGAT TTTTGGCTCA AATTCCATGA GTGGATTATT AGAGGCTTAT | 1020 |
| AACACGCAGA TTTTAGCCAA GCTCCCTTTA GAGCCTAAAG TCGTCTAGG GGGGGATAAG | 1080 |
| GGTGAACCGA TTGTGATTTT TCATCCCACT AGCGTGAGTG CTAAAATTTT TGAAAAAATG | 1140 |
| GCAAAGGATT TGAGTGCTTT TTTAGACAAG GTGGAAAGGG AAAAAGTAGC CGATAATAAG | 1200 |
| GACATCCAGC CCACACAAAC GCATGCTTAT TCGCAT | 1236 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGGGTGTGG TGATTGGCGA GACCACAGAG ATTGGAGATG ATGTTACCAT TTATCATGGC | 60 |
| GTAACTCTGG GGGGTACGGG CAAGTTTAAG GGCAAACGCC ACCCTACTTT AGGCAACCGA | 120 |
| GTGGTAGTTG GGGCAGGGGC TAAGGTCTTG GCGCGGATTT GCGTGGGCGA TGATGTGAGG | 180 |
| ATTGGGGCTA ATGCGGTGGT GCTTTCAGAT TTACCCACGG GTTCTACGGC TGTAGGTGCT | 240 |
| AAAGCCAAAA CCATCACAAA GGATCGT | 267 |

(2) INFORMATION FOR SEQ ID NO:35336707_c3_3.nt:

305

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 576 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGCTATCTT TTATAAGCGC GTTTGATAAA AGGGGCGTTT CAATACGCCT TCTAACAGCC | 60 |
| TTGTTACTGC TTTTtagTTT GGGTTTGGCT AAAGATTTAG AAATCCAAAC TTTTGTGGCT | 120 |
| AAATACCTTT CTAAAAATCA AAAAATACAA GCCCTACAGG AGCAAATTGA CGCTTTAGAT | 180 |
| TCTCAAGAAA AAGTCGTTAG CAAATGGGAT AACCTATTT TGTATTTAGG CTATAACAAC | 240 |
| GCTAACGTGA GCGATTTTTT CAGGCTGGAT AGCACCTTAA TGCAAAACAT GAGCTTGGGT | 300 |
| TTGTCTCAAA AAGTGGATTT AAATGGTAAA AAATCAGCG AGTCTAAAAT GATCAATTTA | 360 |
| GAAAAACAAA AAAAAATATT AGAGCTTAAA AAAACCAAGC AGCAATTGGT GATTAATTTA | 420 |
| ATGATAAACG GCATTGAAAA CTATAAAAAC CAACAAGAAA TAGAGCTTTT AAACACAGCG | 480 |
| ATTAAAAATT TAGAAAACAC CCTCTATCAA GCCAACCATT CCAGTTCGCC CGATTTAATA | 540 |
| GYGATYGYCA AGTTRGAAAW TTTAAAAATC GCCAWT | 576 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| GTGCCGGCTG TTGGGGGGGC TTTGATTGG ATYCYTATAG YGATTTATGA GCTTTATCAT | 60 |
| GGGYATGTGA ATGAGGYTAT TTTTAYYGTT TTGTATTCCA TTTTGTTAAT TGGTGTGTTG | 120 |
| ATTGATAGCG TGATCAAGCC AATTTTAATC GTTTTTATCA AAAAAAGAAT CTTTAAACC | 180 |
| ACCCTTAAAA TCAATGAAAT ATTGATTTTC TTTTCTATGA TTGCTGGGAT TTCTCAATTT | 240 |
| GGTTTTTGGG GGATTATCGT AGGGCCTACC ATCACGGCGT TTTTATCGC GTTACTGCGA | 300 |
| TTGTATGAAA ATTACTTTAT TCAAAAGGAG CAAAAACAT GCGAATGT | 348 |

(2) INFORMATION FOR SEQ ID NO:35417942_c2_10.nt:

304

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 489 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | |
|--|-----|
| GTGGTTGTCA TTATTTTAGT GGTCGTTATC ATTCAAAACA GCTCTTCTTT AAAAGAAGAG | 60 |
| AGAGAGCAAG AACGCGCTAT TAAGCCCGAC ACCAAAAATA ATTCTTTCAA TGAAACTAAT | 120 |
| CCTACAGAAG AAAAAAAGTT AGAGCCAACG CCTAAATTAG AAGAAAAACA CAAAGAACAA | 180 |
| GACAAGCAAG GCAAAGAAGC GATCAAAGAA AATCCTAATA CCATTTACAT TATCCCTAAA | 240 |
| CGAGATATTT GGGTAGAAGT GATTGATTTA GATGAGAAAA AAAACTCTTT TCAAAAGGTT | 300 |
| TTTAAAAAAA GTTATCCTTT AGAGGCTAAA AACCACCGCT TGTTGTTACG CTTTGGGCAT | 360 |
| GGGCATCTTA TTCTTAAAAA CAACCATCAA GAACAAGATT ATAACGACAG CAAAAC TAGG | 420 |
| CGGTTTTTAT ACGAGCCAAA TAAAGGTTTA ACGCTCATCA ATGAGGCCCA ATACAAAGCG | 480 |
| CTCCAGCAA | 489 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: HAEMOLYSIN SECRETION ATP-BINDING PROTEIN

```
ATGGATGAAA TCTATCAAAT CGCTAAAAAT AAAACCCTAA TCGTTATCGC CCACCGCTTA      60
AGCACGATTG AACGCTGTGA AGTCATCATT GACATGAGCC AACACAAAGA CAATCTCGGC      120
```

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| GTGGCGGGCA GCTTTATTAT TGCTCTTTTT AGCGTTTTAG CGGATCAATT TGTGAGCGTG | 60 |
| TTTCAGCATG AAAACGCCTT GCAACGCCTA TTTTCTCAAA ACGCCACCCA AAAACAAAAA | 120 |
| AAGAAGAGTT TATGT | 135 |

(2) INFORMATION FOR SEQ ID NO:35445843_f3_7.nt:

307.

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGGTAGCTT TAAGCAACGC TCTTCAAGG GTTTTGGTT CTGTGGCTGG CTATAAATTC | 60 |
| CCTTCTTTTA TCCAAAAAG CATCAACGCT CTTTATGTTA AGATCTTTAA AATTGATTG | 120 |
| AGCGAGTTTG AGCCTTTAGA AAATTATAAG AGTTTGAACG CTCTTTTCAT GCGCTCTTTA | 180 |
| AAAAAAGAAC GCCCCTTTGA CAAAGCCCCT ATATTGTCAT TGCGCCTTGC GATGGCTTTA | 240 |
| ATCACTGAAT GCGCTTTTTT AGACAACGAT AGCGCTTTAC AAATTAAAGG CATGCCCTAT | 300 |
| AAAGCGCATG AATTAGTGGG CGAAATCAAC CCCTTAAGCC CTCTTTTTTC TATG | 354 |

(2) INFORMATION FOR SEQ ID NO:35704718_c1_23.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 600 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGGCAGTGT TAAAAAAGAT GATAGGTTTG GTGGCGGTTT TAAGCGTTTT ATTAGCCAGA | 60 |
| GACAACCCTT TTGAGCCTGA AATCAATTCC AAGAATTTCG AAGGGGGCTT TAGCGGGATC | 120 |
| TATGATGACT ACCTCAAAGA AATCCATGTG GATTTGCCCA CGAGCGCTAG GATCTTAAAA | 180 |
| AAAATCACGC TCACTTACCA AGATATTGAT GGCTCTATCC ATTCTAAAGT CGTGGGTATT | 240 |
| GATAAAAGCA TTGATTGGCA CTACCCCTTA AAACCTTCCC AACACACCCT TAATCAAGAC | 300 |
| GCCTTTGAAA AACGCTACCA GATCCAAGAT TTTGATTTTT TAATGGCAA CAACACGATG | 360 |
| ATTTTGCGTT CCCCTTATAA AATTTTGCGC TCTTTTGTGT TAGTCAATCC TTATAGAATC | 420 |
| GTGTTAGACA CGCAAAAAGG CCCTTTGGAT ATTTATCAAA ACATGGATTT AAACCAGAAG | 480 |
| TTTTTTTCTC ACATTAAAGT CGGCACGCAC AAAGATTATT ACCGCATCAC GCTCATTTTA | 540 |
| GACGGGAAAT ACCGCTATCT TTTGGAAGAA AAAAACGGGG CGTATGAATT AAAACTGAAA | 600 |

(2) INFORMATION FOR SEQ ID NO:35837767_c2_13.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 237 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|--|-----|
| ATGGGCGGAT TCACAAGCAT ATGGCATTGG GTCATTGTTT TATTAGTGAT TGTGTTGTTA | 60 |
| TTTGGGGGCTA AAAAGATCCC AGAATTGGCT AAAGGTTTAG GCAGTGGGAT TAAGAATTTC | 120 |
| AAAAAAGCCG TGAAAGACGA TGAAGAAGAG GCTAAAAACG AGCTAAAAAC CCTAGACGCT | 180 |
| CAAGCAACAC AAACCAAAGT GCATGAAACT AGCGAAATTA AAAGCAAACA AGAAAGT | 237 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 618 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| GTGCGTTTGA ATGCGGCGGT TGTGGTGGAT GGCAAGTATA AAATCGCGCT CGAAGACGGG | 60 |
| GCAAACGCTT TAGAATACGA GCCTTTAAGC GATGAATSGS TTAAAAAAT CAACGYCCTA | 120 |
| GTCAAACAAG CCATTGGTGA TAACCAAAAT AGAGGCGATG ACGTGGCGGT GAGTAATTTT | 180 |
| GAGTTTAACC CTATGGTGCC TATGATTGAC AACGCCACCT TGAGTGAAAA AATCATCTAT | 240 |
| AAAACCCAAA AAATTTTAGG TTTATTTATG TTTTAAATCA AGGTATATTT GGTGTTTATA | 300 |
| GTGTTATTCA TTTTCTATAA AAAAGTGATC GTGCCTTTCA GCGAACGCAT GCTGGAAGTG | 360 |
| GTGCCTGATG AAGATAAGGA AGTGAAATCC ATGTTTGAAG AAATGAACGA AGAAGAAGAT | 420 |
| GAGTTGAACA AACTCGGCGA TTTGAGGAAA AAAGTAGAAG ATCAATTAGG GCTTAATGCA | 480 |
| AGCTTTAGCG AAGAAGAAGT AAGATATGAA ATTATTTTAG AAAAGATTAG AGGAACCCTT | 540 |
| AAAGAGCGTC CTGATGAAAT CGCCACGCTC TTTAACTCT TAATCAAAGA TGAAATCTCT | 600 |
| TCAGACAGCG CGAAAGGT | 618 |

(2) INFORMATION FOR SEQ ID NO:36131282_f3_10.nt:

311

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 294 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| GTGTGTTTTA TATTGCCTTT TTGTTTAGGG GTTTTAGGCA CGCAAATCTT TAAACAAGAG | 60 |
| ACCCCAAGAC AGCTCCCTAT CGTGGTGGTG GATTGATA AGACCACTAC AAGCCATCAA | 120 |
| GTGGCGTTTG AATTAGGCGC AACGAGTGCG GTTGAAATCA AATACCAAGT GACTAGCCTT | 180 |
| TCAGAAGCTA AACGCTTTTT AACTCCGCT GAAGTGTATG GGGCGTTAAT TTTGCCTAAG | 240 |
| GATTGAGAGA GAAAAATCAA AATGGGGCGA AAAGTGGSAT TTGCCCTTTT ATTA | 294 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 591 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGAAAGGCT TATGGCTTGT AATCTCTTTA GTTTTTGTTG GTTTTTTGTG GGCTAATGAA | 60 |
| TCTTATGTTT TTAACAATTC TAAGGGGCGT TTAACAGAAA AAAGCGTTGC GTTTATAGAG | 120 |
| GGCGTTTCTA AAGAGCTTTA TCTTAAAACC GCGTGCGTT TTGCGATTGA TATGACGGAT | 180 |
| TTTGAAAAAA ATCCTATCGC TCTAGCGAAT AAAAAAGAGC GCCAAAGCTA TCAAGAGGGC | 240 |
| TTTTTAAAGC AGCTCAAACC CCTTTTGTG GTATTCTTTT TCTACCATGA CGCTCAAAAA | 300 |
| ATAGAATTAG TGGCTAACCC TAAAGATTTG CTAGACACTG ATAAAATCTT TTTTGAAAAA | 360 |
| ATCGCTCCCT TACTCCCCAC AAACGCTAAA GAATACACGC CCCAAAGAAT TTCAGCCATG | 420 |
| CTCATTAACG GCTATTCGGT CGCAGTAGAT GCTTTAGCGG AAAAATATCA TGTGAATATC | 480 |
| ACGCAAAATT TTAGCGCTCC TAAGGGAGTA ACTTTTGTA AGGTGGTTAT TTATATTTTG | 540 |
| TTATTGACGC TTTTGGGCGC GTTTTTGGGG CTTTATTTTT TAAAAAATC T | 591 |

(2) INFORMATION FOR SEQ ID NO:36335436_f2_4.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|--|-----|
| ATGTGTTCTA AAAAAATAAG AAATCTCATT TTATGCTTTG GTTTTATTTT AAGCTTGTGC | 60 |
| GCTGAAGAAA ATATCACCAA AGAAAACATG ACTGAAACGA ACACGACTGA AGAAAACACC | 120 |
| CCTAAAGACG CTCCCATTCT TTTGGAAGAA AAACGCGCCC AAACCTCTAGA GCTTAAAGAA | 180 |
| GAAAATGAAG TGGCAAAAAA GATT | 204 |

2) INFORMATION FOR SEQ ID NO:36523442_c3_14.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | |
|--|-----|
| GTGCTAAAGA CATTATCCAT ACGATTAGTC ATACTTTTAA ATTGCTCCCT AGCGACAAAC | 60 |
| GCTTGCACTG GGGTGCAAAA ATTGCGCGAT GAAAGCCACC GGTATGCGAT AAAC TTCCAT | 120 |
| AGATCCACTA AACTTAAAAA CATGAAACAA ATCGCTCTTT TAAAAGAAAA GGGCATAGGA | 180 |
| GAAGCCAGCG TGAAAAAATT GTTGGATTAT TTTGGGAGTT TTGAAGCGAT AGAAAAAGCG | 240 |
| AGCGATCAGG AAAAAAACGC CGTTTTAAAA AAACGAAAA | 279 |

(2) INFORMATION FOR SEQ ID NO:36573502_f2_2.nt:

315

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SULFATE TRANSPORT ATP-BINDING

| | |
|---|-----|
| GTGGGCATTA TTAGGGGGAT TATCCACAGG CCAGAACTCA TTTTATTAGA TGAGCCTTTT | 60 |
| AGCGCTTTAG ATAGTTTGAA TCGTAAGAAT TTACAGGATC TCATCAAAGA AATACACCAA | 120 |
| AATTCTTGCG CTACTTTCAT TATGGTAACG CATGATGAAA ACGAGGCGCA AAAGTTAGCC | 180 |
| ACAAAAACCC TAGAAATCAA AGCCCTTAAA CAAGAGCAG | 219 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 804 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | | | | | | |
|-----------|----------------|-------------|------------|------------|------------|-----|
| GTGATTTT | TA TCGCTACCGC | TAATAATATT | GACAGGATCC | CAGCTCCTTT | AAGAGACAGA | 60 |
| ATGGAATT | TA TCAGCGTGTC | CAGCTACACG | CCTAGCGAAA | AAGAAGAGAT | CGCTAAAAAC | 120 |
| TACCTCAT | CC CAAGAATT | AGAAAAGCAC | GCCTTAAAGC | CTAGCGAAGT | GGATATTAGC | 180 |
| CATGAATG | TT TGAAACTCAT | TATTGAAAAA | TACACCAGAG | AAGCGGGCGT | TAGGGATTTA | 240 |
| CGAAGACA | GA TCGCAACGAT | TATGCGTAAA | GCGGCTTTAA | AATACCTAGA | AGATAACCCG | 300 |
| CACAAAAA | AG GGC GGACCAA | AAAAAGCGAA | GACAAAGATA | AAAAAGGCGG | AAATGAAGAA | 360 |
| AACGAAAA | AA GAGGTGAGAG | TAAAGATTTT | TGCGTCTCTA | TCACGCCTGA | TAACCTTAAA | 420 |
| GAGTATTT | AG AACGCATGGT | GTTTGAAATT | GRCCCCATAG | ATGAAGAAAA | TAAAATCGGT | 480 |
| ATCGTCAAT | GG GCTTGGCATG | GA CTCCAGTG | GGCGGTGATG | TGCTTAAAT | TGAAGCGGTT | 540 |
| AAGATTAG | AG GCAAGGGGGA | ATTGAAACTC | ACCGGGAGTT | TGGGCGACGT | GATGAAAGAA | 600 |
| TCCGCCAT | TA TTGCCTTTTC | TGTTGTCAAA | GTCTTGTTGG | ATAACGAAAC | CTTAAAAGTG | 660 |
| CCTAAAAT | CC CTAGCGAGAC | CGATGCAGAG | AATWAGAAAA | AGAAAAAAGT | GCTGAAAGTT | 720 |
| TWWAACGCT | TT ACGATTTGCA | CTTG CATGTC | CCTAAGGGGC | TACGCCTAAA | GACGGCCCGA | 780 |
| GCGCTGGG | AT CGCTATGGCG | AGCG | | | | 804 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 498 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGGGGTGTT CGTTTATCTT TAAAAAAGTT AGGGTTTATT CTAAAATGTT GGTTGCTTTG | 60 |
| GGGCTTTCAA GCGTGTTGAT CGGTTGCGCG ATGAATCCAA GCGCTGAGAC AAAAAACCA | 120 |
| AATGACGCCA AAAACCAACA ACCAGTTCAA ACTCATGAAA GAATGACAAC AAGTTCTGAA | 180 |
| CATGTTACGC CACTAGATTT TAATTACCCG GTGCATATTG TTCAAGCCCC ACAAACCAT | 240 |
| CATGTTGTAG GTATTTTAAT GCCACGCATT CAAGTGAGCG ATAATCTAAA ACCCTATATT | 300 |
| GATAAGTTTC AAGACGCTTT AATTAATCAA ATCCAAACTA TTTTGGAAAA AAGAGGCTAT | 360 |
| CAAGTGTTGC GTTTTCAAGA TGAAAAAGCT TTGAATGTGC AAGATAAGAA AAAGATTTTT | 420 |
| TCCGTTTGG ATTTGAAAGG GTGGGTAGGA ATCTTAGAAG ATTTGAAAAT GAATTTAAAA | 480 |
| GATTCCCATG GTCCCAT | 498 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | |
|--|-----|
| ATGGATAGAA AACTCTTAAG ATTATACCAG CCCTTAAACG CTTATTCTTA CAATAGCGAT | 60 |
| TCGCTTTTTT TATACGATTT TTCACGCCCT TTTATCAAAA ATAGCGGCGC GATTTTAGAC | 120 |
| ATAGGCTCAG GGTGTGGGGT TCTAGGCTTG CTCTGCGCTA GAGACAACCC GCTAGCGAGC | 180 |
| GTTCAATTTAG TGGAAAAGGA TAGCAAAATG GCGTTTTGCT CCCAAAAAAA CGCCCTTAAA | 240 |
| TTCCCTAACG CTCAAGTGTT TGAGAGCGAT TTTTLAGATT TTAACCCTCC GATTTTGTAT | 300 |
| GATGCGATTG TGTGCAACCC TCCTTTTTTAT GCTTTAGGAT CTATTAAATC TCAAATTAAA | 360 |
| GGGCATGCGA GGCACCAGAG CGAATTAGAC TTCGCTTCTT TGGTGGCTAA AGTGAAAAAA | 420 |
| TGCCTGAAAC CC | 432 |

(2) INFORMATION FOR SEQ ID NO:391313_f2_5.nt:

319

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGTTGAGTG CGTTGGTGAT GCTGCCTTTT ATGGAGGTTT TTTATTATTT CAATTTTCCG | 60 |
| TTGTGGCTCA ATCTTTTCTT AGGGCAAACC ATTGGAGCGG TGATTTTTTT CAAGTTGGAT | 120 |
| AAGTTGATTT TTTCTAAAAA A | 141 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 387 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGAATACTA TTATAAGATA TGCGAGTTTA TGGGGCTTGT GTATTACTCT AACTCTAGCG | 60 |
| CAAACCCCCT CTAAAACCCC TGATGAAATC AAGCAAATCC TTAACAATTA TAGCCATAAG | 120 |
| AATTTAAAGC TCATTGATYC GCCGACAAGT TCTTTARRAG CGACACCGGG TTTTWWCCC | 180 |
| TCGCCTAAAG AAACAGCGAC CACGATCAAT CAAGAGATCG CTAAATACCA TGAAAAAAGC | 240 |
| GATAAAGCCG CTTTGGGGCT TTATGAATTG CTAAAGGGGG CTACCACCAA TCTCAGTTTG | 300 |
| CAAGCGCAAG AACTCAGTGT CAAGCAAGCG ATGGAAGAAC CACACCATCG CCAAAGCGAT | 360 |
| GTTTTTGCCT ACTTTGAACG CGAGTTA | 387 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 726 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | |
|--|-----|
| ATGGTTTTGT TTCTATCCAT TTTTAAAAA AGCTTTAATG ATTTTTTAAG CGCTAGAATG | 60 |
| CTTTTAATCA ATCTTGGCCC TATCCTTTTG AGTTTGGCGT TTTTGGAGC TATCTTTTAT | 120 |
| TACAATGGCG GGAGTATTGT GAATTATTGC CAAACTTTAT TACCGCAATC TTTGAATGAT | 180 |
| TACGCTCATT CTCAAGGCTT TTTTGCCGGT GTGTTTCGCAT GGGTTTTTAA AGCGTTAGTG | 240 |
| TATTTTCTTA TTTTGGGAT CGTAATTCTT TTGAGTTTAG TCATCAATAT TTTTGCGTCT | 300 |
| ATTTTTTACA CCCCTTTAGT GGTCTCTTAT TTGCACCAAA AATATTATCC CCATGTCGTT | 360 |
| TTAGAAGAAT TTGGCTCTAT CCTTTTTTCT ATTAAATATT TTTTAAAATC GCTCACTTTT | 420 |
| ATGCTTTTAT TCTTAGCGGT TTTAACGCCC CTTTATTTC TCCCTTTAT AGGGGTCTTT | 480 |
| GGGGTCTTTT TTTCTATAGT CCCGCATTC CYCTTTTTC AAAACACCAT GAGTTTGGAT | 540 |
| ATAGCCAGCA TGATTTTCAA CCATCAAAGC TATCAAAATT TACTCAAACA GCACCGATTG | 600 |
| AAGCATTATC GTTTTTCGTT TTTTGCTAT CTTTTTCCT TGATTCCTTT TTTTAATTTT | 660 |
| TTTGCCACCT TGTTGCAAAC CCTAAYGCTA ACGCACTACY TTTTATCTT TAAAGAGAAA | 720 |
| GAATGC | 726 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 378 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: flagellar protein flis

| | |
|---|-----|
| ATGCAATACG CTAACGCTTA TCAAGCCTAC CAGCATAACC GAGTGAGTGT GGAATCCCCG | 60 |
| GCAAAACTCA TTGAAATGCT TTATGAAGGG ATTTTAAGAT TTTCTTCGCA AGCCAAACGC | 120 |
| TGTATTGAGA ATGAAGACAT TGAAAAGAAG ATCTATTATA TTAATAGGGT TACGGATATT | 180 |
| TTCACGGAGT TGTTGAATAT TTTAGACTAT GAAAAAGGGG GGRAAGTGGC GGTGTATCTT | 240 |
| ACAGGCTTAT ACACCCATCA AATCAAAGTT TTAACGCAAG CCAATGTGGA AAATGACGCG | 300 |
| AGTAAGATTG ATTTGGTGTT GAATGTGGCT AGGGGGTTGT TAGAGGCATG GAGGGAAATC | 360 |
| CATTCAGATG AACTCGCC | 378 |

(2) INFORMATION FOR SEQ ID NO:3953143_f2_1.nt:

323

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 429 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|--|-----|
| ATGATGTTTG ATAACACGCT TATCAATTTA TTTGAGACAG CGCCTCTTTT AACYTCTGCTT | 60 |
| TTAGCTGGGA TTTTAACTTT TTTAAGCCCT TGCCTGTTGC CTTTGATCCC GCGGTATATG | 120 |
| TCTTATATTT CGCAAATTTT TTTAGAGGAT ATTAAAGATG GTAAGGCTAA AAGGGTTTCG | 180 |
| GTTTTTTTAA AATCCTTGAT GTTTGTGGTG GGGTTTTTCGC TCGTGTTTTT GGGCGTGGGC | 240 |
| ATGTCTATGG CCAAGCTTAT CCATAGCTTT TCGTTTTCTT GGGTGAATTA TATCGCTGGG | 300 |
| GGGATTGTGA TCCTTTTTTG TTTGCATTTT TTAGGCGTGT TTCGTTTTGC ATTTTGTAT | 360 |
| AAAACCCAAA GCGTTGGTTT AGCGAGCAAA TCTAACAGCA TGCAGCGCTT TACCCCTTTC | 420 |
| TTTTTGGCA | 429 |

(2) INFORMATION FOR SEQ ID NO:3958537_f1_2.nt:

324

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: *Plasmodium falciparum* gametocyte specific antigen

| | |
|--|-----|
| GTGCTGGTGG TGGGCAAACC CAACGAAAGC TATGCAGATA CCCACGCCCCG CATTGAGCAT | 60 |
| TTTATCAAGC TTGTAGATTT TAAGGGCGAA ATCGTTTTTA TCAATGAAGA TAATTCTAGC | 120 |
| GTAGAAGCTT ATGAAAATTT AGAGCATTTG GGTAAGAAAA ATAAGCGGAT CGCTACCAA | 180 |
| GATGGCCGGT TAGACTCTTT GAGCGCTTGT AGGATTTTAG AGCGCTATTG CCAGCAGGTT | 240 |
| TTAAAAAAGG GC | 252 |

(2) INFORMATION FOR SEQ ID NO:3964593_f2_5.nt:

325

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGCGGATAT TAATTCTCAA AAACAAGCCA CCAACGCTAC GATCAAAGGC TTTGACGCGC | 60 |
| TCTTGGGGTA TCAATTTTTC TTTGAAAAAC ACTTTGGCTT ACGCCTTTAT GGGGTTTTTT | 120 |
| GACTACGCTC ATGCCAATTC TATTAAGCTT AAAAACCCTA ACTATAATAG CGAAGCGGCG | 180 |
| CAAGTGGCTA GTCAAATTCT TGGGAAACAA GAAATCAATC GTTTAACAAA CATTGCCGAT | 240 |
| CCCAGAACTT TTGAGCCGAA CATGCTCACT TATGGGGGGG CTATGGACGT GATGGTTAAT | 300 |
| GTCATCAATA ACGGCATCAT GAGTTTGGGG GCTTTTGGCG GGATACAATT GGCCGGCAAT | 360 |
| TCATGGCTTA TGGCGASACC GAGCTTTGAG GGCATTTTAG GGGAACAAGC CCTTGTGAGC | 420 |
| AGAAAGCCAC TTCTTTCCAA TTTTATTCA ATGTGGGGGC TCGCM | 465 |

(2) INFORMATION FOR SEQ ID NO:3991067_c3_21.nt:

326

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGAATGTCA AAAAAAAGGA AAAGCCACAA AGTGGAAGA TTGATAGGGT GGATTGTTTG | 60 |
| GAGAACTTG GGAAAGAAAA CACTACTTTT TTAAGCAGTA TAGCTATGGG GAGCATTGGT | 120 |
| CAATTAGCGA TCCCCATTCC TGGAGTTGGA GTGCTCATTG GGGGCTTTGT GGGTGGGGTG | 180 |
| ATGAGTAAAA CTTTTTATGA TGTCTCGCTA ACGATTTTCA AAGAGGCTAA ATTAGCGCGT | 240 |
| CAAAGGCGTA TTGAGATTGA AAAAGAATGC CGTGAGAGTA TCAGACAGTT AGAGATGTAT | 300 |
| CAAATCAAT TTAATGAAGT GTTTGAGCGG TATTTTCATG GGACTATAAA ATTCTTTAAT | 360 |
| GAAAGTTTTG ATGAGCTGGR GAGGGCGCTT TGTGCGGGCG ATGCGGATTT GGCTATAGCA | 420 |
| GTCAATAACA AGATCCAAGA GGGGATGGGT CAAGAGTTGC TGTTTGACAA TAAGCAAGAG | 480 |
| TGCTGGGAAT TTATCACTAG CCGTAAAGAG GGT | 513 |

(2) INFORMATION FOR SEQ ID NO:40339452_f3_2.nt:

327

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 423 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGTGGCCGT RAAAGCTTTT TCTAAAACCC CTAAAAGAAA CGAGCCTTGC CCTTGTGGGA | 60 |
| GTGGCAAAAA ATATAAGAT TGTGCGCTA AAAGCGGGCC TAAAAGGGC TTATTGCCA | 120 |
| AATAGATCCT TAATCTTTTT CCTTATCAAG CGTTATTGTC GTTTTGATAA AAGCCAGCCT | 180 |
| TTCATTAGTA TCACTGCTTT GTTAGCCTTT TTTGGCGTGG CGGTTGGCGT GATGGTTTTA | 240 |
| ATTGTGGCTA TGGCGATCAT GAACGGCATG AGTAAGGAAT TTGAAAAAA GCTTTTTGTG | 300 |
| ATGAACTACC CCTTAACGCT CTATACCACA AGCCCTTATG GGATCAGCGA AGAAGTGGTT | 360 |
| CAAGCTTTAG AAAAAAGTT CCCTAATTG CCTTTTTCAG YCCCTATTTG CAAACCCAAA | 420 |
| GCC | 423 |

(2) INFORMATION FOR SEQ ID NO:4035262_c2_16.nt:

328

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|--|-----|
| ATGGTATCGT TGCTTGGCGC GCTTAAACGC ACCCCTTGCA CTAATCGCTT TTATCTTAAA | 60 |
| GCACTACTAT TTGCTATATT CTATCATGCA GTAAATAATT TTCTAACGCA ATGCCCCGCCC | 120 |
| CATCAAGTCC GGGAGTTTTT TTCATCACGA CATGCACAGG GATGGAAGCG AGAAACGCTC | 180 |
| CCATGCGCCC TTTCGTTTCA AAACGCGCTC | 210 |

(2) INFORMATION FOR SEQ ID NO:4035783_f3_4.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 459 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| GTGCATCATT TGAAACGGCT TTTAGACTCA GGCTCTGAAA GGTGTATAGG CTGTGGGCTG | 60 |
| TGCGAAAAGA TTTGCACGAG CAACTGCATA AGGATCATCA CGCATAAGGG CGAAGACAAC | 120 |
| CGCAAAAAGA TCGATTCTTA CACGATCAAT TTGGGGCGTT GCATTTATTG CGGGTTGTGT | 180 |
| GCGGAAGTTT GCCCAGAATT GGCGATCGTT ATGGGGAATC GGTTTGAAAA CGCCAGCACC | 240 |
| CAACGCTCCC AATACGGCTC TAAAAGCGAG TTTCTAACGA GCGAACAAGA CGCTAAAAAC | 300 |
| TGCTCGCATG CCGAATTTTT AGGCTTTGGT GCGGTAAGCC CTAATTATAA CGAACGCATG | 360 |
| CAAGCCACCC CTTTAGATTA TGTCCAAGAA CCTTCAAAG AAGAATCCAA AGAAGAGTTT | 420 |
| YCCACAAGCC CAGAAAGCCA TAAGGGAGAT GAAAATGTT | 459 |

(2) INFORMATION FOR SEQ ID NO:4040928_f2_3.nt:

330

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 549 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|--|-----|
| ATGGCTATTT GGGGGTGGTG TTTTATTATTT TTATCGTCCT TGATGTGGGG TTCAAGCATG | 60 |
| CATGAGTTGG TTTTAAGATC CCAAGCTTTA GGGTTTGAAA CGCGCTTAGT CCAGTGCGAT | 120 |
| TTATCGTTTT CTTATGAAAG GTTTATTTCT AAAACCAAAC GCTCTTTAGC GGTGTTAGAA | 180 |
| GAATTTGATT GGTAAATTC TGGCTTTGAT TTTTCACGCT TGAACGTTGA AAATGACACT | 240 |
| CTGGAATTAC TCAAAGCGCT GTATTTTAAA TTAGAAAAAT TAGAGAGCCT GCTTTTAAAA | 300 |
| GAAAATTTAC TTGAATTGGA GCAAAAGGAT CGCATCATCG CTTTAGGGCA TGGGCTAGTT | 360 |
| TGCCTAAAAA AACAAAGCCT GATAGCGCCT CAACTTACT ATGGGCGTTG CGTGTTAGAG | 420 |
| GGGAAAATCC TAGCCTTTTT TGGCGTGGCA AGGGATAAAG ATTTTTTAGA AATCACTCGC | 480 |
| ATGCACGCCT TAGACATTAA GCGTTATGAT TCCTTCATTG TTGATAGCGA AAGAAAAGGC | 540 |
| TTGAAATTA | 549 |

(2) INFORMATION FOR SEQ ID NO:4062813_c2_20.nt:

381

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 201 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|--|-----|
| ATGCCGAAA ATTCTAAACT ACAACCTGCT AAGTTAGGGA AAAATTTTGA CCCTGTGGAT | 60 |
| CATTCTAACA GGAATTTTTT CTTTCTCTC ATTCTGTCTG TATTGTTACA CTGGTTGATT | 120 |
| TATTTTTTAT TTGAACACAG AGAAGATTTT TTTCTTCAA AACCCAAGCT CGTTAAATTA | 180 |
| AATCCTGAAA ATTTATTGGT Y | 201 |

(2) INFORMATION FOR SEQ ID NO:4177212_c2_9.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 519 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

332

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| GTGTTTTTAG TTCAATCGTG GGCTTTGAGC TTGAAAATAG ACAGCCTGTT TTCTCTTTTT | 60 |
| AGCGTGGGTA AAATCCCTAG CGGATCTAAA GATCCCTTTG CGTTAAGGCG TTTGAGTTTT | 120 |
| GGGCTATTGA AAATCATCGC GCATTACGGG TTAGAATTTG ATTTGAAAGC GGATTTAAAA | 180 |
| AACCTCTTTG AAAAAGTGGG CGTTTATCAA AGCTTTGATT TAGAGGTTTT AGAAAAGTTT | 240 |
| TTACTGGAGC GCTTTCATAA TTTAATAGAT TGTAACCTCT CTATTATAAG AAGTGTGTTA | 300 |
| AACACCAACG AGCGAGACAT TGTTAAAATC ATTCAAAAAG TCAAAGCCTT AAAACGCTTT | 360 |
| TTAGACAATC CTAAGAACGC TCAAAAAAAA GAGTTGCTTT TTAGCGCTTT CAAACGATTA | 420 |
| GCTAATATCA ATAAAGACAG AAACCCTAAC GAATCAAGCG GGTTTTCTAC GAGTCTTTTC | 480 |
| AAAGAATTAC AAGAGCATGC CCTTTTTTGAA GCGTTCAAC | 519 |

(2) INFORMATION FOR SEQ ID NO:422937_c2_11.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 777 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

333

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | |
|--|-----|
| ATGAGTCTTG CTCCAAGCGT TATGGCGGGC TTCTTGTTTT GTGCCGGCTC TTGCTCGCTT | 60 |
| CGCTTCCCTA ATTATTCTAA AATCATTTCC ATAGATGTGG ATACGGTGTT TTTAGGCGAT | 120 |
| GTTGCAAGCG CTTATTTTGC GCTGGATAAT GAACCCACTA AATTGCTTGG CATGGTGAGA | 180 |
| GAACTTTTTT CCCACCTTCC TTTTGAAGCC TTTTGTGATT TTTGCGAACG CACATGCAAG | 240 |
| AATTTTAAAA TTGATCTTTT GCGCTTTAGC CAAAACGAAT TAAAACGCAT CCATCAGGGC | 300 |
| TTTAACATGG GCTTTTTTGGT GCGGAATTTA GATTTATGGC GCGAAAATGG GTTTGAAAAA | 360 |
| ATCGCTTTAG AGTTTTTGAA AACTAGGGGA AAGGATCTTT TCTACCCTGA GCAGTGTTTA | 420 |
| ATCAATATGG TGTTTTTAGA GCGTATTTTA GAATTGCCTA TTCATTATAA TTGCTATTCT | 480 |
| GATTTTTTCA AAGAGCACTA CCCTAAAAGT ATCATCATGC TCCATTTTCAT CAAATACAAG | 540 |
| CCGTGGCGTT CTGTCAGTTC TTTGAACGGG CGTTTGATTT GCTATGAAGC TGAAGCGAGT | 600 |
| TTTTGGCTCG CCAACCTTTT TTGCACCCCT TTTAAAAACG ATTTTTTTTAA AGAACGCCTT | 660 |
| GAAATGGCTA AAGACCAACA AATGCAATCT TTTAAAACCC ACATCCGATC AAAAACGATT | 720 |
| AGGGATTATT TTTATTTTAG GATAAAAAAT ATTTTGAAAA AAGTTTTTCGA ACTCTCT | 777 |

(2) INFORMATION FOR SEQ ID NO:42683_c2_6.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 582 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

334

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|--|-----|
| GTGATTGTTT GCAGCGCGGC GGGGTTGAGC CATTTTTTTTG GGTTTTCTAT GTCTTTGGGG | 60 |
| GCGTTCATTG TGGGCATGGC GATTTCTAAA TCGCGCTATA AAATCAATGT CCAAGAAGAA | 120 |
| TTTCGCGCAAT TAAAAAACCT CTTTTTGGCC CTTTTTTTCA TTACGATAGG GATGCAGATT | 180 |
| AATGTGAGTT TCTTCATGGA GAAATTCTTT GTCGTCATCT TTTTACTCAT TTTAGTGATG | 240 |
| AGTTTTAAGA CTTTTATCAT TTATGCGCTA TTGCGTTTTT TTAGAGACGC TAAACCGCC | 300 |
| ATCAAAACCG CTCTTTCTTT GGCGCAAATT GGGGAGTTTT CTTTCGTGAT CTTTTTAAAT | 360 |
| TCAGGCTCGC ACCAGCTCTT TAATTTGCAA GAAAAAAAG GGATTCTTGG TTTTTTACAC | 420 |
| CAAAAAAATA TCTTAAATAT TGCTCAAAAT GACATCCACC AGCTCCTTAT TCTCATGGTG | 480 |
| GTCTTTTCTA TGTTAGCAAC CCCTTTTATT TTAAAATACC TAGAATCTAT CGCTCAATTT | 540 |
| ATTTTGCACC AAAAGAGCCA AGAAAACGAG CCGGCTAAAA AA | 582 |

(2) INFORMATION FOR SEQ ID NO:429192_f1_1.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 396 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

335

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|--|-----|
| ATGTTCTATC TTATCAATAC AGGAGTGCCT CATTTAGTGG GATTTGTGAA AAATAAAGGG | 60 |
| TTATTAAATT CTCTTAACAC ACTGGAATTA AGGGCTTTAA GGCATGAATT TAACGCTAAT | 120 |
| ATTAAACATCG CTTTTATAGA AAATAAAGAG ACGATTTTTT TACAAACTTA TGAGAGAGGG | 180 |
| GTTGAAGATT TCACGCTAGC TTGCGGGACA GGCATGGCAG CGGTTTTTAT CGCCGCGCGC | 240 |
| CTTTTTTCATA ACACCCCTAA AAAAGCCACT CTCATCCCTA AAAGCAACGA ATTTTTAGAG | 300 |
| CTTCTTTTAA AAAATGATGG AATTTTTTAT AAAGGAGTCG CGCGTTATAT CGGCATGAGC | 360 |
| GTTTTAGGCA TGGGTGTTTT TAAAAATGGG TGTTTT | 396 |

(2) INFORMATION FOR SEQ ID NO:4338438_c3_16.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 639 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

336

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: hypothetical abc transporter n tesA region

| | |
|---|-----|
| ATGATTAAAG CGATTGATAT TTCTCATGST TTTGAAAARC CTCTTTRTRA TGGCGTGAAT | 60 |
| TTGCGCATT AACCCAAAGA AAGCYTGGYG ATTTTAGGCG TGAGCGGGAG CGGTAAAAGC | 120 |
| ACGCTTYTAA GCCATTTGGC CACCATGCTA AAACCGGATA GCGGAACAGT CAGTTTGTTA | 180 |
| GAACACCAAG ATATTTATGC CCTAAATTCC AAAAAGCTTT TGGAATTGCG GCGCTTAAAA | 240 |
| GTGGGCATCG TTTTCAATC GCATTACCTT TTTAAGGGTT TTAGCGCTTT AGAAAACTTG | 300 |
| CAAGTCGCTT CAATCCTAGC CAAGCAAGAA ATAAATCATT CCCTTTTAGA ACAATTAGGC | 360 |
| ATAGCCCACA CCCTAAAACA AGGCGTGGGC GAATTGAGCG GCGGCCAGCA ACAACGCTTA | 420 |
| AGCATCGCCA GAGTGCTTTC TAAAAAACC CAAATCATT TCGCTGATGA ACCCACC GGG | 480 |
| AATTTAGACA CCACTAGCGC TAATCAAGTC ATCAGCATGC TGCAAAATTA CATTACAGAA | 540 |
| AACGAAGGGG CGTTAGTCTT AGCCACGCAT GATGAGCATT TAGCCTTCAC TTGCTCTCAA | 600 |
| GTCTATCGCC TAGAAAAAGA ATCTTTGATT AAGGAAAAA | 639 |

(2) INFORMATION FOR SEQ ID NO:4339708_f3_3.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

337

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|--|-----|
| ATGCTTGATA AACGCATTAA AACGCTTTTA CTTTTTTTTG GTCTTAATAT GGTGTGTTTG | 60 |
| AGCGTGAGTT TTACCAATAA GCCTCATTTG TGTTTTTTGGT TTTTAGTGTT AGGTTGTTAT | 120 |
| TTAGTTTATG AGTGGCAAAA GAAACAAAAA AAAGATTTTC AAAGCGCTAA AAGTTTGAAA | 180 |
| TTTGACAGCG TTAGCGAATT AGAAAAGGAT TTTGAACATG GAAGTAAC | 228 |

(2) INFORMATION FOR SEQ ID NO:4414000_c2_5.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

338

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGAAAACAA TTAAAAATGG TATTATGATC GGCACACTCG GTGCGTTGTT ATTGAGCGGT | 60 |
| TGTTCTAGCT TTGATGCTCA GCGTTTCGCT TGTCTCCCTA AAGACCATTC TTCAAAAGAC | 120 |
| GCTTCTACCA AAAAAGAAGC GCAATACATT CCTAAGGGCT TTTTGGACCC TTATTCTTCT | 180 |
| AACTTAAACC ATTGGGATTC TACATTC | 207 |

(2) INFORMATION FOR SEQ ID NO:4486092_f1_1.nt:

339

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 570 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|--|-----|
| ATGGAGCTTA TTTTAGGCTC TCAATCCAGC GCTAGGGCGA ATCTTTTAAA AGAGCATGGG | 60 |
| ATTAAGTTTG AACAAAAAGC GCTCTATTTT GATGAAGAAA GCCTAAAAAC CACAGACCCT | 120 |
| AGGGAGTTTG TCTATTTGGC GTGCAAGGGG AAATTAGAAA AAGCTAAAGA GTTACTTGCG | 180 |
| AATAATTGCG CTATCGTGGT GGCTGATAGC GTGGTGAGCG TGGGTAATCG CATGCAACGA | 240 |
| AAAGCTAAAA ACAAGCGAGA AGCCCTTGAA TTTTTTAAAAC GCCAAAATGG CAATGAAATA | 300 |
| GAGGTTTTTAA CTTGCTCTGC ATTGATTTCT CCTGTGTTGG AATGGCTGGA TCTATCGGTT | 360 |
| TTTAGAGCGC GTTTAAAGGC GTTTGATTGC AGCGAAATAG AAAAATATTT AGAGAGCGGT | 420 |
| TTATGGCAAG GAAGTGCGGG CTGTGTGCGT TTAGAGGACT TTCATAAGCC TTATATTAAA | 480 |
| AGCTCAAGCA AGAATTTAAG CGTGGGGTTG GGGCTGAATG TGGAAGGCTT GTTAGGGGCA | 540 |
| CTAAAATTAG GGGTTAAACT TTCATTATTA | 570 |

(2) INFORMATION FOR SEQ ID NO:4491093_c1_9.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 405 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

340

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | |
|--|-----|
| ATGCTTATTT TAGGACACCC TTTAATCCCT AGCGCTCGTT TTGTTTTTCAT TAAAAACACC | 60 |
| GATGCTATTC ATTCCAGCGC CAATAACGAT ATAGTGTGTT TTGAAGCAAA CCCAAAAAAT | 120 |
| TTGGAATTAG CCAATATTG CTGTGAAAAT GCGGTCCATT TTAGCGTGAT CTTTTTATCG | 180 |
| CACAAGATAG AGACGGACAC CTTTTTTTTTA TTCAACGCTT TCAAACCGCT CTATTGTATT | 240 |
| TTTAAGGATA TTAAGCAAGC CATACTCGCC CAACAACACG CCACTAATTA CTTGTTAGAT | 300 |
| AGCAAAATCT TGTTTTCTAT GGATTTTAAC GATACAGAGT CATGGGAGAT TTGCGCTAAA | 360 |
| AATCAAATAG ATGGTGTCAT TTCTAAAGAT TCACTCCTTT TGAAA | 405 |

(2) INFORMATION FOR SEQ ID NO:4492217_c3_15.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 765 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

341

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|--|-----|
| ATGAAAAAAAA GATTGAATAT AGGGCTTGTG GGTTTAGGGT GCGTGGGGAG CACGGTCGCT | 60 |
| AAAATCTTAC AAGAAAATCA AGAAATCATT AAAGACAGAG CCGGCGTGGA AATTAAAATT | 120 |
| AAAAAAGCGG TGGTGCGAGA CGTGAAAAAA CACAAGGGCT ATGCTTTTGA AATCAGTGAT | 180 |
| GATTTAGAAA GCGTGATAGA AGATAAAGGG ATTGATATTG TCGTGGAGCT TATGGGTGGG | 240 |
| GTGGAAGCGC CTTATCTTTT AGCTAAAAAA ACTTTAGCCA AACAAAARGC CTTTCGTTACA | 300 |
| GCCAATAAAG CCATGTTAGC GTACCACCGC TATGAATTAG AACAAATCGC TAAAAACACC | 360 |
| CCCATAGGCT TTGAAGCGAG CGTGTGTGGG GGTATCCCCA TTATCAAGGC TTTAAAAGAC | 420 |
| GGCTTGAGCG CTAATCACAT CCTTTCTTTT AAAGGGATTT TAAACGGCAC GAGCAATTAC | 480 |
| ATTTTAAGCC AGATGTTTAA AAATCAAGCG AGCTTTAAGG ACGCTTTGAA AGACGCGCAG | 540 |
| CATTTAGGCT ATGCGGAATT GAACCCTGAA TTTGACATTA AGGGCATTGA TGCGGCGCAC | 600 |
| AAATTATTGA TTTTAGCGTC TTTAGCGTAT GGCATTGATG CGAAATTAGA AGAAATCTTG | 660 |
| ATTGAAGGCA TTGAAAAGAT AGAGCCAGAT GACATGGAAT TTGCAAAAGA GTTTGGTTAT | 720 |
| AGCATCAAAC TTTTAGGCAT CGCTAAAAAA CACCAGGGAT TGCAT | 765 |

(2) INFORMATION FOR SEQ ID NO:4531568_c3_16.nt:

340

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 729 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGCAAGAAA AACGACTTAA AGCCATTCAA AACAAAATCG CTTCTTGGAT CAAGGAAATT | 60 |
| GAAAGCGGCT TTATAGATGC ATTGTTTTCT AAGATTGGCC CTTCAAAGAT GCTGCGCTCC | 120 |
| AAACTCATGC TCGCTTTGTT AGACGAAAAA ACAGACGCTA TTTTATTAGA TAAAGCGCTC | 180 |
| AATTTGTGTG CGATTGTGGA AATGATACAG ACCGCTTCTT TATTGCATGA TGATGTGATT | 240 |
| GACAAGGCGA CCATGCGCCG AAAGCTCCCT AGCATTAACG CTCTTTTTTG GAATTTTAAC | 300 |
| GCCGTGATGC TTGGGGATGT GTTTTATTCT AAAGCCTTTT TTGAGTTGTC TAAAATGGGC | 360 |
| GAATCCATCG CTCAAGCCCT CTCTAATGCG GTTTTAAGGC TCTCTAGGGG CGAGATTGAA | 420 |
| GACGTGTTTG TGGGGGAATG TTTTAATAGC GACAAACAAA AATACTGGCG TATTTTAGAA | 480 |
| GACAAGACCG CCCATTTTCAT AGAAGCGAGC TTAAAAAGCA TGGCGATTCT TTAAATAAA | 540 |
| GACGCCAAAA TGTATGCGGA TTTTGGGTTG CATTTTGGCA TGGCGTTTCA AATCATTGAT | 600 |
| GATTTGTTAG ACATCACTCA AGACGCCAAC ACTCTAGGTA AGCCCAATTT TAGCGATTTT | 660 |
| AAAGAGGGCA AGACCACTCT ACCCTACTTG CTTTATATG AAAAATTGAA TCAGCATGAA | 720 |
| CAGGGCTTT | 729 |

(2) INFORMATION FOR SEQ ID NO:4548792_c1_27.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 756 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

343

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|--|-----|
| ATGTTAGGGA AAAAAACGA AGAAGTCTTG ATTGATGAAA ATTTGGTTGG GGGTGTGATA | 60 |
| GCCCTTGATA GATTGGCAAA ACTCAATAAG GCCAATAGGA CTTTCAAAAG GGCTTTTTTAT | 120 |
| CTCTCTATGG TGCTCAATGT CGCCGCTGTA ACGAGTATTG TGATGATGAT GCCTTTGAAG | 180 |
| AAAACAGATA TATTTGTTTA TGGCATTGAT CGATACACAG GAGAATTTAA AATCGTCAAA | 240 |
| CGCTCCGATG CTAGGCAAAT CGTCAATTCT GAAGCCGTTG TGGATAGTGC AACTTCAAAA | 300 |
| TTTGTCTCAT TGCTGTTTGG TTATAGCAAA AATTCTTTGA GGGATCGCAA GGATCAACTA | 360 |
| ATGCAGTATT GCGATGTGAG TTTCCAAACC CAAGCAATGA GAATGTTCAA TGAAAATATC | 420 |
| AGACAATTCG TAGATAAAGT CCGAGCAGAA GCTATCATTG GCTCCAACAT ACAAAGAGAA | 480 |
| AAAGTCAAAA ATAGTCCCTT AACGAGATTA ACATTTTTC AATTACCATCAA AATCACGCCT | 540 |
| GATACAATGG AAAATTATGA ATATATCACT AAAAAACAAG TAACTATTTA TTATGATTTT | 600 |
| GCTAGAGGTA ACTCTTCTCA AGAAAATCTT ATCATCAACC CTTTGGCTT CAAAGTGTTT | 660 |
| GACATTCAAA TCACGGATTT ACAAACGAA CAGACAGTAA GCGAAATTTT GAGAAAGATT | 720 |
| AAAGAAGTGG AATCAAAAAA TAAGGCATTA AATAAA | 756 |

(2) INFORMATION FOR SEQ ID NO:4562712_c3_10.nt:

344

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 495 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGAGAGCGA TCGCTATTGT TTTAGCCAGA AGTTCCAGTA AAAGGATTAA GAATAAAAAT | 60 |
| ATGATTGATT TTTTCAATAA ACCCATGCTC GCTTACCCTA TTGAAACAGC ACTAAATTCC | 120 |
| AAGCTCTTTG AAAAAGTGTT TATCTCTAGC GATAGCATGG AGTATGTCAA TTTAGCCAAA | 180 |
| AATTATGGGG CGAGTTTTTT GAATTTACGC CCTAAAAATT TAGCAGACGA CAGGGCCACG | 240 |
| ACTTTAGAAG TGATGGCCTA TCACATGAAA GAATTAGAAT TAAAAGATGA AGACATTGCG | 300 |
| TGTTGTTTGT ATGGCGTTTC AGTATTTTCA CAAGAAAAGC ATTTACAAAA CGCTTTTGAA | 360 |
| ACTTTAAAAC AAAATCAAAA TACGGATTAT GTTTTACAT GCTCTCCCTT TAGCGCTTCG | 420 |
| CCTATCGTTC TTTTAGCCTT GAAAACGGCG TTCAAATGGC TTTTAAAGAG CATTCAAACA | 480 |
| CGCGCACGCA AGATC | 495 |

(2) INFORMATION FOR SEQ ID NO:4569693_c2_11.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

345

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: Cell division inhibitor

| | |
|---|-----|
| ATGAGTAATC AAGCGAGCCA TTTGGATAAT TTTATGAACG CTAAAAATCC CAAAAGTTTT | 60 |
| TTTGATAATA AGGGGAATAC CAAATTCATC GCTATCACAA GCGGTAAGGG GGGCGTGGGG | 120 |
| AAATCCAACA TTAGCGCTAA TTTAGCTTAC TCTTTATACA AGAAAGGTTA TAAGGTAGGG | 180 |
| GTATTTGATG CGRATATTGG TTTAGCGAAT TTAGATGTCA TTTTGGGGT GAAAACCCAY | 240 |
| AAAAATATCT TGCATGYCTT AAAAGGCGAA GYCAAATTGY AAGAAATCAT TTGCGAGATT | 300 |
| GAACCCGGGC TTTGCTTAAT CCCTGGGGAT AGCGGCGAAG AAATTTTAAA ATACATCAGC | 360 |
| GSSGCGGAAG YTTTCGATTC ATTCTTAGAT GAAGAGGGGG TTCTAAGCGC TTTAATTTAT | 420 |
| ATTTTAATTA ATACATTTTC TAAAAATTG GGTCCACTAT CTCAACTTT TCTTAATTTT | 480 |
| CAGTCATTTT TTTTATTTT TATTCAATCT CCC | 513 |

(2) INFORMATION FOR SEQ ID NO:4570262_c2_30.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

346

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | |
|--|-----|
| ATGCAGCATT TAGTCTTAAT CGGTTTTATG GGGAGCGGTA AAAGCTCTCT AGCACAAGAA | 60 |
| TTGGGGCTGG CTTTGAAATT AGAAGTGCTG GATACGGATA TGATCATTAG CGAGAGGGTG | 120 |
| EGCTTGAGCG TGAGAGGGAT TTTTGAAGAG CTTGGCGAAG ACAATTTTCAG GATGTTTGAA | 180 |
| AAAATT | 186 |

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 654 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Helicobacter pylori*
- (xi) SEQUENCE DESCRIPTION:

| | | | | | | |
|-----------|-----------|-----------|-----------|-----------|-----------|-----|
| ATGAGCATT | AGGAAAATT | AGAGCAAGT | AGAAACGA | TTAAAAGCG | TGAAAAGCT | 60 |
| TTAGAAGG | CGTTTAGAT | AGAAAAGTT | TTCAAACG | ACAAGTGGG | GTTGTTGTT | 120 |
| ATCGTGGT | CTTTTATCG | TTATTTAGG | GATACAAA | TACAAGATT | TAAGCATG | 180 |
| CAAACGAG | AGCGGATCA | TCAAATTT | AATGAAGT | GATAGAGTC | TAATAATAT | 240 |
| GCCTTGCAA | AAAGATTGA | AGAAGTCGC | CCAGAGTT | ATGACTTG | TCAGTTCGC | 300 |
| AGAGCGAG | TG | AGAGGAACG | TGCAAACG | TTTAAAAGG | TTTCGCAAT | 360 |
| ATCGTTAA | AG | CGTTCGCCA | ATATTCTTA | GCATCGCT | CTAGAGATA | 420 |
| GAAAAAAG | CCATTCTTA | AGAAATGAG | GCTTTACA | AAGTGAAC | GTTGTATGA | 480 |
| GAAAATTCT | AAGACGCA | CAAAAAAGC | CATCAAAG | TATCAACT | CCCTCTAAG | 540 |
| TCTTCACT | CT | ATGCTATA | AT | CTCTGTTT | AAACATTAT | 600 |
| CAAAACCCT | T | CCAAACCA | AC | CAATCTAA | AG | 654 |

(2) INFORMATION FOR SEQ ID NO:45914063_c2_9.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

348

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| GTGCATTTCA ATCAGGTTGT TCTCCCAAAA GCGGTGGGCG CGATTTTAGT CGCACCAAAA | 60 |
| GGGCCCCGGA GCGCTTTAAG AGAAGAATAC CTTAAAAATA GGGGTTTATA CCATCTAATC | 120 |
| GCCATAGAGC AAGAAAGCTC AATTCATAAC GCTAAAGCGG TGGCTTTAAG CTATGCTAAA | 180 |
| GCGATGGGTG GGGGGAGAAT GGGGGTTTTA GAAACGAGTT TTAAAGAAGA ATGCGAGAGC | 240 |
| GATTTATTCG GCGAGCAAGC GGTCTTGTGC GGGGGGTTAG AAGTCGATCG TAAGAATGGG | 300 |
| GTT | 303 |

(2) INFORMATION FOR SEQ ID NO:4687507_f1_3.nt:

349

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGAAAAAAT TTTTTTCTCA ATCTTTGTTA GCTCTTATTA TCTCTATGAA TCGGGTATCT | 60 |
| GGCATGGATG GTAATGGCGT TTTTTTAGGG GCGGGTTATT TGCAAGGACA GCGCAAATG | 120 |
| CATGCGGATA TTAATTCTCA AAAACAAGCC ACCAACGCTA CGATCAAAGG CTTTGACGCG | 180 |
| CTCTTGGGGT ATCAATTTTT CTTTGAAAAA CACTTTGGCT TACGCCTTTA TGGGGTTTTT | 240 |

(2) INFORMATION FOR SEQ ID NO:4698838_f2_3.nt:

350

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1341 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|------|
| ATGCTAAAAA AGATTTTTTA TGGTTTTATC GTTTTATTTT TGATTATCGT AGGGTTGTTG | 60 |
| GCCGTTCTTG TCGCTCAAGT TTGGGTAAGT ACGGATAAGG ATATTGCTAA AATTAAAGAT | 120 |
| TATCGCCCCA GTGTCGCTTC ACAGATTTTA GACAGAAAAG GGCGTTTGAT CGCTAATATT | 180 |
| TATGATAAGG AATTTCGTTT TTATGCGCGT TTTGAAGAAA TCCCCCACC GATTGTTGAA | 240 |
| AGCCTTCTAG CGGTAGAAGA CACCCTCTTT TTTGAGCATG GGGGGATCAA TTTAGACGCT | 300 |
| GTCATGCGCG CTATGATTAA AAACGCTAAA AGTGGTCGTT AACTGAAGG GGGTAGCACT | 360 |
| CTAACCCAAC AACTCGTTAA AACATGGTG CTCACACGGG AAAAAACCCT AACCAGAAAA | 420 |
| CTCAAAGAAG CTATCATCTC CATACGCATT GAAAAAGTCT TAAGCAAAGA AGAAATTTTA | 480 |
| GAGCGTTATT TGAACCAAAC TTTTTTTGGG CATGGGTATT ATGGCGTGAA AACCGCAAGT | 540 |
| TTAGGGTATT TTAAAAAACC CCTTGACAAA CTCACGCTTA AAGAAATCAC CATGTTAGTC | 600 |
| GCCTTACCTA GGGCTCCAAG TTTTATGAC CCTACCAAAA ATTTAGAATT TTCACTCTCT | 660 |
| AGGGCTAATG ATATTTTAAG GCGGTTGTAT TCTTTAGGCY GGATTTCTTC TAACGAGCTC | 720 |
| AAATCCGCTC TCAATGAAGT GCCAATCGTC TATAACCAAA CTTCCACGCA AAATATCGCT | 780 |
| CCCTATGTCG TGGATGAAGT GTTGAAGCAA TTGGATCAAT TAGACGGGTT AAAAACTCAA | 840 |
| GGCTATACCA TAAAACTCAC GATAGATTTG GATTACCAAC GCTTAGCGTT GGAGTCTTTG | 900 |
| CGTTTTGGGC ATCAAAAAAT CTTAGAAAAA ATCGCTAAAG AGAAGCCAAA AACTAACGCT | 960 |
| CTAATGATA AAGATGAAGA CAACTTAAAC GCCAGCATGA TAGTTACAGA AACGAGCACC | 1020 |
| GGTAAGATTT TAGCCTTAGT GGGGGGGATT GATTATAAAA AAAGCGCTTT CAATCGCGCC | 1080 |
| ACGCAAGCCA AACGGCAGTT TGGGAGCGCR ATCAAGCCTT TTGTGTATCA AATCGCTTTT | 1140 |
| GATAATGGCT ATTCCACCAC TTCCAAAATC CCTGATACCG CGCGAAATTT TGAAAATGGC | 1200 |
| AATTATAGTA AAAACAGCGT GCAAAACCAC GCATGGCACC CTAGCAATTA TRCTCGCAAA | 1260 |

TTTTTAGGGC TTGTAACCTT GCAAGAAGCC TTGAGCCATT CGTTAAATCT GGCTACGATT

1320

351

AATTTAGCGA TCGCTTGGCT A

1341

(2) INFORMATION FOR SEQ ID NO:4708337_f1_7.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 654 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGAACGATA CAACAGAGCA CCATGGATCC AATCCGCTAA ACGCCCCACC ACCTAGCAAC 60
TCACAGAGCA ACGATCTCTT AAATTGCTA GACTCGTTAT ATCCTAAAGG GAGTTTAGGG 120
GAACAAAGAT TTCACGAAGC TTAAAGAAT CAAGAAGAGT TGAAAAATAT CCTAATAGAA 180
ATAGAAAAGC TACCGCAAGA AAAAAGGTAT GAACTTCTGA TGCAGATAGG ACAAGCCAAA 240
CAGAGAATAA TGGAAGCATA CGCTCATTC A TTCTTAGGAT ATATAGGGGG ACTAGAGCAT 300
CTGTTAGGAT TGTGTATGGG TGGGATATTT GTTTTGTTTG CAATCTATTT TGTATTTTTA 360
AGAACTAGCA AAAACACAGA GCTAGTGGAA AGTCTAAAA CAAAATTAAA ACTTCAGTAT 420
TTTTACTATG CCTTTGGTGT GGGTGCGGTT TTGTTTTTTG GATTAGAAAC AATTAGATCG 480
ATTTATGAAC TATATATCTT AGGAATTGGT AGCACTAACG ACAAGGTGCT CTTTGTTTTG 540
AAAAACATTT GCTTCATAGG TATGGGCTAT TTGATTATA AAGTTATTAA AGTTATTGGT 600
ATAAAAAATT TTATCAATGG TCTTTTCGCT TCAAAGAAAC AAGGCGGTGC AGAA 654

(2) INFORMATION FOR SEQ ID NO:4714375_f2_7.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 576 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGATGGATA AGGTGGGTTT TAAATCTCAA GGCATCTTTG TGATGGACGC TAGCAAGAGG 60
GATGGGCGTT TGAACGCGTA TTTTGGAGGC TTGGGTAAAA ACAAGCGGGT GGTGTTGTTT 120
GACACTTTGA TCTCTAAAGT TGGGACAGAA SGGCTTTTAG CCATTTTAGG GCATGAGTTA 180
GGGCATTTTA AAAATAAGGA TTTGTTGAAA AATTTAGGGA TTATGGGAGG CTTGCTCGCT 240
CTTGTTTTTG CTTTGATCGC TCATTTGCCG CCGTTGGTTT TTGAAGGCTT TAATGTCTCG 300
CAAACGCCAG CGAGTTTGAT CACGATTCTA CTCTTGTTTT TGCCGGTGTT TTCCTTTTAC 360
GCCATGCCTT TGATTGGGTT TTTTAGCCGC AAGAACGAAT ACAATGCGGA CAAGTTTGGG 420
GCGAGTTTAA GCTCTAAAGA GACTTTAGCC AAAGCGTTAG TGTCCATTGT GAATGAAAAT 480
AAAGCGTTCC CCTATTCGCA CCCTTTTAT GTTTTCTTGC ATTCACGCA CCCGCCGCTA 540
TTAGAACGCC TAAAAGCTTT GGATTATGAA ATTGAA 576

353

(2) INFORMATION FOR SEQ ID NO:4726503_c2_12.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 603 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

354

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGAATATTT ATCAAAAAA CTTGCAAGCT CTTTTCAAAA AAGACCCTCT TTTGTTCGCA | 60 |
| AAGCTCAAAG CCATTAAAGA AAACAAAAA TACGAAGTGT TTTTAGGGAA TGATAGCGCG | 120 |
| AATTTCAACC TCTTAGATAA AGAAACAAAC ACGCCCTTAT TTGAAAAAAG CCCGCTAGAT | 180 |
| TCAAGCTTAG AGCTATATAA AAATAGCGAA ATTCACATGC TCTATCCTTA TTTGTATTAT | 240 |
| TTTGGCTTGG GTAATGGGGT GTTTTATCGC TTGCTTTTAG GCAATGAAAA TTTAAAACGC | 300 |
| TTGGTGGTCA TTGAGCCTGA AATAGAGGTG ATTTTCATTG TGCTGAATCT TTTGGATTTT | 360 |
| TCCACTGAGA TTTTAGAAAA TCGTTTGATT TTATTGCATG CAAGTTTTTG CAATTACAAC | 420 |
| ATGATTGCTT CATTATTTGA TATGGATAAA AAGTCTCGTT TATACGCAAG AATGTATGAT | 480 |
| TTAAAACTTT TTAACGCTTA TTATGAACGA TACTCTCATC AAATGATAGA AATCAACCAG | 540 |
| CATTTACGC GCGCTTTAGA GCATGGCGCT ATTAGCGTAG GCAATGACGC TAAAGCGCAC | 600 |
| TCA | 603 |

(2) INFORMATION FOR SEQ ID NO:4728193_f1_2.nt:

355

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 390 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGAAAAAGA TTATTCTTGC ATGCCTTGTG GCTTTTGTGG GTGCCAATTT AAGCGCAGAG | 60 |
| CCTAAGTGGT ATAGCAAGGC CTATAACAAA ACAAACGCCC AAAAAGGCTA TCTTTATGGG | 120 |
| AGTGGTTCAG CCACTTCTAA AGAGGCTTCT AAACAAAAAG CGTTAGCGGA TTTAGTGGCG | 180 |
| TCTATTAGCG TGGTGGTCAA TTCACAAATC CACATTCAAA AAAGTCGTGT GGATAATAAG | 240 |
| TTAAAATCCA GCGATTCACA AACGATCAAC TTAAAAACCG ATGACTTGGA ATTGAATAAT | 300 |
| GTAGAAATTG TCAATCAAGA AGCGCAAAAA GGGATCTACT ACACCAGAGT GAGGAATCAA | 360 |
| TCAAAACTTG TTTTTCAGG GTTTAAGGGA | 390 |

(2) INFORMATION FOR SEQ ID NO:4740887_f3_10.nt:

356

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|--|-----|
| ATGAAAATCC AAACAATTTT AACACTTGTC CTTACAATAA TAATGGTAAT ACAAAAAATG | 60 |
| ATTGTTGGCA AAATTTTCACC CCACAAAACC GCAGAAGAAT TCACYAATTT AATGTTGAAC | 120 |
| ATGATCGCTG TTTTAGACTC CCAATCTTGG GGCGATGCGA TCTTAAACGC TCCTTTTGAG | 180 |
| TTCACTAACA GCCCAACAGA TTGCGATAAT GATCCTTCAA AATGCGTAAA TCCTGGGACA | 240 |
| AACGGGCTTG TCAATTCTAA AGTCGATCAA AAATATGTGT TAAACAAACA AGACATTGTC | 300 |
| AATAAATTTA AAAACAAAGC RGATCTTGAT GTAATTGTTT TAAAGGATTC AGGGGTTGTA | 360 |
| GGGTTRGSCA ATGGATATGG CAATGATGGT GAATATGGCA CATTAGGGGT AGWAGCCTAT | 420 |
| GCTTTAGGAT CC | 432 |

(2) INFORMATION FOR SEQ ID NO:4744128_c3_102.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 927 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

357

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| GTGGTAATAA GGTTAGTCCT AAACATGCTA ACATGTCAAA TTAGCTATAT AAGGATAAGT | 60 |
| TATCTTGTCT CTGTTAGCGA TTTTGTGATT TGCAAGGAAA GATTTATGGA TGAAATTAAA | 120 |
| ACGCTGTTAG TGGATTTTTT CCCGCAGGCA AAGCATTTTG GGATAATCTT AATCAAGGCT | 180 |
| ATTGTTGTCT TTTGTATAGG TTTTATTTT TCGTTTTTCT TACGGAACAA AACCATGAAA | 240 |
| TTCTTATCCA AAAAGGATGA GATTTTGGCG AATTTTGTCT CGCAGGTTAC TTTTATCTTA | 300 |
| ATCCTTATCA TTACTACAAT CATCGCGCTC AGCACGCTAG GCGTCCAAAC CACCTCTATT | 360 |
| ATCACTGTTT TAGGAACGGT GGGGATTGCG GTGGCGTTGG CTTTAAAAGA TTATCTTTCA | 420 |
| AGCATTGCTG GAGGGATAAT CCTTATTATT TTACACCCTT TCAAAAAGG AGACATCATT | 480 |
| GAAATCTCTG GCCTAGAGGG CAAAGTAGAA GCGCTTAATT TTTTAAATAC TTCTTTACGC | 540 |
| TTGCATGACG GGCGCTTGGC GGTTTTGCCT AATAGAAGTG TCGCTAATTC TAATATTATC | 600 |
| AATAGCAATA ACACTGCGTG TCGGCGCATT GAATGGGTCT GTGGGGTAGG GTATGGGAGC | 660 |
| GATATTGAAC TGGTGCATAA GACTATAAAA GATGTTATTG ACGGGATGGA AAAAATTGAT | 720 |
| AAAAACATGC CCACTTTCAT TGAATCACG GATTTTGGAC AAAGTTCGCT GAACTTCACC | 780 |
| ATTAGGGTTT GGGCAAAGAT TGAAGACGGG ATCTTTAATG TGAGGAGCGA ACTCATTGAA | 840 |
| TCGATCAAAA ACGCCCTGGA CGCTAATCGT ATTGAAATCC CTTTCAACAA GCTAGATATT | 900 |
| TCTATCAACA AACAAGACTC TTCTAAG | 927 |

(2) INFORMATION FOR SEQ ID NO:4766691_f1_2.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 491 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

358

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGAAAAACT TTTCCCCACT CTATTGTCTT AAAARGCTCA AAAAACGCCA TTTAATCGCT | 60 |
| CTGAGTCTGC CCTTGCTTTC TTATGCGAAT GGCTTTAAAA TCCAAGAGCA AAGCTTGAAT | 120 |
| GGCACGGCTT TAGGCTCGGC GTATGTCGCT GGGGCTAGGG GTGCTGACGC TTCTTTTAC | 180 |
| AACCCGGCTA ACATGGGCTT TACTAACGAT TGGGGCGAAA ACAGAAGCGA ATTTGAAATG | 240 |
| ACCACCACCG TGATCAATAT CCCGACCTTT AGCTTTAAAG TCCCTACGAC CAATCAAGRC | 300 |
| TTATATTCGG TAACAAGTTT AGAAATTGAT AAAAGCCAAC AAAATATTTT AGGCATCATC | 360 |
| AACACTATAG GGTTAGGCAA TATCCTTAAA GCGCTTGGCA ATACGGCCGC TACCAATGGC | 420 |
| TTATCACAAG CTATCAATCG TGTTCAGGG CTTATGAACT TAACCAATCA AAAAGTCGTA | 480 |
| ACCCTCGCTT C | 491 |

(2) INFORMATION FOR SEQ ID NO:4787562_c3_5.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

359

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGTGTTTAG CGATCCCCTC TAAAGTCATA GCCATTAACG ATAATGTGGC ACTCTTAGAG | 60 |
| ACTTTGGGCG TTCAAAGAGA AGCGAGCTTG GATTTAATGG GCGAGTCCGT TAAAGTGGGC | 120 |
| GATTATGTGC TACTACACAT CGGCTATGTG ATGAGTAAAG AT | 162 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 606 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|--|-----|
| ATGAAATATT TATGGCTTTT TTTAATATAC GCTATAGGGC TTTTGTGCAAC AGATAAAACG | 60 |
| CTAGATATTA TTTAAACCAT TCAAAACTT CCTAAGATTG AAGTGCCTA CTCCATAGAT | 120 |
| AACGATGCCA ATTACGCTTT AAAATTGCAT GAAGTCTTAG CGAACGATTT AAAGACTAGC | 180 |
| CAGCATTTTG ATGTTTCTCA AAACAAAGAG CAAGGTGCTA TCAATTACGC AGAACTCAAG | 240 |
| GATAAAAAAG TCCATCTTGT AGCGCTTGTG AGCGTGCGG TAGAAAACGG CAATAAAATT | 300 |
| TCACGATTAA AACTTTATGA TGTGGATACA GGAACGCTCA AAAAGACTTT TGACTACCCC | 360 |
| ATTGTAAGTT TAGATCTATA CCCTTTTGCA GCGCACAACA TGGCCATTGT GGTGAATGAT | 420 |
| TATTTAAAAG CCCCTTCTAT CGCTTGGATG AAGCGCCTGA TTGTTTTTTC TAAATACATT | 480 |
| GGACCAGGAA TCACAAACAT CGCACTAGCG AATTATACGA TCGGTTATCA AAAAGAAATC | 540 |
| ATCAAAAACA ACCGACTCAA TATTTTCCCC AAATGGGCGA ACGCTGAGCA AACGGAGTTT | 600 |
| TATTAC | 606 |

(2) INFORMATION FOR SEQ ID NO:4826401_f2_2.nt:

361

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 615 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| GTGGTGAGCG GGGTGGTGAT CATTATTGTG TTTTTTGTGC CGATTCTAAC CTTACAGGGG | 60 |
| TTAGAGGGCA AGATGTTTAG GCCTTTAGCG CAAAGCATTG TGTATGCGCT TTTAGGCACT | 120 |
| TTAGTTCTAT CCATCACTAT CATTCCTGTA GTGAGCTCTC TTGTCTTAAA AGCCACGCCC | 180 |
| CATAGCGAAA CCTTTTTAAC GAGGTTTTTA AACAGAATCT ACGCCCCTTT ATTGGAATTT | 240 |
| TTTGTGCATA ACCCTAAAAA AGTGATTTTA GGAGCGTTTG TTTTTTTAAT CGCAAGCCTT | 300 |
| TCTTTATTCC CTTTGTGGG GAAGAATTTC ATGCCTGCTT TAGATGAGGG CGATGTGGTT | 360 |
| TTGAGCGTGG AAACCACCCC CTCTATTTCC TTAGATCAAT CTAAAGATCT CATGTTAAAC | 420 |
| ATTGAAAGCG CGATTAAAAA GCATGTCAAA GAAGTTAAAA GCATTGTCGC GCGCACAGGG | 480 |
| AGCGATGAAT TGGGGCTGGA TTTAGGGGGT TTGAATCAAA CCGATACTTT TATTTCTTTC | 540 |
| ATCCCTAAAA AAGAATGGAG CGTTAAAACC AAAGATGAAT TGGTTAGAAA AAATCATGGA | 600 |
| TTCTTTAAAA GACTT | 615 |

(2) INFORMATION FOR SEQ ID NO:485375_f2_1.nt:

362

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| GTGGGATATA TCCCTARGGA AAAGATTGTA GGCATTAGCG CGATCGCTAA ACTCATTGAA | 60 |
| ATTTATAGCA AACGCCTGCA AATCCAAGAA AGGCTGACCA CTCAAATTGC AGAAACTTTT | 120 |
| GATGAAATCA TAGAGCCAAG GGGCGTGATC GTGGTTTGTG AAGCCAAGCC ACTTGTGCAT | 180 |
| GAGCATGCAA GGGGTGCAAA AGCAAAATGC GATCAT | 216 |

(2) INFORMATION FOR SEQ ID NO:487750_c1_42.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

363

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

GTGGCTCTTG TGTTTGATAG TTTGATAGAG AACAAGAAG

(2) INFORMATION FOR SEQ ID NO:4882318_c3_7.nt:

364

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 297 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|--|-----|
| ATGAAAAAAA TTGGTTTGAG CTTGTGTTTG GTTTGTAGTT TGGGTTTTTT AAAAGCCCAT | 60 |
| GAAGTGAGCG CTGAAGAGAT TGC GGATATT TTCTACAAAC TCAACGCCAA AGAGCCTAAA | 120 |
| ATGAAAATCA ACCACACGAA GGGGTTTTGC GCTAAAGGCG TGTCCTCCC TAACCCGCAA | 180 |
| GCAAGAGAGG ATTTAGAGGT GCCACTACTC AATGAAAAAG AAATCCCTGC GTCTGTAAGG | 240 |
| TATTCTTTAG GGGGCGTGGT CGATTGGACG ATAAAAGCAA GGTTAGGGGA ATGGCGT | 297 |

(2) INFORMATION FOR SEQ ID NO:4882652_f2_2.nt:

365

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| GTGATCAAAC CTCATAGCGT GGGATTGGTA AGGATTGGGA TTTGTTTGTC TTTAGAAGTG | 60 |
| GGGTATGAAC TGCAGGTACG CACCCGTAGC GGCTTGGCTT TGAATCATCA GGTGATGGTG | 120 |
| TTAAATTYCC CTGGCACGGT GGATAATGAT TATAGGGGCG AAATTAAGGT CATTTTAGCG | 180 |
| AATTTGAGCG ATAAAGATTT TAAAGTTCAA GTAGGGGATA GGATCGCTCA AGGGGTGGTT | 240 |
| CAAAAAACTT ATAAAGCCGA ATTTATAGAA TGCGAACAAT TAGATGAAAC CTTCAAGGGG | 300 |

(2) INFORMATION FOR SEQ ID NO:4882842_c3_11.nt:

366

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 765 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGGAAATCA TTTTATTAAT TGTTGCGGCG GTTGTGTTGT TTTATTTTTA CAACACCCTC | 60 |
| AAAGAATATT TGAAAAACCC CCTAAACCCT AAAACCAAAA CCGAAGAATA CGACTTGAAA | 120 |
| AATGACCCCT ATTTGCTGGT GCAATCTAGC CCCCTAGACA AATTCAAGCA AACCCAAATA | 180 |
| GGCGCGTATA TGCGTCTTTT AAAATTTTTA GACATTCAAA AAAACGCCTT GGATAACGCT | 240 |
| TTAAGAACGC TTTTATCCA TGAATTGGAG CAGCCCTTAA ACAGCGAACA GCAAAATTTA | 300 |
| GCCAAAGAGC TTCTCAATGA GCCSGTGGAT AAAAAAGAAA ATTTTGAATC CTTATGCCAA | 360 |
| GAAATCGCCG ACCACACGCA TGGAGAATAC ACCAAACGCC TGAAATTAGT GGAATTTCTT | 420 |
| ATGCTATTAG CCTATGCTGA TGGGATTTTG GACAGCAAAG AAAAAGAATT GTTTTTAGAT | 480 |
| GTGGGGGCGT TTTTGCAGAT AGACAATCAA GATTTTAACG AGCTTTATGA CAATTTTGAA | 540 |
| CACTTCAATT CAATAGAAAT CCCTATGTCT TTAGAAGAAG CAAAAAATCT TTTTGAAATC | 600 |
| CAAACCCACA CCACCATGCA AGATTTAGAA AAAAAAGCTT TGGATTTAAG CGCCCCCTAT | 660 |
| TACCATAAAA TGAATGACAA CAAACGCTAC AGCGAACAAG ATTTTATCTC TTTGAAAAAA | 720 |
| ATCGCCCTCG CTTCCCAACT TTTAGAAAAT GATTTAAAAG ACTCA | 765 |

(2) INFORMATION FOR SEQ ID NO:489057_c3_5.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

367

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGGAAGTAG AGCATGGCAA GATTGAAACC ACTTTAAGCT TGGGGGCGTC TCATTGGA | 60 |
| GTCATTAAAA TGATGCTTTT AGAGAGCCTG CCTTCTTTAG TGAATAATAT CACCATCACT | 120 |
| TTAATTTCTC TAATAGGCTA TTCGGCTAWG GCYGGAGCGT TAGGGGCTGG GGGATTGGGG | 180 |
| GATTTAGCCA TTAGGATTGG CTATCAAAGT TATAGGGGCG ATGTGCTTTT TTATGCGGTG | 240 |
| GTCGTGATCA TCGTTTTAGT GCAAATCATT CAAAGCGCGG GGGATTATGT GGTGAAACGC | 300 |
| TTGAGAAAGA ATAAGTAT | 318 |

(2) INFORMATION FOR SEQ ID NO:4895327_c1_11.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1581 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

368

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|--|------|
| ATGAACGAAA TTGACAAATC CGTTGATATC GGATTCTTAC GGATTCTGGA TGTTATTAAA | 60 |
| AAAGTTAAAA CCCCAAAGGG TGGTATTGAG GTTTTAAGGA CTTTAATTGA TTTCACGCCC | 120 |
| AAAATTGAAA ACGCCCTAAA TTTAGCGACC AAAAGCCATA AGGGGCAATA CAGAAAGAGC | 180 |
| GGTGAGCCTT ATATTGTCCA TCCTATTTGC GTGGCGAGCG TGGTGGCGTT TTGTGGGGGC | 240 |
| GATGAGGCGA TGGTGTGCGC CGCGCTTTTG CATGATGTGG TAGAAGACAC GCCTTGTGAG | 300 |
| ATTGAAACGA TTGAGCGAGA ATTTGGGCAA GATGTGGCTA ATTTAGTGGA TGCGCTCACC | 360 |
| AAAATCACTG AAATCAGGAA AGAAGAGTTA GCGGTGAGTT CTCAAGATCC CAGAATGGTG | 420 |
| GTTTCAGCCC TCACTTTTAG AAAGATCCTT ATTAGCGCGA TACAAGATCC AAGAGCCTTA | 480 |
| GTGGTAAAGA TTAGCGACAG GTTGCAACAAC ATGCTCACCT TAGACGCCTT GCCTCATGAC | 540 |
| AAGCAGGTGC GTATTTCTAA AGAAACTCTA GCGGTGTATG CCCCATAGC GAGTCGATTG | 600 |
| GGCATGTCTT CAATCAAAAA CGAATTAGAA GACAAGAGCT TTTATTATAT TTATCCAGAA | 660 |
| GAGTATAAAA ATATTAAGGA GTATTTGCAC AAAAACAAC AGTCTTTACT CTTAAAACTC | 720 |
| AACGCTTTTG CGAGCAAGTT AGAAAAAAG CTTTTTGACA GCGGGTTTAG CCATTCGGAT | 780 |
| TTTAAACTCG TTACAAGGGT GAAACGCCCT TATTCTATTT ATCTTAAGAT GCAACGAAAA | 840 |
| GGGGCGGTTA ATATTGATGA AATTTTGGAC TTGTTAGCCA TTAGGATTTT ATTGAAAAAC | 900 |
| CCGATTGATT GCTACAAGGT TTTAGGGATT ATTCATTGA ATTTCAAACC CATTGTTTCT | 960 |
| CGTTTTAAAG ATTACATCGC TTTGCCCAA GAAATGGCT ATAAGACAAT ACACACGACG | 1020 |
| ATTTTTGATG AATCTTCTGT TTATGAAGTG CAGATCCGCA CTTTTGATAT GCACATGGGG | 1080 |
| GCGGAGTATG GTAATTCAGC CCATTGGAAG TATAAAGCCG GGGGCGTGGA TCATGAAGAA | 1140 |
| CATCATGAGG GCATGCGGTG GTTGCAAAAT TTTAAATACC ATGACAGCGA TTTGAAAAAC | 1200 |
| GACCCTAAGG AATTTTACGA ACTCGCTAAG AACGATTGT ATCGTGAAGA TATTGTCGTT | 1260 |

| | |
|---|------|
| TTTTCGCCCC ATGGGGACAC TTACACTTTA CCGGTGGGCG CGATCGCTTT AGATTTCGCT | 1320 |
| TACATGGTGC ATAGTGATTT GGGCGATAAA GCCACGGACG CTTATATCAA TAGTAAAAAA | 1380 |
| GCCTTACTCA ATCAAGAATT AAGGAGTGGG GATGTGGTTA AAATCATTAA AGGCGATAAA | 1440 |
| GTAATACCTC GTTTCATTTG GATGGATCAG CTTAAAACCTT CTAAGGCTAA AAACCATTG | 1500 |
| CGCATCCAAA GAAGAAACCG CTTGAAAGAA ATTGACACTA AGAGCATGAT CAATATCTTA | 1560 |
| GCGACTTTTTT TTTGGGCGCT C | 1581 |

369

(2) INFORMATION FOR SEQ ID NO:4897177_f1_1.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

370

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| GTGGTGGTGG TTGAGAATAT AAAAGACGCT GTGCCTTTAG CGCAAAGCCT RATARAGGGG | 60 |
| GGTATTCCAA TCATAGAAGT AACTTTGCGA TCAAAGTGTG CTTTAGAGGC CATAGAGCTT | 120 |
| ATCGCTAAGA ATGTGCCAAA AATGCGCGTG GGTGCTGGCA CGATACTCAA TCTCACTCAA | 180 |
| TTAGAGCAGG CTCAAATAG GGGGGCAGAG TTTTGTGATTA GCCCGGGTCT TACGATAAAG | 240 |
| CTTTTAGAAC ACGCAAAGAA AAAAGACATG CCTTTAATAC CTGGGGTTTC TAGCAGCAGT | 300 |
| GAAGTCATGC AAGCTTTAGA ATTGGGTTAT AACGCTTTGA AATTTTCCC GCGGAGTAT | 360 |
| TGCGGGGGCC GT | 372 |

(2) INFORMATION FOR SEQ ID NO:495312_c2_4.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

371

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: UDP-N-ACETYLMURAMOYLALANYL-D-GLUTAMATE--2 & 6-DIA

| | |
|---|-----|
| GTGGAAAAAA TCAAACCCTA TGCCCCTAAA GATAGCCCTT TAATAGACTA TTCTAGCCTA | 60 |
| GTTAGAAACG TCCAATCCAC TTTAAAAGGC ACTTCTTTTG AAACGCTTAT CAATGGCGTT | 120 |
| TGGGAAAGCT TTGAAACGAA GGTTTTAGGG GAGTTTAACG CCTATAATAT CGCTTCAGCG | 180 |
| ATTTTAACCG CTAAGCATTT AGGCTTAGAG ACAGAAAGGA TCAAACGGCT TGTTTTTGAG | 240 |
| CTTAAGCCTA TTAACCATCG TTTGCAACTG TTGGAAGCGA ATCAAAAAAT CATTATAGAC | 300 |
| GATASCTTTA ATGGGAATTT AAAGGGCATG | 330 |

(2) INFORMATION FOR SEQ ID NO:50253_c1_13.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1791 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

372

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: heat shock protein C62.5 - chaperone-ATPase activ

| | |
|---|------|
| ATGTCTAATC AAGAATACAC CTTCCAAACT GAAATCAACC AGCTTTTGGA TTTGATGATC | 60 |
| CACTCTTTGT ATTCTAATAA AGAGATTTTT TTAAGGGAGT TGATTTCTAA CGCGAGCGAC | 120 |
| GCTTTGGATA AGCTGAATTA TTTGATGCTA ACCGATGAGA AATTAAAAGG GCTGAATACC | 180 |
| ACGCCTAGCA TCCATTTGAG TTTTGATAGC CAAAAAAAAA CCTTAACGAT TAAAGACAAT | 240 |
| GGTATAGGCA TGGATAAAAG CGATCTCATC GAGCATTTAG GCACGATCGC TAAATCAGGC | 300 |
| ACGAAGAGTT TTTTAAGCGC TTTGAGTGGG GATAAGAAAA AAGATAGCGC CTTAATTGGC | 360 |
| CAATTTGGCG TGGGCTTTTA TTCGGCGTTC ATGGTAGCGA GTAAGATTGT CGTTCAAACC | 420 |
| AAAAAAGTTA CCAGTCATCA AGCTTATGCA TGGGTGAGCG ATGGTAAGGG CAAGTTTGAA | 480 |
| ATCAGCGAAT GCGTCAAAGA GGAGCAAGGC ACAGAAATCA CCCTCTTTTT AAAAGAAGAA | 540 |
| GATTCTCATT TTGCGAGCCG TTGGGAGATT GATAGCGTTG TTAAAAAGTA TTCTGAGCAT | 600 |
| ATCCCTTTCC CTATTTTTTT AACTTACACC GATACGAAAT TTGAGGGCGA AGGGGATAAT | 660 |
| AAAAAAGAAG TTAAAGAAGA AAAATGCGAT CAGATCAATC AAGCGAGCGC TTTATGGAAA | 720 |
| ATGAATAAGA GCGAATTGAA AGAAAAGGAT TACAAAGACT TTTACCAATC GTTTGCGCAT | 780 |
| GATAACAGCG AGCCTTTGAG CTATATCCAT AATAAAGTGG AAGGCTCTTT AGAATACACG | 840 |
| ACGCTTTTTT ATATCCCTAG CAAAGCGCCC TTTGATTGTG TTAGGGTGGA TTATAAAGC | 900 |
| GGGGTCAAAC TTTATGTTAA ACGGGTGTTT ATCACTGATG ATGACAAAGA ATTGTTGCCG | 960 |
| TCTTATTTGA GGTTTGTTAA AGGCGTGATT GACAGCGAAG ATTTGCCCTT GAACGTGAGT | 1020 |
| CGTGAAATCT TACAGCAGAA TAAGATTTTA GCCAATATCC GTTCGGCTTC AGTGAAAAAG | 1080 |
| ATTTTAAGCG AGATTGAAAG GCTGAGCAAG GATAACAAGA ATTACCATAA ATTCTATGAG | 1140 |
| CCTTTTGGGA AAGTGTTAAA AGAAGGCTTG TATGGGGATT TTGAAAACAA AGAAAACTT | 1200 |
| TTAGAATTGT TGAGATTCTA TTCTAAAGAC AAAGGAGAAT GGATTTCTTT AAAAGAATAC | 1260 |

| | | | | | | |
|------------|------------|------------|------------|------------|------------|------|
| AAAGAAAATT | TAAAAGAAAA | TCAAAAAAGC | ATTTACTACC | TTTtagGCGA | AAATTTAGAC | 1320 |
| TTATTAAAAG | CGTCCCCCCT | TTTAGAAAAA | TACGCTCAAA | AAGGCTATGA | TGTTTTGTTA | 1380 |
| TTGAGCGATG | AAATTGATGC | GTTTGTGATG | CCAGGCGTGA | ATGAATACGA | TAAAACGCCC | 1440 |
| TTTAGAGACG | CTAGCCATAG | TGAGAGTTTG | AAAGAGCTTG | GTTTGGCAGA | AATCCATGAT | 1500 |
| GAGGTAAAAG | ATCAGTTTAA | AGATTTAATC | AAAGCGTTTG | AAGAAAATCT | TAAAGATGAG | 1560 |
| ATTAAGGGCG | TAGAGCTTTC | TGGTCATCTC | ACTTCAGCGG | TGGCTTTAAT | AGGCGATGAA | 1620 |
| CCAAATGCGA | TGATGGCTAA | TTGGATGCGT | CAAATGGGGC | AAAGCGTGCC | TGAAAGCAAG | 1680 |
| AAAACTTTAG | AATTAAACCC | TAACCATGCG | ATTTTGCAAA | AACTCTTAAA | ATGCGAAGAT | 1740 |
| AAAGAGCAGT | TGAGCGCTTT | TATCTGGTTG | CTTTATGATG | GGCGAAGCTT | T | 1791 |

(2) INFORMATION FOR SEQ ID NO:5078593_c2_6.nt:

374

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 468 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|--|-----|
| GTGAATTTAG GGGCTTACTA CACGCCCCCT TATTTAGTGG ATTGCGCTTA CAAGCTTTTA | 60 |
| AAAAAGCATG TTGGTATTGA AAACCTACACG CTTTTAGACA CCGCATGTGG TAATAAAGAG | 120 |
| TTTTTAAAGC TCCACCACCC TAAAAAATA GGAGCGGATA TTGACCCTAA GTGTGATGCT | 180 |
| TTAATAATAA ACGCTCTAGC CAATCCTAAA AGAGAAAATT ATGGCATTAG CCAAGATGAA | 240 |
| CCTTTAATCA TCGTGGGCAA TCCCCCCTAT AACGATAGAA CTTCTTTTAT CAAACAAGAT | 300 |
| ATTAAAAATA AAGATTTTCAT TTTTGAGATA GACAACGATT TGAAATCCCG AGATTTAGGG | 360 |
| ATAAGTTTTT TAAATCTTT TGCAATTTTA AAGCCGGCGT TTATTTGCGT GCTACACCCT | 420 |
| TTATCTTATC TCATCAAAGA AGCTAATTTT AAGCAATTTA AAGCTATT | 468 |

(2) INFORMATION FOR SEQ ID NO:5083193_c1_3.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGAAAAGCA TTTTGCTCTT TATAATTTTT GTAGTTTGTC AGTTAGAAGG CAAAAAATTT 60
TCACAAGATA ATTTTAAGGT GGATTATAAC TACTATTTGC GCAAACAGGA TTTGCACATC 120
ATTAAAACGC AAAACGATTT GTCCAATGCC TGGTATCTCC CTCCACAAAA AGCCCCCAAA 180
GAACATTCTT GGGTGGATTT TGCTAAAAAA TATTTAAACA TGATGGATTA TCTAGGCACT 240
TATTTTTTGC CTTTTTATCA TAGTTTCACC CCCATTTTTT AATGGTACCA CCCTAATATC 300
AACCCTTACY AACGCAATGA GTTTAAGTTC CAAATCAGTT TTAGAGTGCC TGTATTTAGG 360
CATATTCTTT GGACTAAAGG CACGCTTTAT CTGGYTTATA CCCAACTAA CTGGTTTCAA 420
ATTTATAATG ACCCTCAATC CGCCCCCATG CGAATGATTA AATTCATGC C 471

(2) INFORMATION FOR SEQ ID NO:5083577_f3_15.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 573 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

376

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGGGCTTGA TGGGCGTGTC GCAAGGCTTA CCAAACACCA CTAGCAAGTT TGGTATTGAA | 60 |
| TTTGACTCTT TAGCTGATGT GGTCGCTTTT GGAGTCGCCC CAAGCCTTAT TACTTACTTT | 120 |
| TATGTGGGGT ATAAC TTTGG GCGTATAGGC ATGGCGGTGA GCGCGTTGTT TGTGATTTTT | 180 |
| GGAGCGATAC GATTAGCGCG ATTCAATATC AGCACCAACA CAAGCGATCC CTATTCTTTC | 240 |
| ATCGGTATCC CCATTCCTGC GGC GGCGGTA TTGGTG GTGC TTTGCGTGTT ATTAGATAAT | 300 |
| AAATACCATT TCTTAGAAGG CAATACCGAA AAGTTATTTT TAGGCTTTAT TGTCTTATTA | 360 |
| GGGGTGCTTA TGGTGAGCAA TATCCGCTAC CCTAATTTTA AAAAAGTCAA GTGGAATCTC | 420 |
| AAGCTTTTCA TCTTAGTGTT GATCTTTTTC TCGTTAGTGT TTGTGCGCCC TTTAGAGGCT | 480 |
| TTGAGCGTGT TTATGGGGTT GTATTTGATC TATGGCATCA TTCGGTGGAT CTTTTTAATG | 540 |
| GTAAAAATTA cTttTAATAA AAATAAAAGC GCA | 573 |

(2) INFORMATION FOR SEQ ID NO:5111308_f2_1.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGATAGGAG TTTACCCCAA TTATTCCAAA AAGCAACTAA AACGCCCCTT AGTCATATTT | 60 |
| GTAAGTAGGG AGTTAGCGCT GGCTAATGGT ATTCTTACAG ACGCCTATGA CATTGAAGCA | 120 |
| AATCTTTACA TGAATGCTCG TATCGTTATG AARAATAATA AAAGGAAACA TTATGAGCAG | 180 |
| CGGGTTAATT TACATTTCRT TAGAAGTCTT GGTARCGTGT TTGATCACCG CTCTAATCAT | 240 |
| GTATTATGTG ATGAAAAAGA TCTATTACGC | 270 |

377

(2) INFORMATION FOR SEQ ID NO:5138_f2_6.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 831 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

378

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|--|-----|
| GTGAAAATAA CCATAATGAT TAAAGATTTT AACCACTATT GTAGAAAAAT AACGAGAGGG | 60 |
| TTTGTAAGAAA TTCCACACAA AAAACAAGGA GCAAAAAAGA TGAAAAAAGC GGGTTTTCTT | 120 |
| TTTTTGGCGG CGATGGCTAT CATTGTTGTG AGTTTAAACG CCAAAGATCC GAATGTGTTG | 180 |
| CGTAAGATTG TTTTGTAGAA ATGTTTGCCT AATTATGAGA AAAATCAAAA TCCTTCACCA | 240 |
| TGCATAGAAG TCAAACCCGA CGCCGGCTAT GTGGTTTTAA AAGATATTAA CGGTCCGTTG | 300 |
| CAATATTTGT TGATGCCAAC GACTCACATT AGTGGCATTG AAAACCCTTT GTTGCTTGAT | 360 |
| CCTTCTACGC CTAACCTTTT TTAATTGTCA TGGCAAGCGC GCGATTTTAT GAGTWAAAAA | 420 |
| TACGGAAAAC CCATTCCTGA TTATGCGATC TCTTTGACGA TCAATTCTAA AAAAGGGCGA | 480 |
| TCGCAAAACC ATTTTCACAT CCATATTCTT TGCATTAGCC TTGATGTGCG CAAACAGCTG | 540 |
| GATAATAATC TAAAAAATAT CAACAGCCGT TGGTCGCCAT TATCAGGTGG CTTGAACGGG | 600 |
| CATAAATATT TGGCGCGTCG GGTAACAGAG AGCGAATTAG CGCAAAAAAG CCCGTTTGTC | 660 |
| ATGCTTGCTA AAGAAGTGCC TAACGCGCAC AAACGCATGG GAGACTATGG CTTGGCGGTG | 720 |
| GTGCAACAGA GCGATAACTC CTTTGTCTTG TTAGCGACAC AATTTAACCC ATTGACTTTA | 780 |
| AATCGCGCTT CAGCCGAAGA GATTCAAGAT CATGAATGCG CGATTTTGCG T | 831 |

(2) INFORMATION FOR SEQ ID NO:5265957_c2_5.nt:

379

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: surface antigen

| | |
|---|-----|
| GTGCTAACGA GTGGGGACAT GATCACTTGT CCGTATTGCG GCGGTATTTT RTACGCTGAG | 60 |
| AGTACGCATG AAAGTAACGC TCAACCTCCA AAAGAAAGCC AACCAAAGA AAGCCAAGAA | 120 |
| GAAAGCCAAG AAGAAAGCCA AGAAGAAAGC CAAGAAGCCG TCCGTTTGAT TGTT | 174 |

(2) INFORMATION FOR SEQ ID NO:5312712_f3_10.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 837 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

380

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|--|-----|
| ATGAAATTGA ATGACCCTTT CACAAGCCCT AATAAAGCCA AAAAAGAATT ATCGCCAAAA | 60 |
| GGCTTTAGGG GGGGGTTAGA GTCTGAAATT TTATTAGGCT TTGTCTTGCA AAAAGAAAGG | 120 |
| GTTTTTTTGC ACACGCATGA GCATTTGGAA TTAAGCCACG AAGAAGAAAC ACGCTTTTTT | 180 |
| GAATTGGTAG GAAAGCGTTT GAATGACTGC CCCATAGAGT ATTTATTAGG AAGCTGTGAT | 240 |
| TTTTATGGGC GCTCTTTTTT CGTGAATGAG CATGTTTTAA TCCCACGGCC TGAAACCGAG | 300 |
| ATTTTAGTCC AAAAAGCCCT TAATATTATT TCTCAATACC ATTTAAAAGA AATAGGCGAA | 360 |
| ATCGGCATAG GGAGCGGATG CGTGTCCGTG AGTTTGGCTT TAGAAAACCC TAATCTCTCT | 420 |
| ATTTATGCGA GCGATATTTT ACCAAAAGCT TTAGAAGTGG CGTTAAAAAA TATTGAACGC | 480 |
| TTTGTCTAA AAGAGCGTGT TTTTTTAAAA CAAACGCGCC TTTGGGATCA TATGCCAACG | 540 |
| ATAGAAATGC TTGTCTCTAA CCCGCCCTAT ATCGCTAGAA ATTATCCTTT GGAAAAATCC | 600 |
| GTTCTCAAAG AACCGCACGA AGCCCTTTTT GGGGGGGTTA AAGGCGATGA AATCTTAAAA | 660 |
| GAAATCGTTT TTTTAGCCGC TAAATTAAAA ATCCCTTTTT TGGTTTGTGA AATGGGGTAT | 720 |
| GACCAGTTAA AGAGCTTGAA AGAATGCTTG GAGTTTTGCG GTTATGATGC AGAGTTTTAC | 780 |
| AAGGATTTGA GCGGCTTTGA TAGAGGGTTT GTGGGCGTTT TAAAAAGTTT TTTAAGA | 837 |

(2) INFORMATION FOR SEQ ID NO:5325005_f1_2.nt:

381

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

ATGATTTCTT TCATTGGGTT TGAATGCTCC GCATTAAAAG TTTTTTTAAC TTTTGGTTAC 60

ATAGTTTTTA AAAGYTGGCA CTATAGCGCT ATAAGACTAA TTGTTATA 108

(2) INFORMATION FOR SEQ ID NO:55843_c1_3.nt:

382

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 387 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| GTGATCCAGT CTCACCCTAA ACAAACTCTA ATTGAAGATG AAAATTATTT TTATGCTAAC | 60 |
| AAGGGTCTTT ATAAAACCAA CAAAGAAGCC TTTTAAAGGG TTTATAAAAT CCCAGAGAGC | 120 |
| ATGCCCATAG AAAAACGAGA AAGTTTAAGC AAGGTTTCTA AAATCTTTTT AGCGTTGCTT | 180 |
| TTTTTCATTT CTAGCATGCT TTTTGGGATC TTTTGGCGTT TGCCCAAACG ATTGGACACT | 240 |
| AAAATGAGTT TAGAGAGCGC GCACAAAAAC GAATTAGAAA ATGCATTCCA ACGATACGAT | 300 |
| GCGCTAGGGG TGCGTTTTGA AGACATTGCA GGGGTGAATG AAGTCAAAGA AGAATTACTA | 360 |
| GAAGTGATRG ATTWTTTWAA AAAACCC | 387 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGTTTGTAG TTAAATGGT GTTAGGGTTT TTGATCCTTT TAAGCCCTTT GTGCGCTACT | 60 |
| GGATTGGATA TTTCACAAAC AGACATTATA GAGCGTTCTT TAAATTCCT CTTGTTTGTG | 120 |
| GGGATTTTGT GGTATTTTTT GGCTAAAAGA TTGCGTTCAT TTTTGCATTC CAAAAGCCTT | 180 |
| GAAATCTCCA AACGCTTAGA AGAGATTCAA GCCCAACTTA AAGTGAGTAA AGAACATAAG | 240 |
| AAAAAACTCC TTAAAGAATT AGAGCAAGCC AAAGAAAAAG CTGAATTGAT TATTTCTGAT | 300 |
| GCGAATAAAG AAGCCCTACA CGATCACGCA AAAATACGAA TTACAAACCA AAATGGATGT | 360 |
| GGAAAATTTG ATCAAAAATT C | 381 |

(2) INFORMATION FOR SEQ ID NO:5875152_f1_2.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 885 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

384

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|--|-----|
| ATGAGGGTTT TAGAGTGGAA ATATTGGTTA AATACTGATA AGTGGGATAC GCCCACCAAC | 60 |
| AAACCGCCTC AAACCTTTTAA AATACAAATT TTTAAGATAC AAATAGGTAT AATCAATAAC | 120 |
| TTCAATCATT TAATCAAAGG GAGTTCTATG AAAAACGCTT TCAAAGCGTT TGCCTTGTTA | 180 |
| ATCGTATTTT TCTCAAACGC TCTATTAGCG CAGGATTTAA AAATCGCTGC TGCTGCTAAT | 240 |
| CTCACGCGCG CTTTAAAAGC CCTTGTTAAA GAATTTCAAA AAGAACACCC AAAAGACGCT | 300 |
| ATTAACATTA GCTTTAATTC TTCAGGCAAA CTCTACGCTC AAATCGCTCA AAACGCCCT | 360 |
| TTTGATTTAT TCATTTTCAGC GGATATTGCT AGACCCAAAA AACTTTATGA TGAAAAAATA | 420 |
| ACCCCTTTTA AAGAAGAAGT CTATGCTAAA GCGTGTTGG TTTTATGGAG TGAAAATCTA | 480 |
| AAAATGGATT CTTTAGAAAT TCTTAAAGAC CCTAAAATTA AACGTATCGC TATGGCTAAT | 540 |
| CTTAACTAG CCCCTTATGG AAAAGCCAGC ATGGAAGTCT TGGATCGTTT AAAACTCACT | 600 |
| CTAGTCTTA AATCTAAAAT CATTTATGGC GCTTCTATTT CTCAAGCCCA TCAATTCATC | 660 |
| GCCACCAAAA ACGCTCAAAT AGGCTTTGGA GCGTTATCTT TGATCGATAA AAAAGACAAA | 720 |
| AACCTCTCTT ATTTTCATCAT TGATAAAACC CTTTATAACC CTATTGAACA AGCCTTAATC | 780 |
| ATCACTAAAA ATGGGGCTAA TAACCCTTTA GCCAAAGTTT TTAAAGATTT TTTATTCAGC | 840 |
| CTTAAAGCTA GAGCTATCTT TAAAGAATAC GGCTATATTG TGGAT | 885 |

(2) INFORMATION FOR SEQ ID NO:5878208_f2_7.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 378 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

385

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| GTGGCTTTAT TAGAGCCAAG CGTGATGTAT CTTACCGAAA AGTATCAATA CTCTCGTTTT | 60 |
| AAGGTTACTT GGGGTCTTGT AGCGTTAATC TTTGTGGTAG GCGTGGTGTT GATTTTCTCG | 120 |
| CTCCATAAGG ATTATAAAGA CTATCTCACT TTCTTTGAAA AAAGTCTTTT TGATTGGTTG | 180 |
| GATTTTGCAT CAAGCACCAT TATCATSCCT TTAGGCGGGA TGRCAACCTT TATTTTATG | 240 |
| GGCTGGGTTT TGAAAAAAGA AAAATTGCGT CTTTGTAGCG CGCACTTTTT AGGCCCTAAA | 300 |
| TTGTTTGCAA CTTGGTATTT CTTGCTTAAA TACATCACCC CTTTAATTGT GTTTTCCATT | 360 |
| TGGTTGAGCA AGATTTAT | 378 |

(2) INFORMATION FOR SEQ ID NO:5879160_c3_26.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 726 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

386

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|--|-----|
| GTGGGGCTTA TGAAAATAAG ATTTATGGGG CGGAGTGTTT TTGTGGGGGA TTTGGAACGC | 60 |
| ATTGAAGAAG TGGCTAGATT TGAAGAATTT TGGCTTTTAG GGGGGCAAAA AGCGATCAAA | 120 |
| GAGCCTAGAA GATTGGTTTT AGAAATCGCT TTAAAACACC AGCTCAACAA GCTTTTAAAA | 180 |
| CGCGTTCAAA AGCATTTCAA AGAAGACGAA TTAGGAATTT TTAAACAAAT GCATGACAAA | 240 |
| AAAATTCAAA GCGTCGCCAC CAATTCCATA GGGCGTTTGT TTGATATAGT GGCGTTTAGT | 300 |
| TTGGGCGTGG TGGGAACGAT TAGTTTTGAA GCCGAGAGCG GGCAGGTTTT AGAAAATCTA | 360 |
| GCCCTACAAA GCGATGAGAT CGCTTTTTTAC CCTTTTGAAA TCAAAAACAG CGTGGTGCGT | 420 |
| TTGAAGGAAT TTTATCAAGC GTTTGAAAAG GATTTGGGCG TTTTAGAACC CAAACGCATC | 480 |
| GCTAAGAAAT TTTTAAACAG CTTAGTAGAA ATCATTACCG CTTTGATTGC GCCTTTTAAA | 540 |
| GGGCATGTCG TGGTGTGCAG TGGGGGCGTG TTTTGCAACC AATTGTTGTG CGAACAATTA | 600 |
| GCCAAGCGAT TGAAAAAGCT TCAAAGGGAG TATTTTTTCC ACAAGCATTT CCCCCCTAAT | 660 |
| GACAGYAGTA TCCCTGTCGG TCAAGCCTTA ATGGCGTATT TCAACCCTAC AATCATCAAA | 720 |
| AAAGGA | 726 |

(2) INFORMATION FOR SEQ ID NO:598933_c2_16.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 453 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

387

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| GTGAGCGATT CTAACGCTTT AAAGGAAGTG TTTTAAACA TCAGCGCTAA AGAAGATCAT | 60 |
| TGCGACGTTT TGATCAATTC CGCCGGTTAT GGGGTGTTTG GGAGCGTGGA AGACACGCCC | 120 |
| ATTGAAGAGG TAAAAAGCA ATTTAGCGTG AATTTTTTCG CCCTTTGTGA AGTGGTGCAA | 180 |
| CTTTGTTTGC CTTATTAAA AAACAAGCCT TATTCTAAGA TTTTCAATCT TTCTTCCATA | 240 |
| GCGGGGCGTG TGAGCATGCT CTTTTTAGGC CATTACAGCG CGAGTAAGCA TGCCTTAGAG | 300 |
| GCTTATAGCG ATGCCTTGCG TTTAGAGCTT AAGCCCTTTA ACGTTCAAGT GTGTTTGATT | 360 |
| GAGCCAGGCC CGGTGAAAAG CAATTGGGAA AAAACCGCTT TTGAAAATGA TGAGCGGAAA | 420 |
| GATAGCGTTT ATGCTTTGGA AGTGAATGCG GCT | 453 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 462 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| GTGATAGTGG CGTGGCTTTT TAGGTTTAAA AGCATTGCGT TTTCTATTTT AATCACTCTG | 60 |
| TTGGTTATTT TAGTGGATAT TTGGGTGTAT AGCGATGTGC GCCAGTTTTT ATTGGACACT | 120 |
| TCTAGCTCTT TTATTTGGCT TTTAATCGCT TTACTAATCA AGTGGGGCGT GATTGTTATA | 180 |
| AGTGCGCGCA AATGCTACCA ATTCAGCCAA AAAATGTTTG CGTTAATCCA AAGAAAAGG | 240 |
| CAAATCAGAG AGAATTTAAA AAACCGCTCC AATCGCAAAG ATGCTAAAAA TTTTGAAAAA | 300 |
| CTCTCTAACA TCGCTGAAGA AATCATTTCA AAAAAACAAG AAGAGTCCCA CCACAAAGAA | 360 |
| GATTCTAATG ATGAAAACCA CAAAGACAAG CTTTCTAACA TTACCGAAGA AATGATTCTC | 420 |
| AAAAAACAAG AGGAACTGAA AGCTAGAAAG GATAAGGGGG AT | 462 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 537 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGAACTACC CTAATCTACC TAACAGCGCT TTAGRGATAA GCGAACAGCC AGAAGTGAAA | 60 |
| GAAATCACTA ACGAGCTTTT AAAGCAATTA CAAAACGCTT TAAGGAGCAA CGCGCATTTT | 120 |
| AGCGAGCAAG TGGAATTAAG CCTTAAATGC ATCGTTAGGA TTTTAGAAGT GCTTTTGAGT | 180 |
| TTGGATTTTT TTAAGAATGC GAATGAGATT GATAGCAGTT TAAGAAATTC CATTGAGTGG | 240 |
| CTGACTAACG CCGGCGAGAG CTTGAAATTA AAAATGAAAG AATACGAGCG CTTTTTTAGC | 300 |
| GAGTTTAATA CGAGCATGCA TGCCAACGAG CAGGAAGTAA CCAATACCTT AAACGCTAAC | 360 |
| GCCGAGAACA TTAAAAGCGR AATTAAAARG CTAGAAAATC AATTGATAGA AACCACGACA | 420 |
| AGACTTTTAA CGAGCTATCA AATCTTTTTT AACCAAGCCA GAGATAACGC TAACAACCAA | 480 |
| ATCACAAAAA ACAAACCCR AAGCCTTGAA GCGATTACAC AAGCTAAAAA CAACAGC | 537 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 480 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|--|-----|
| GTGTTTGCCA CTGACAGCAG TAGCTTTTCT ATGGGGCTTA CCATGGCGAG TGCTTATGAY | 60 |
| CCCATTTCAG GATCGCAAAA ACCCATTGTG GGGCAAGCCC TTTTATTGTT AGCGATTTTA | 120 |
| ATTTTATTGG ATTTATCGTT CCACCATCAA ATCATTTTAT TTGTGGATCA CAGCTTAAAA | 180 |
| GCCGTCCCTT TAGGGCGATT TGTCTTTGAG CCAGAAATTAG CTAAAAACAT TGTCAAAGCC | 240 |
| TTTTTCACACT TGTTTGTCAT AGGGTTTTCT ATGGCGTTCC CTATTTTATG CTTGGTGTTA | 300 |
| TTGAGCGATA TTATTTTGG CATGATCATG AAAACCCACC CTCAATTCAA CCTGCTCGCT | 360 |
| ATCGGGTTTC CGGTAAAAAT TGCATCGGG TTTGTGGGCA TTATTTTAAT CGCTTCGGCT | 420 |
| ATCATGGGGC GTTTTAAAGA AGAAATCAGC CTGGCCTTTA GCGTTATTRG TAAAATCTTT | 480 |

(2) INFORMATION FOR SEQ ID NO:6495137_f1_1.nt:

391

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|--|-----|
| ATGTATGGCG TGAAAGAGAT TAAAGATAAA ATTGACAAGC AACTCCACAA TAACGATCAT | 60 |
| TTGTTTGAAG GGCTTTTTTGG GGAAAAAGAA GATTTGAAAA AATTGGTGAG CATGTTTGGG | 120 |
| CAGTTGCGTT TCCAAAAGCG CTGGAGCCAA ACCCCAAGAG TGCCACAAAC CAGTGTTCTA | 180 |
| GGGCATACTT TATGCGTGGC GATTATGGGG TATTTATTGA GTTTTGACTT GAAAGCTTGT | 240 |
| AAAAGCATGC GGATCAATCA TTTTTTGGGC GGGCTTTTTC CA | 282 |

(2) INFORMATION FOR SEQ ID NO:6517040_c3_27.nt:

392

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 438 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGACTTTAG ATGACTTATT AGGGGGGAGT TTGGACCCGC ATTGTTTTTG CAAACCCTTA | 60 |
| ATCAAAACCA AAAAAGACCA AGAAAGGCTC TTATCCCTTG CTTTAAAAGC CCACCCTAAA | 120 |
| ATCTCTTTTG GAWWGGACAG TGCCCCGCAT TTCATTTCTA AAAAGCATAG CGCTAACATC | 180 |
| CCGGCGGGCA TCTTTTCTGC CCCTATTTTG TTGCCTGCGT TGTGCGAACT TTTTGAAAAA | 240 |
| CACAACGCTT TAGAAAATTT GCAAGCCTTT ATCAGTGATA ACGCTAAAAA AATCTACGCG | 300 |
| CTAGACAATT TACCCAGTAA AAAAGCGCAT TTGTCTAAAA AACCTTTTAT AGTCCCTACG | 360 |
| CACACGCTTT GCTTGAATGA AAAAATCGCT ATCTTAAGAG GGGGCGAAAC GCTATCTTGG | 420 |
| AACCTTCAAG AAATCGCC | 438 |

(2) INFORMATION FOR SEQ ID NO:663530_f1_2.nt:

393

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 519 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGGGCGTTT TGGGCATGTT CGCTTTTTTT TCATGGGTTT TTTTATTCAA GCACAATCTC | 60 |
| AGCCATAAAA TCCGCTTATA CCATGAAAAA AAGGATTTTG ACAAATTGCT CAAACAAATC | 120 |
| CTATCCCAAG ACACCCAAAA GACTTTTTTT AAAACAAAAT TAAAAGCGA TCTCGCTAAA | 180 |
| AACCTCTCTC AAATCTTAGC CCGCTATGAT TAAAAGCTG ATTTAAACAC GCCAAATAGC | 240 |
| GGGTGCGAAA AAGTGGATAA CCTTTTTTAA CATTACCACA ATATAGAAAA TAACACCCTT | 300 |
| GAGCCTAAAG ATCACGCTAA ACATTCCCTA GCTTATGAGC ATGCTTATTT TTCTAAACGC | 360 |
| TTGAAGGCTT TCATTCATAA CGATTTGAAA AACGCCTTTG AAGTTTTAAC AAACGCGCAA | 420 |
| ATCCCTTTGG AATTACGCCG CTACGCTTAT AGAAATCGCC CAAAAGGCA GCAAAAAGA | 480 |
| GGTTTTAAAG GCTGTGAATG CGATGCAAGA GGATTTGGA | 519 |

(2) INFORMATION FOR SEQ ID NO:6696887_c1_3.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

GTGAGTG TTC CTGCAACGAG TCGGAATTTA GGCCCCGGTT TTGATTGCTT GGGTTTGAGT 60
TTGAATTTAC GCAATCGTTT TTTTATTGAG CCTAGTAATA TCCATGCGGT GAAATTGGTT 120
GGGGAGGGTG AAGGGATCCC TAAATTTTTTA ACCAACAATA TTTTCACCAA AGTGTTTTAT 180
GAGATTTTAA AAAAGCATGG GAATGACGGC TCGTTTAAAT TTTTATTGCA TAATAAAGTC 240
CCTATTACAA GGGGCATGGG GTCTAGCTCA GCGATGATTG TGGGGGCGGT CGCTTCAGCG 300
TTTGCGTTTT TAGGGTTTGC TTTTGATAGA GAAAACATTC TCAATACTGC TCTAATTTAT 360
GAAAACCACC CGGATAATAT CACCCCGGCG GTGTTTGGGG GGTATAATGC AGCGTTTGTG 420
GAAAAAAGA AAGTGATAAG TTTAAAAACC AAAATCCCTT CTTTTTTAAA AGCGGTGATG 480
GTGATCCCTA ATAGGGTCAT TTCTACCAAG CAATCGCGCC ATCTCTGCCC AAGCGTTACA 540
GCGTGCAAGA AAGCGTGTTT AACCTTTCGC ATGCGAGTT 579

(2) INFORMATION FOR SEQ ID NO:677088_f3_6.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

395

| | |
|---|-----|
| GTGGCTAAAA ATTTGGTAGC GAGCGGGGTT TCGATAAAG CGACCGTGCA GCTTGCTTAT | 60 |
| GCGATTGGGG TGATAGAGCC TGTGTCTATT TATGTGAACA CGCATAACAC GAGCAAGCAT | 120 |
| TCAAGCGCGG AGTTGGAAAA ATGCGTGAAA TCGGTTTTCA AACTCACGCC AAAAGGCATC | 180 |
| ATTGAAAGCT TGGATTTGTT AAGACCCATT TATTCGCTCA CTCAGCTTA TGGGCATTTT | 240 |
| GGGCGCGAGT TAGAAGAATT CACTTGGGAA AAGACTAACA AGGTTGAAGA GATTAAAGCG | 300 |
| TTCTTTAAGC GT | 312 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1065 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|--|------|
| GTGCGTTTGT TTAGATTTGT GGGGTGGTAT TATTTCAAAT ACTTTTAAAT CGTGCTTTTA | 60 |
| GCTTTGGAAT TGTTTTTTGT AGGCATTGAC AGCCTGAAAT ACGCCGATAA AATGCCTGAT | 120 |
| TCTGCGAACA TGATCATTTT ATTTTTCACC TATGATATTT TATTCGCTCT CAATTACACC | 180 |
| TTGCCCATTT CCTTGCTTTT AGCGATGGTT TTATTTTATA TCACCTTCAT TAAATCCAAC | 240 |
| CAATACACCG CCCTGCTCTC TATTGGATTT TCCAAATGCC AGATTTTAAG CCCTATTTTTT | 300 |
| TTGATTAGCC TGTTTTTCAC GGCTGTTTAT GTGGGGTTGA ACGCGACTCC TTTTGTGTAT | 360 |
| ATGGAAGAAA AAACGCAAAA TTTAATTTAT AAAGACAATT CTTTGAGCGT TTCAGAGCAT | 420 |
| TTGTTAGTGA AATACAACGA TGATTACGTG TATTTTGATA AGATTAATCC CTTATTGCAA | 480 |
| AAAGCCCAAA ATATCAAGGT TTTTCGCCTA AAAGATAAAA CTTTAGAATC TTATGCTGAA | 540 |
| GCTAAAGAAG CTTTTTTTGA AGACAAATAT TGGATTTTAC ATGACACTAC TATCTATGAG | 600 |
| ATGCCCTTGA GTTTTGAACT GGGCGCGAAC GCTTTAAACA CCACGCATTT AGAAACCTTT | 660 |
| AAAACGCTCA AAAATTTCCG CCTTAAAGTT TTAGACACCA TTTATCAAAA CAAGCCTGCG | 720 |
| GTTTCTATCA CAGACGCTCT TTTATCCTTG CATGCTTTAG TGCGCCAAAA CGCGGACACG | 780 |
| AAAAAAGTGC GCTCGTTTTT GTATGTGTTT GCGATTTTGC CCTTTTTTGT GCCGTTTTTA | 840 |
| AGCGTTTTAA TCGCTTATTT TTCGCCCAGT CTCGCCCCTG ATGAAAACCT GGCTCTTTTA | 900 |
| GGGCTAAAGT TTATCATTAT CACGCTCGTT GTTTGGGGGC TATTCTTTGC TTTAGGGAAG | 960 |
| TTCAGCATTT CAGGGATACT CATTCCTGAA ATAGGCGTTC TATCGCCCTT TTTCGTATTT | 1020 |
| CTAGCTCTCA GTCTTTGGTA TTTTAAAAAA CTTAATAAGA GATTG | 1065 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 717 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|--|-----|
| ATGATTTATG GCGTTTTAGA CGGCTTGTTT TTGGCTATTT TACAGGCTCA AAATTACCGC | 60 |
| TTCCATTCGC TTTATTTGTT TGAAGAAAAT TTAGACTTGT TTAAATCAG TTGCTATTTT | 120 |
| GCGCGTTATG AAGATTTGAT TAAAAAAGGG GCTAAACTTT TTATTCAAGG GTTTTTTAAAC | 180 |
| CCTAATGAAT TGAAAATGGA TTTTTTGAAA CGCCCTATCA CGCATTCTTT TTTAAAGCTA | 240 |
| GAAATCATGC CCTATAAAG CGCTTTTAAT TTGCGCATGC GAGAAAACAT TCAAAGCTAT | 300 |
| TACAAACAAG CCTTAAGGGG TTGGGGGAGT TTTGAAGACG AATTGCTAGG GTTAAAGAAC | 360 |
| ACGCTTAAAA ACTTACCCCT ATACCAAACC CTAAAAACCA AACCCAAAAA AATTAACGCC | 420 |
| CCCATTTGCG TGGTGGGTAA TGGGCCAAGC CTGGATTTAT TGTTAGATTT TTTAAAAGAA | 480 |
| AATGAAGAAA AATTCATCAT TTTTTCATGC GGAACCGCTT TAAAGCCTTT AAAAGCGCAT | 540 |
| GGCGTTAAAG TGGATTTTCA AATAGAAGTG GAGCGCATAG ACTATCTTAA GGAGGTTTTA | 600 |
| GAAAGAGCCC CCCTAGAAGA CACCCCTTA ATGGGCGCTA ACATGCTCAA TCCTAACGCT | 660 |
| TTTGATTTAG CCAAAGAAGC GTTGATGTTT ATGCGTGGGG GGAGCGCTTG CGCAGTA | 717 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 867 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|--|-----|
| ATGCTGGCGT TTTTAAAAAC CCCTAGAAAC AGCGCTTTTG CTTTGGGTYT TTTCGTGGGG | 60 |
| GCGTTATTGT TTTACTGGTG CGCTTTAAGG CTTTCGCATT CGGATTTTAC YTATTTATTG | 120 |
| CCCTTAATCA TTGTTTTAGT AGCGTTAGTT TATGGGGTTT TATTTTATTT GTTGCTCTAT | 180 |
| TTTGAAAACC CCTACTTCAG GCTTTTGAGT TTTTLAGGCT CTAGTTTTAT CCACCCTTTT | 240 |
| GGATTTGATT GGTTAGTCCC GGATAGCTTT TTTTCTTATA GCGTGTTTAG GGTGGATAAA | 300 |
| TTATCTTTAG GGCTTATTTT TTTAGCTTGC ATTTTTTTGA GCGCTCAAAA TCTTAAAAAA | 360 |
| TACAGAATGA TAGGGGTTTT ATTGCTGCTT GGCGCGTTGG ATTTTCATTT TTTTAAATA | 420 |
| AGCGATTTAA AAGAGGTTGG AAATATTGAA TTAGTCTCTA CAAGAACGCC CCAAGATTTG | 480 |
| AAATTTGACT CAAATTACCT TAATAATATT GAAAACAACA TTCTTAAAGA AATCAAATC | 540 |
| GCTCAAAGCA AGCAAAAAAC CTTGATTGTT TTTCCAGAGA CCGCTTACCC TATCGCTTTA | 600 |
| GAAAACTCCC CTTTTAAAAAC CCAACTAGAA GATTTAAGCG ACAAGATCGC CATTTTAATA | 660 |
| GGGACATTGC GCGCTCARGG CTATAGCCTT TATAACAGCT CGTTTTTATT TTCTAAAAAA | 720 |
| AGCGTTCAAA TCGCTGATAA AGTGATCTTA GCCCCCTTTG GCGAGATAAT GCCTTTACCG | 780 |
| GAGTTTCTTC AAAAACCCTT TGAAAAGCTC TTTTGTGCGA GAGCGCTTAT TTATACCGCA | 840 |
| ACGCTCCCCA TTTCAGCGAT TTTACAT | 867 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1308 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|--|------|
| ATGAACGATC CTAAGCATGT GGTGTATGTT TGGCTGGACG CTTTATTGAA TTATGCGAGC | 60 |
| GCGTTAGGGT ATTTGAACGG TTTAGACAAT AAAATGGCGC ATTTTGAACG CGCTAGGCAT | 120 |
| ATTGTGGGTA AGGATATTTT ACGCTTCCAT GCCATTTATT GGCCAGCCTT TTTGATGAGT | 180 |
| TTGAATTTGC CCTTATTCAA ACAGCTCTGT GTGCATGGGT GGTGGACGAT AGAGGGCGTG | 240 |
| AAAATGAGTA AGAGCTTGGG TAATGTTTTA GACGCTCAAA AGCTCGCCAT GGAGTATGGG | 300 |
| ATTGAAGAAT TACGCTATTT TTTATTGCGT GAGGTGCCTT TTGGGCAAGA TGGGGATTTT | 360 |
| TCTAAAAAAG CGTTAGTAGA ACGGATTAAT GCGAATTGTA ATAACGATTT GGGGAATTTG | 420 |
| TTGAATCGTT TGCTAGGCAT GGCTAAAAAG TATTTCAATT ATTCTCTAAA AAGCACCAAA | 480 |
| ATCACTGCGT ATTATCCTAA AGAGCTAGAA AAAGCACATC AAATTTTAGA TAACGCTAAT | 540 |
| TCTTTTGTGC CTAAAATGCA ATTGCATAAG GCTTTAGAGG AATTGTTTAA TATTTATGAT | 600 |
| TTTTTTGAATA AACTCATCGC TAAAGAAGAG CCGTGGGTCT TGCACAAAAA CAACGAATCA | 660 |
| GAAAAATTAG AAGCCTTATT GAGTTTGATC GCAAACACGC TACTACAATC AAGCTTCTTG | 720 |
| CTCTATGCGT TCATGCCAAA GAGCGCTATG AAATTAGCGA GCGCTTTTCG TGTAGAAATC | 780 |
| ACGCCCAATA ATTACGAACG CTTTTTTAAG GCTAAAAAAT TACAAGATAT GGTTTTACAA | 840 |
| GACACCGAGC CTTTATTTTC CAAAATTGAG AAAATTGAAA AGATTGAAAA GATTGAAAAG | 900 |
| ATTGAAAAGA TTGAAAAGG GGAGGAAGCC CTAGCAGAAA AAGCAGAAAA AAAAGAAAAA | 960 |
| GAAAAAGCCC CACCAACACA AGAAAATTAT ATTAGTATTG AGGATTTCAA GAAAGTAGAG | 1020 |
| ATTAAAGTGG GGCTTATCAA AGAAGCTCAA AGGATTGAAA AATCCAATAA ATTACTGCGC | 1080 |
| TTAAAAGTGG ATTTAGGCGA AAATCGTTTG AGGCAGATCA TCTCAGGGAT CGCTTTGGAT | 1140 |
| TATGAGCCTG AAAGCTTGGT GGGTCAAATG GTGTGCGTGG TGGCTAATTT AAAACCCGCA | 1200 |
| AAGCTTATGG GTGAAATGAG TGAGGGCATG ATTTTAGCGG TGCGAGATAA TGATAATCTG | 1260 |

GCTTTAATCA GCCCTACCAG AGAAAAAATT GCAGGAAGTT TGATCAGC

1308

400

(2) INFORMATION FOR SEQ ID NO:80257_c1_23.nt:

401

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 342 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | |
|--|-----|
| ATGAAACGAC CGATCAGCAA ATTGAAACAA AACTTTTTTAC AATTCAAACA TTCTTTCAAC | 60 |
| AAACATTTAG ATAAGTACAG CCTTTATTAT AGGCTGTTCA ATATCAGCTC TATCGTTATA | 120 |
| GGTTTTTTTAA TAGCGCTTTT TTCTTATGGG GCAGGGGTGA TTTTAGTTTA TCCAATATTA | 180 |
| TTCTTGTTTG CTCTTATAAT AAAACCTAGC TTTTTTTATT ACACTACTTA TCTTTTGCTA | 240 |
| CTCGTTTCTC TCAGCATAAT AAGCAAATAC TATCTCCTAA GCCACGCAAA TTTCACAATG | 300 |
| AAGCTAATCA TGCTTATGAC TCAATGGCAA AATTGGTTCT TA | 342 |

(2) INFORMATION FOR SEQ ID NO:85786_c1_10.nt:

402

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

ATGGG

(2) INFORMATION FOR SEQ ID NO:875042_f1_2.nt:

403

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|--|-----|
| GTGTTCACTT ATTCCTTGGG GCAGGTTTTT TTTTCTCTAA GTATCGGTTT AGGGATCAAT | 60 |
| ATCACTTATG CTGCCGTTAC GGATAAAACG CAGAATTTGC TTAAAAGCAC GATTGGGTG | 120 |
| GTTTTATCAG GRATTTTAAT TTCTCTTG TG RCAGGGCTTA TGATTTTCAC TTTTGTGTTT | 180 |
| GAATATGGGG CTAATGTCTC ACAAGGCACA GGGTTAATCT TCACTTCTTT ACCGGTGGTT | 240 |
| TTTGGCCAAA TGGGAGCGAT AGGCGTTCCT TGTTTCAATT CTTTTCTTGC TCGCGCTCGC | 300 |
| TTTTGCTGGC ATCACTTCTA CGGTGGCTTT ATTAGAGCCA AGCGTGATGT ATCTTACCGA | 360 |
| AAAGTATCAA TACTCTCGTT T | 381 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 537 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGAAACCAT TGCATTTTTC ACACCTGGAC AGAGAGCAAT CAGGCGATGT GGGTTTTATC | 60 |
| ATTAAAAACC TTATTTTTTT AGGGGTTTTT TCCTTATTGG GTTGGTTGAA TACCGAGTAT | 120 |
| TTTCTATGGC CTAGCATGCT GGAATTAAAA AAAATCCTTT TAGAAGAAAA TCGTAAAAAA | 180 |
| AGCGTTTTAG AATACGCGCA AAGGCATTTT GAAACAGCCC TAGCAAATA CCGCAATCAA | 240 |
| AAAGAAACCA GCGAATCTTT GTTAAAGATT TTTAATGATG AAGAGTCCAG GCGGATTTTA | 300 |
| GAAAAGATCT TAAAAAATG TTTTGACGCC TATAAATCA AACCTTGCT CTCTCAAAAC | 360 |
| CCCTCCCAA AAACCCAATT TTTTATCATG GCTAGAGCGA GCGAATTGGA AAAAATTAT | 420 |
| CTTTTTTTCA CCTTAATCAA CAAGTATTTA CCGAGCGCTC AAAGCCAATT GCCCTTAAAG | 480 |
| ATTTCTAAAG ATAGCGACGG GTTGTGGTG CAATTTGGCG TGAGTATTGA TCTCAA | 537 |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 627 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|--|-----|
| ATGAATGCAT TGAAGCGTGC GTGTTTAAGA TTGATGGGCG AAACCAATAC CGATGATTTA | 60 |
| ASCCARYGA GCGACGCTTT CACACGGAGC GATATTCCTT TACACGCCAA AGCCATGCTA | 120 |
| AAAACCGGA TTGAAAATTA CGAACAACGC ATTGAAGCCA TTAAAACTAA AGGCGTTCCT | 180 |
| GTAGCGTATG TGGGCGATGT GGTGGCACA GGAAGCTCTA GAAAAAGCGC GACTAACTCT | 240 |
| ATCATGTGGC ATTTTGGTAA GGACATTCCT TTTGTGCCTA ATAAAAGGAG TGGAGGCATT | 300 |
| GTGATTGGGG GGGTGATCGC TCCGATTTTC TTTGCGACTT GTGAAGATAG CGGGGCGTTA | 360 |
| CCCATTTGTGG CTGATGTTAA GGATTTGAAA GAGGGCGATA TCATTAAAAT CTACCCTTAT | 420 |
| AAAGGCGAAA TCACGCTGAA CGATAAGGTG GTTAGCACCT TTAAGCTAGA GCCTGAAACT | 480 |
| TTATTAGATG AAGTCAGGGC TTCTGGGCGT ATCCCCTTAA TCATTGGTAG GGGTTTGACC | 540 |
| AATAAAGCGC GTAAATTTTT GGGCCGGCGA ATCGGAAGCG TTCAAAAAAC CTTCCGCCCC | 600 |
| TCAAGCGCGC TAAGGCTACA CTTTGCC | 627 |

(2) INFORMATION FOR SEQ ID NO:914087_f2_5.nt:

406

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 702 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGCTTTCAG CCCACCAACC TTTTAAAAAT TACCCTGATC TGATTAAAAA AGAGTTGCAA | 60 |
| GAGCATAACG CCTATGCGAG CGTCGCTAGT GGGGTGCCAG CGATGTGTGA TGGTATCACG | 120 |
| CAAGGTTATG AGGGAATGGA ATTGAGCTTG TTTAGTAGAG ATGTGATCGC ATTAAGCACC | 180 |
| SCCGTAGGGT TAAGCCATAA TGTTTTTGAC GGGGCGTTTT TTTTGGGCGT GTGCGATAAA | 240 |
| ATTGTGCCAG GCTTGCTCAT AGGAGCGTTA AGCTTTGGGA ATTTAGCGAG CGTGTTTGTG | 300 |
| CCAAGCGGGC CTATGGTGAG CGGGATAGAA AATTATAAAA AAGCCAAAGC GCGCCAAGAT | 360 |
| TTTGCAATGG GAAAGATCAA CAGAGAAGAG CTTTTAAAAG TGGAAATGCA AAGCTATCAT | 420 |
| GATGTGGGCA CTTGCACTTT TTATGGCACG GCTAATTCTA ATCAAATGAT GATGGAGTTT | 480 |
| ATGGGGTTGC ATGTGGCCAA TTCTAGCTTT ATCAACCCTA ACAACCCCTT ACGAAAGGTT | 540 |
| TTAGTAGAAG AGAGCGCTAA AAGATTAGCG AGCGGGAAAG TCCTGCCTTT AGCCAAACTC | 600 |
| ATTGATGAAA AAAGCATTCT TAACGCTCTT ATAGGCTTAA TGGCAACAGG GGGTTCTACT | 660 |
| AACCACACTT TGCATTTGAT CGCTATCGCA GATCTTGTGG GG | 702 |

(2) INFORMATION FOR SEQ ID NO:9776562_c3_13.nt:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 795 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: circular

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | |
|---|-----|
| ATGAAATTTT TAAATTTCTT TGCCAGTAGC GTAACCTCTAG ATGAAAAATT TTTAATGTTC | 60 |
| CTTCTTTTGCA ACGCTCTTTC TAACGCTTAC AAAAATAGCG ATTTGTTTTTC TTTCTCTAAA | 120 |
| EGCTTTTTTAG GCGCTTTTTT AATCGGGTTT GTGGTGTATT ATGGTTGCGC GCTAATCCCT | 180 |
| AAAAAACGCT TGAAATATTC ATTAGAATGG CTGTTTATAG GAAGCGGTAT TATTTTTAGC | 240 |
| GTGGCAGAAA TTTTACGCT GTTTATGTTT AAAATGCCTT TTTCCAAAGG CTTGATTGAC | 300 |
| ACGCTTTTAG CCACAAACAG CTCTGAAACG ATGGCGTTTA TAAAAAGCTA TAAAAATTAT | 360 |
| TTGCTTTACT ACGCTTTGAT TTTGATCGCT TTGTTGATCG CCATTAAAAT CATTCGCTTT | 420 |
| AGAGCGCTTG TGCCTGGTGT GATAGCGAGC GTTTTAGGGC TTTCTATCCT TACAATAGGG | 480 |
| AGCGTTCGTA ACATTAAACA CCTTACAAAG AACGATGCGA TTTTAAAAG ATCACTCTTT | 540 |
| TCTCTTTCTT TAGCTAGGGG GTTTTATTCC GCTTATTTGA GTTTGTTTGA TCGCCAACAA | 600 |
| GCCATAAAAT TTTATAGCTT TTTAAATAAT CTTTATTTAC CAAGCGATTA TCTTTCTAGC | 660 |
| ACGGGCGATA TTTCAAATGT CGTCTTAGTC ATCGCGAAAG CGCGAGCAGA AATTTTCATGC | 720 |
| AACTCTATGG CTATAGCGTT CCTAATAATC CTTATSCGA GCGAACTCGC CAACGAGAGA | 780 |
| GAGAGAGAGA GAGAG | 795 |

Figure 560

| Sequence Identifier | Sequence Name | BLAST hit | Description |
|---------------------|---------------|-------------------------|---|
| 1, | 3987580, | | |
| 2, | 55843, | | |
| 3, | 1365943, | | |
| 4, | 914087, | | |
| 5, | 23438887, | | |
| 6, | 24409641, | | |
| 7, | 26258562, | sp P20021 CADA_STA AU, | probable cadmium-transporting ATPase, |
| 8, | 5138, | | |
| 9, | 21647676, | | |
| 10, | 207817, | | |
| 11, | 116018, | | |
| 12, | 486075, | | |
| 13, | 30708287, | | |
| 14, | 6828218, | | |
| 15, | 24089087, | | |
| 16, | 35163962, | | |
| 17, | 6288949, | | |
| 18, | 35345228, | | |
| 19, | 24406567, | sp P10408 SECA_EC OL I, | flagellar biosynthetic protein, norepinephrine transporter, Protein secretion secA subunit, |
| 20, | 24409577, | | |
| 21, | 15126875, | | |
| 22, | 25595387, | | |
| 23, | 5869090, | | |
| 24, | 23912807, | sp P26276 ALGC_PSEAE, | phosphomannomutase, |
| 25, | 598933, | | |
| 26, | 24500088, | | |
| 27, | 4882842, | | |
| 28, | 4062813, | | |
| 29, | 35269000, | | |
| 30, | 23535937, | sp Q03523 MURE_BACSU, | UDP-N-ACETYL MURAMYL-TRIPETIDE SYNTHETASE, |
| 31, | 2042312, | | |
| 32, | 30478562, | | |
| 33, | 34161500, | sp P31548 YABJ_EC OL I, | HYPOTHETICAL ABC TRANSPORTER, |
| 34, | 33203192, | | |
| 35, | 12505125, | sp P18783 EXBB_EC OL I, | biopolymer transport exbB protein, |
| 36, | 22379952, | sp P31547 YAE EC OL I, | HYPOTHETICAL 23.3 KD PROTEIN-INTEGRAL MEMBRANE, |
| 37, | 489057, | | |
| 38, | 5312712, | gi 311022 gp L08012 , | major surface LPS-antigen, |
| 39, | 24220627, | | |
| 40, | 12698442, | sp P31219 YBBA_EC OL I, | hypothetical abc transporter n tesA region, |
| 41, | 4338438, | | |
| 42, | 2149041, | | |
| 43, | 4569693, | | |
| 44, | 3179505, | sp P33916 YEJF_EC OL I, | Cell division inhibitor, |
| 45, | 33397538, | | |
| 46, | 917152, | gp M82917 WOLFLAG_1, | HYPOTHETICAL ABC TRANSPORTER, |
| 47, | 34172639, | | minor flagellin flaB precursor-H.pylori, |
| 48, | 30730068, | sp P33024 , | similar to E.coli hypothetical nucleoside transport protein, |
| 49, | 23631292, | | |
| 50, | 3962777, | sp P31122 YDEA_EC OL I, | similar to CHLORAMPHENICOL RESISTANCE PROTEIN, |

| | | |
|----------------|-----------------------|---|
| 51, 24215, | sp P19933 GLTS_ECOLI, | sodium/glutamate symport carrier protein, |
| 52, 3964593, | | |
| 53, 3991067, | | |
| 54, 24410643, | | |
| 55, 47290919, | | |
| 56, 10742963, | | |
| 57, 16422591, | | |
| 58, 23490686, | | |
| 59, 875042, | sp P28573 NTPR_RAT, | SODIUM-DEPENDENT PROLINE TRANSPORTER, |
| 60, 4562712, | | |
| 61, 23594838, | gp U09005 VPU09005_4, | channel component of the sodium-type flagellar motor, |
| 62, 2150290, | | |
| 63, 30471091, | sp P08089 , | encodes the serologically diverse protein M in Streptococcus, |
| 64, 4821082, | | |
| 65, 23631317, | sp P03819 KEFC_ECOLI, | potassium efflux system protein, |
| 66, 19531291, | sp P16676 CYSB_ECOLI, | SULFATE TRANSPORT ATP-BINDING, |
| 67, 36573502, | sp P26093 HEL_HAEIN, | outer membrane protein P4 precursor, |
| 68, 7116626, | | |
| 69, 12617677, | | |
| 70, 34495938, | | |
| 71, 24218968, | sp P33916 YEJF_ECOLI, | HYPOTHETICAL ABC TRANSPORTER, |
| 72, 24634750, | | |
| 73, 24132293, | | methyl-accepting chemotaxis protein; transmembrane receptor, |
| 74, 20173437, | | |
| 75, 22441050, | | |
| 76, 3942217, | gp Z31376 BSFLIDST_3, | probable cadmium-transporting ATPase, |
| 77, 12520952, | | flagellar protein flis, |
| 78, 31681556, | | |
| 79, 3907042, | | |
| 80, 24222885, | | |
| 81, 17497107, | | |
| 82, 19556290, | | |
| 83, 34427317, | | |
| 84, 11132778, | sp P30750 ABC_ECOLI, | PREPROTEIN TRANSLOCASE SECA SUBUNIT, |
| 85, 24645837, | | ATP-BINDING PROTEIN ABC, |
| 86, 35887, | | |
| 87, 21487501, | sp P13511 CZCA_ALCEU, | cation efflux system membrane protein czcA, |
| 88, 33601578, | | |
| 89, 26355390, | sp P33913 YEJA_ECOLI, | homology to HYPOTHETICAL PROTEIN IN BCR 5'REGION (FRAGMENT), |
| 90, 3319687, | sp P37732 MODD_AZOVI, | molybdenum transport atp-binding protein, |
| 91, 7225666, | gp U05670 HIU05670_2, | influenzae type B lipooligosaccharide, |
| 92, 4826401, | sp P13511 CZCA_ALCEU, | cation efflux system membrane protein czcA, |
| 93, 867183, | | |
| 94, 21573938, | gi 495471 gp U07145 , | vacuolating cytotoxin of Hpylori, |
| 95, 21563752, | | |
| 96, 2111040, | | |
| 97, 10037799, | | |
| 98, 23437502, | | |
| 99, 32462543, | | |
| 100, 20976500, | | |
| 101, 1038312, | | |
| 102, 14494077, | gp Z12001 RFCRP_1, | chloramphenicol resistance protein, |
| 103, 4714375, | | |

| | | | |
|------|-----------|-----------------------|--|
| 104, | 23564012, | gp U05670 HIU05670_2, | influenzae type B lipooligosaccharide, |
| 105, | 5879160, | sp P16439 FLGG_SALTY, | flagellar basal-body rod proteins, |
| 106, | 12694087, | sp P12699 ATPE_BACME, | H+-transporting ATP synthase, |
| 107, | 22667967, | sp P35100 , | reacts with antibodies to chloroplast envelope proteins, |
| 108, | 14063518, | sp P37388 XYLG_ECOLI, | D-XYLOSE TRANSPORT ATP-BINDING PROTEIN, |
| 109, | 23531562, | gi 439981 gp U04619 , | flagellar hook polypeptide, |
| 110, | 6845425, | | |
| 111, | 22265691, | sp P22188 MURE_ECOLI, | UDP-N-ACETYLMURAMYL-TRIPETIDE SYNTHETASE, |
| 112, | 26588588, | | weak homology to membrane-associated c-type cytochrome, |
| 113, | 14094816, | | |
| 114, | 26366312, | sp P31134 POTG_ECOLI, | putrescine transport atp-binding, |
| 115, | 26423583, | | |
| 116, | 23441078, | | |
| 117, | 6696887, | | |
| 118, | 29531590, | gp X79134 EHK18SAW_1, | antigen [Entamoeba histolytica], |
| 119, | 6848287, | sp P08006 OPPC_SALTY, | oligopeptide permease membrane protein, |
| 120, | 36131282, | | |
| 121, | 16100038, | | |
| 122, | 2548562, | | |
| 123, | 1581937, | sp P37446 , | PHOSPHOLIPASE A1, |
| 124, | 35156938, | sp P13511 CZCA_ALCEU, | cation efflux system membrane protein czcA, |
| 125, | 1071890, | | |
| 126, | 20836042, | | |
| 127, | 2082012, | | |
| 128, | 6136430, | | |
| 129, | 5083193, | | |
| 130, | 33399142, | | |
| 131, | 40339452, | | |
| 132, | 917200, | | |
| 133, | 4490717, | | |
| 134, | 22140787, | | |
| 135, | 2855006, | | |
| 136, | 10664078, | | |
| 137, | 24416083, | sp P23894 , | HEAT SHOCK PROTEIN HTPX PRECURSOR, |
| 138, | 1411681, | sp P35620 FLHA_BACSU, | flagellar biosynthesis protein flha, |
| 139, | 1181418, | | |
| 140, | 24407533, | | |
| 141, | 24089437, | | |
| 142, | 24651083, | gp M13463 ECOCH3, | chemotaxis protein cheY, |
| 143, | 16219090, | gp U07145 HPU07145_2, | vacuolating cytotoxin - Helicobacter pylori, |
| 144, | 14572133, | | |
| 145, | 5325005, | | |
| 146, | 34574062, | | |
| 147, | 24070250, | | |
| 148, | 23439633, | | |
| 149, | 26614041, | | |
| 150, | 24798427, | | |
| 151, | 24806290, | | |
| 152, | 9776562, | | |
| 153, | 32140663, | | |
| 154, | 34194093, | | |
| 155, | 4339708, | | |
| 156, | 36134661, | | |

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| 157, | 3261306, | sp P28635 YAEC_ECOLI, | Outer membrane 30K protein, |
| 158, | 16225006, | | |
| 159, | 33595708, | sp P30858 ARTP_ECOLI, | ARGININE TRANSPORT ATP-BINDING PROTEIN |
| 160, | 17787558, | | |
| 161, | 24396937, | | |
| 162, | 35360843, | gp U05676 HPU05676_2, | vacuolating cytotoxin, |
| 163, | 32609403, | sp P10740 , | PHOSPHATIDYL SERINE DECARBOXYLASE, |
| 164, | 32705252, | | |
| 165, | 429192, | | |
| 166, | 22692187, | sp P33979 , | FLAGELLAR P-RING PROTEIN PRECURSOR, |
| 167, | 10009666, | sp Q03203 , | INTEGRAL MEMBRANE PROTEIN, |
| 168, | 19536458, | sp P37169 MVIN_SALTY, | VIRULENCE FACTOR MVIN, |
| 169, | 5194840, | | |
| 170, | 3906963, | | |
| 171, | 23486342, | sp P14900 MURD_ECOLI, | UDP-N-ACETYLMURAMOYLALANINE--D-GLUTAMATE LIGASE, |
| 172, | 195336375, | | |
| 173, | 17089217, | | |
| 174, | 23635968, | sp P13511 CZCA_ALCEU, | cation efflux system proteins, |
| 175, | 25922137, | sp Q02114 CWL_B_BACSU, | N-ACETYLMURAMOYL-L-ALANINE AMIDASE CELL WALL HYDROLASE AUTOLYSIN, |
| 176, | 14455461, | | |
| 177, | 45914063, | | |
| 178, | 16984442, | sp P35528 FLIP_BACSU, | flagellar biosynthetic protein flip, |
| 179, | 12120938, | | |
| 180, | 23439055, | | |
| 181, | 32636635, | | |
| 182, | 3933437, | | |
| 183, | 24328910, | | |
| 184, | 29479681, | sp P13036 FECA_ECOLI, | IRON(III) DICITRATE TRANSPORT PROTEIN FECA PRECURSOR, |
| 185, | 4177212, | | |
| 186, | 26351567, | | |
| 187, | 20415937, | | |
| 188, | 24003758, | sp P21458 SP3E_BACSU, | spoIIIE gene product, |
| 189, | 23853165, | | iron(II) transport system, |
| 190, | 26052137, | | |
| 191, | 23468781, | | penicillin-binding protein 2, |
| 192, | 14726542, | | |
| 193, | 6523427, | | |
| 194, | 13704718, | | |
| 195, | 23440814, | | |
| 196, | 14642217, | | |
| 197, | 5875152, | sp P37734 MODB_AZOVI, | molybdate-binding periplasmic protein precursor, |
| 198, | 104792, | sp P15932 FLGK_SALTY, | FLAGELLAR HOOK-ASSOCIATED PROTEIN 1 HAP1, |
| 199, | 34265691, | sp Q03523 MURE_BACSU, | UDP-N-ACETYLMURAMYL-TRIPETIDE SYNTHETASE, |
| 200, | 5440436, | sp P07176 PAL_ECOLI, | peptidoglycan-associated lipoprotein, |
| 201, | 24078837, | sp P23452 , | component of flagellum, |
| 202, | 12343763, | | |
| 203, | 19626250, | pir S S09411, | spoIIIE gene product, |
| 204, | 4728193, | | |
| 205, | 1416312, | | |
| 206, | 31413433, | | |
| 207, | 26758437, | | dgTP triphosphohydrolase and periplasmic protease gene, |
| 208, | 10553192, | | |
| 209, | 14480927, | | |

Figure 560

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| 12897656, 260941, 3242337, 21486677, 6933202, 11924177, 3166040, 3360130, 2915903, 203192, 26203402, 36261040, 23492181, 14570443, 22453166, 34573431, 10407625, 35442513, 24256572, 26301059, 13723593, 23945317, 25995917, 26197187, 22164962, 32627125, 16412593, 32453958, 16459375, 3906712, 32595137, 16440842, 31250333, 4708337, 11253, 26306340, 1367157, 35704718, 423131, 186752, 24230058, 24238762, 24276587, 29557266, 43490713, 16251627, 23915877, 4960952, 25925, 23880087, 6093906, 29302003, 13726562, | sp P31438 YICM_ECOLI, sp Q01960 FLHF_BACSU, sp P02913 , gp U13166 RMU13166_3, sp P33650 FEOB_ECOLI, gp M31827 BACDDSA_2, gp X70039 HPCAI_1, sp Q05605 EXBB_PSEPU, gi 531265 gp D21131 , sp P17952 , sp P19933 GLTS_ECOLI, sp P17448 KGTP_ECOLI, sp P13036 FECA_ECOLI, sp P33941 YOJI_ECOLI, | penicillin-binding protein 2, flagellar biosynthesis protein flhF, integral membrane protein, chemotaxis protein cheY, iron(II) transport system, cell division and sporulation protein, cytotoxicity associated immunodominant antigen [H. pylori], biopolymer transport exbD protein, sequence predicts membrane bound protein, N-ACETYLMURAMATE--ALANINE LIGASE, sodium/glutamate symport carrier protein, alpha-ketoglutarate permease, glycerolphosphate auxotrophy in plsB background, iron dicitrate transport protein, HYPOTHETICAL ABC TRANSPORTER, |
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| 5891412, | sp P23282 , | 3-deoxy-D-manno-octulosonic acid transferase, |
| 29386577, | | |
| 264, | | |
| 265, | | |
| 2458267, | gi 495471 gp U07145 , | vacuolating cytotoxin of Hpylori, |
| 24824087, | sp P13738 NHAA_ECOLI; | NA+/H+ ANTIPORTER [E.coli], |
| 33218912, | | |
| 34666680, | gp L36317 YSCCC2A_1, | Cu++-transporting P-type ATPase, |
| 783432, | | |
| 24609431, | | |
| 6495137, | | |
| 4035783, | | |
| 35417942, | | |
| 24414687, | | |
| 259665, | | |
| 23867207, | | |
| 34109763, | | |
| 487750, | | |
| 24411011, | | |
| 4721061, | sp P36175 GCP_PASHA, | O-SYALOGLYCOPROTEIN ENDOPEPTIDASE-lacks signal sequence, |
| 5440436, | sp P10324 PAL_HAEIN, | OUTER MEMBRANE PROTEIN P6 PRECURSOR |
| 24329712, | sp P14788 , | SULFATE TRANSPORT ATP-BINDING PROTEIN CYSA, |
| 10181942, | | |
| 24036302, | | |
| 677088, | | |
| 5111308, | | |
| 29458178, | | |
| 10677187, | | |
| 422937, | | |
| 21511555, | | |
| 1370202, | | |
| 36335436, | | |
| 1962590, | | |
| 21976637, | | |
| 24427340, | sp P10121 FTSY_ECOLI, | CELL DIVISION PROTEIN -- FUNCTIONAL HOMOLOG OF SRP RECEPTOR, |
| 114505, | | |
| 35428912, | sp P10089 HLY2_ECOLI, | HAEMOLYSIN SECRETION ATP-BINDING PROTEIN, |
| 19557055, | sp P15928 FLIF_SALTY, | FLAGELLAR M-RING PROTEIN, |
| 6517040, | | |
| 35837767, | | |
| 289711, | sp P19933 GLTS_ECOLI, | sodium/glutamate symport carrier protein, |
| 21720017, | | |
| 1256885, | | |
| 25422192, | | |
| 719606, | | |
| 272058, | | |
| 23912707, | gp U07173 VCU07173_1, | ToxR-activated (tagE) gene [Vibrio cholerae] (inner membrane), |
| 24611590, | | |
| 179677, | sp P30848 PROP_ECOLI, | proline/betaine transport protein, |
| 5083577, | | |
| 22682813, | | |
| 2843912, | | |
| 24039587, | | |
| 907827, | | |

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| 316, | 2035936, | gp U05676 HPU05676_2, | vacuolating cytotoxin Hpylori, |
| 317, | 978477, | gp L28919 STRFBP5A_1, | fibrinogen-binding protein (FBP54 may be a surface antigen) |
| 318, | 10737627, | | |
| 319, | 3953143, | | |
| 320, | 197166, | | |
| 321, | 33476715, | sp P08776 K2C8_XENLA, | KERATIN- TYPE II CYTOSKELETAL-intermediate filament, |
| 322, | 14313885, | sp P16680 PHNA_ECOLI, | alkylphosphonate uptake genes A through Q, |
| 323, | 34489549, | gp L26016 DVUDCRG_1, | aspartate chemoreceptor, |
| 324, | 3958537, | gi 309688 gp L04161 , | Plasmodium falciparum gametocyte specific antigen, |
| 325, | 1204418, | | |
| 326, | 5267037, | sp P15035 , | ROD SHAPE-DETERMINING PROTEIN, |
| 327, | 21742157, | | |
| 328, | 14257751, | | |
| 329, | 25605166, | sp P15876 MRAY_ECOLI, | PHOSPHO-N-ACETYLMURAMOYL-PENTAPEPTIDE-TRANSFERASE, |
| 330, | 23958179, | | |
| 331, | 4882763, | | |
| 332, | 19531291, | sp P03819 , | GLUTATHIONE-REGULATED POTASSIUM-EFFLUX SYSTEM PROTEIN, |
| 333, | 4455467, | sp P37388 XYLG_ECOLI, | D-xylose transport atp-binding protein xylg, |
| 334, | 12969218, | | |
| 335, | 10312562, | | |
| 336, | 23475342, | | |
| 337, | 35397265, | | |
| 338, | 662933, | | |
| 339, | 14864452, | | |
| 340, | 42683, | sp P03819 , | GLUTATHIONE-REGULATED POTASSIUM-EFFLUX SYSTEM PROTEIN, |
| 341, | 24417212, | | |
| 342, | 24488537, | | |
| 343, | 24492192, | sp P08089 , | ONE OF THE DIFFERENT ANTIGENIC SEROTYPES OF PROTEIN M, |
| 344, | 41552656, | | invasion protein A, |
| 345, | 3157067, | sp P35640 INVA_BARBA, | |
| 346, | 12400007, | | glycerolphosphate auxotrophy in plsB background, |
| 347, | 21687842, | | MEMBRANE-ASSOCIATED HYPOTHETICAL 21.7 KD, |
| 348, | 34097707, | | |
| 349, | 30078126, | | homology to NITROGEN FIXATION; TRANSMEMBRANE [Rhizo. meliloti], |
| 350, | 33986087, | | lipopolysaccharide epitope, |
| 351, | 5993958, | | variable antigen from Treponema, |
| 352, | 24395801, | sp P18399 FIXS_RHIME, | |
| 353, | 1364378, | gp U06471 DNU06471_5, | |
| 354, | 11876471, | | |
| 355, | 625277, | sp P16665 , | |
| 356, | 16131887, | | |
| 357, | 14640637, | | |
| 358, | 22704567, | sp P16439 FLGG_SALTY, | FLAGELLAR BASAL-BODY ROD PROTEIN, |
| 359, | 29298130, | sp P17952 , | N-ACETYLMURAMATE--ALANINE LIGASE, |
| 360, | 24441412, | sp P35652 HRPN_BURSO, | HYPERSENSITIVITY RESPONSE SECRETION PROTEIN, |
| 361, | 14642202, | | |
| 362, | 80257, | | |
| 363, | 30703183, | sp P15929 FLGH_SALTY, | flagellar basal body L-ring protein, |
| 364, | 26054702, | | |
| 365, | 4787562, | | |
| 366, | 23598962, | | |
| 367, | 234391, | | |
| 368, | 34179577, | | |

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| 369, | 34253912, | SP P33134 FLIQ_ECOLI, | flagellar biosynthetic protein fliQ, |
| 370, | 24882763, | | |
| 371, | 50062, | | |
| 372, | 1218751, | | |
| 373, | 4687507, | | |
| 374, | 23494043, | | |
| 375, | 23442642, | | |
| 376, | 38080063, | | |
| 377, | 4572168, | | |
| 378, | 6281956, | | |
| 379, | 23437741, | | |
| 380, | 25478375, | SP Q03475 LAFB_VIBPA, | flagellar distal capping protein homolog, |
| 381, | 10580417, | GP U09868 ECU09868_9, | INVOLVED IN F PILUS ASSEMBLY, |
| 382, | 4035262, | | |
| 383, | 34099062, | | |
| 384, | 85786, | | |
| 385, | 17086587, | SP P08150 PBP2_ECOLI, | D-alanyl-D-alanine carboxypeptidase, |
| 386, | 22542803, | | |
| 387, | 10723412, | SP P33916 YEJF_ECOLI, | hypothetical abc transporter in bcr 5' region, |
| 388, | 11719687, | | |
| 389, | 32236462, | | |
| 390, | 14574201, | | |
| 391, | 40409281, | | |
| 392, | 16281449, | SP P37105 SRP4_BACSU, | signal recognition particle protein, |
| 393, | 36523442, | | |
| 394, | 882827, | | |
| 395, | 2774062, | | |
| 396, | 36111066, | | |
| 397, | 31262, | | |
| 398, | 630, | | |
| 399, | 392900, | SP P15921 , | 190kD surface antigen, |
| 400, | 23646885, | | |
| 401, | 13178562, | | |
| 402, | 4895327, | GP X72832 SEDEXB_5, | stringent response-like protein, |
| 403, | 21503772, | | |
| 404, | 2001403, | SP P35162 YX16_BACSU, | hypothetical protein X, |
| 405, | 5878208, | | |
| 406, | 22303918, | | |
| 407, | 4698838, | SP P02918 , | penicillin binding protein, |
| 408, | 2445812, | | |
| 409, | 22370182, | | |
| 410, | 16406581, | SP P27841 CORA_ECOLI, | H.influenzae lic-1 operon lica-licD genes, |
| 411, | 20023400, | | MAGNESIUM AND COBALT TRANSPORT PROTEIN, |
| 412, | 30603402, | | |
| 413, | 4095342, | | |
| 414, | 23728388, | | |
| 415, | 24406401, | SP P31652 NTS1_RAT, | serotonin transport protein, |
| 416, | 3385833, | | |
| 417, | 14344378, | | |
| 418, | 32600912, | | |
| 419, | 30283516, | | |
| 420, | 25625192, | | |
| 421, | 30081291, | | |

Figure 560

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| 5078593, | sp P23878 FEP_CECOLI, | ferric enterobactin transport protein fepC, |
| 23446896, | gi 471729 gp U05676 , | weak similarity to vacA (duplication?), |
| 19537968, | | |
| 32663212, | | |
| 34189716, | | |
| 24609593, | | |
| 9954743, | | |
| 1408, | | |
| 3930468, | | |
| 84691, | | |
| 13865928, | sp P37169 MVIN_SALTY, | VIRULENCE FACTOR MVIN, |
| 32036462, | | |
| 3953952, | | |
| 291700, | gi 471729 gp U05676 , | weak vacA similarity, |
| 24708129, | | penicillin-binding protein 2, |
| 30100332, | sp P23847 DPPA_ECOLI, | PERIPLASMIC DIPEPTIDE TRANSPORT PROTEIN PRECURSOR, |
| 4492217, | | |
| 10745275, | | |
| 31262, | | |
| 289077, | | |
| 24818802, | | |
| 10353192, | sp Q05605 EXBB_PSEPU, | biopolymer transport exbB protein, |
| 24104558, | pir S B4AG58, | VirB4 homolog, |
| 3203142, | sp P07893 ATSY_SYNP6, | PROBABLE COPPER-TRANSPORTING ATPASE, |
| 32144532, | | |
| 4740887, | | |
| 4548792, | sp P33231 LCTP_ECOLI, | L-LACTATE PERMEASE, |
| 34658285, | | |
| 4766691, | gi 459690 gp L29189 , | methyl-accepting chemotaxis protein, |
| 36520792, | | |
| 4744128, | sp P16439 FLGG_SALT, | flagellar basal-body rod proteins, |
| 29454837, | | |
| 15039062, | | |
| 4805318, | | |
| 36594167, | | |
| 785437, | | |
| 23526667, | | |
| 156587, | sp P07365 CHEW_ECOLI, | chemotaxis protein cheW, |
| 15824052, | gi 459688 gp L29189 , | transmembrane receptor, |
| 4578469, | | |
| 29844512, | | |
| 24415917, | | |
| 24298127, | gp L23426 NGOPHOSPHO_1, | phosphoglucomutase, |
| 32952, | sp P31220 YHBC_ECOLI, | PROBABLE ABC TRANSPORTER, |
| 32422343, | | |
| 23493756, | | |
| 214812, | sp P33231 LCTP_ECOLI, | L-lactate permease, |
| 1179838, | | |
| 98191, | | |
| 14714687, | | |
| 3317501, | sp Q08382 MODEB_RHOCA, | molybdenum transport system permease, |
| 19541302, | gi 495471 gp U07145 , | vacuolating cytotoxin of Hpylori, |
| 23438840, | | |

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|------|-----------|-------------------------|---|
| 475, | 2738378, | gp X76422 NSPEN2_1, | penicillin-binding protein 2, |
| 476, | 22460468, | sp P15933 FLIG_SALTY, | FLAGELLAR MOTOR SWITCH PROTEIN F, |
| 477, | 26380318, | | |
| 478, | 24803280, | | |
| 479, | 29843937, | gi 495471 gp U07145 , | vacuolating cytotoxin of Hpylori, |
| 480, | 1431462, | gp L16627 PASPLP123A_2, | outer membrane 30.2K protein, |
| 481, | 34089087, | | |
| 482, | 35445843, | | |
| 483, | 22687687, | | |
| 484, | 23473437, | | |
| 485, | 23515833, | sp P10408 SECA_ECOLI, | PREPROTEIN TRANSLOCASE SECA SUBUNIT, |
| 486, | 30662792, | sp P35538 FLHB_BACSU, | FLAGELLAR BIOSYNTHETIC PROTEIN FLHB, |
| 487, | 1171928, | | |
| 488, | 21767890, | | |
| 489, | 4882652, | | |
| 490, | 23539006, | | |
| 491, | 6517192, | sp P37105 SRP4_BACSU, | signal recognition particle protein, |
| 492, | 1933, | | |
| 493, | 22447252, | | |
| 494, | 14645905, | gi 520402 gp U03552 , | sensor protein, |
| 495, | 10675632, | sp P23445 FLII_BACSU, | H+-transporting ATP synthase alpha chain homolog, |
| 496, | 23831562, | | |
| 497, | 32704686, | | |
| 498, | 24816915, | | |
| 499, | 24219012, | | |
| 500, | 4897177, | | |
| 501, | 4486092, | sp P25536 YHDE_ECOLI, | E.coli mreD gene Rod shape-determining protein, |
| 502, | 21618785, | sp P05353 VIB4_AGR79, | VIRB4 PROTEIN PRECURSOR, |
| 503, | 16603418, | | |
| 504, | 4551291, | | |
| 505, | 23867687, | | |
| 506, | 25976418, | | |
| 507, | 25525277, | | flagellar motor switch protein flmM, |
| 508, | 32431687, | | |
| 509, | 4531568, | | |
| 510, | 19720300, | | |
| 511, | 24413512, | | |
| 512, | 4570262, | | |
| 513, | 29500075, | sp P38489 NFSI_ECOLI, | OXYGEN-INSENSITIVE NAD(P)H NITROREDUCTASE, |
| 514, | 30089217, | | |
| 515, | 134666, | | |
| 516, | 391313, | | |
| 517, | 4726503, | | |
| 518, | 26172627, | | |
| 519, | 24495312, | | |
| 520, | 30082267, | | |
| 521, | 24300682, | | |
| 522, | 25398250, | | |
| 523, | 23610905, | | |
| 524, | 23573294, | | |
| 525, | 485375, | | |
| 526, | 12066675, | | |
| 527, | 23567137, | gp U07145 HPU07145_2, | vacuolating cytotoxin - Helicobacter pylori, |

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| 528, | 30728393, | sp P32113 ATKA_ENTFA, | POTASSIUM/COPPER-TRANSPORTING ATPASE A, |
| 529, | 1385937, | | |
| 530, | 20032561, | sp P07117 PUTP_ECOLI, | SODIUM/PROLINE SYMPORTER, |
| 531, | 4414000, | | |
| 532, | 34489543, | gi 415692 gp L26015 , | putative chemoreceptor, |
| 533, | 35949212, | | |
| 534, | 1464715, | sp P33231 LCTP_ECOLI, | L-lactate permease, |
| 535, | 35336707, | | |
| 536, | 16839562, | | |
| 537, | 25501501, | | |
| 538, | 23671689, | | |
| 539, | 4491093, | | |
| 540, | 194415, | | |
| 541, | 14713512, | sp P22565 LYTB_ECOLI, | INVOLVED IN PENICILLIN TOLERANCE-has signal peptide seq., |
| 542, | 4882318, | | |
| 543, | 663530, | | |
| 544, | 16305252, | | |
| 545, | 16603381, | | |
| 546, | 33394230, | | |
| 547, | 16406265, | sp P26601 , | integral protein in inner membrane, |
| 548, | 495312, | sp Q03523 , | ACETYLMURAMOYLALANYL-D-GLUTAMATE-DIAMINOPIMELATE LIGASE, |
| 549, | 15807794, | | |
| 550, | 11878127, | | |
| 551, | 3242952, | | |
| 552, | 7031343, | gi 487637 gp U09364 , | similarity with eukaryotic myosins, |
| 553, | 13673328, | | |
| 554, | 50253, | | |
| 555, | 13727311, | sp P10413 HTPG_ECOLI, | heat shock protein C62.5 - chaperone-ATPase activity, |
| 556, | 5265957, | gi 155338 gp M82917 , | flagellin, |
| 557, | 12697338, | gi 160409 gp M69183 , | surface antigen, |
| 558, | 20911583, | sp Q01465 MREB_BACSU, | rod shape-determining protein envB, |
| 559, | 21699087, | | |
| 560, | 2461062, | | |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 508 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

HPP1

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: INTEGRAL MEMBRANE PROTEIN

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Cys | Ser | Gln | Glu | Ile | Leu | Ser | Ser | Leu | Gln | Thr | Ile | Ile | Ala | Glu | 1 | 5 | 10 | 15 |
| Gln | Phe | Ser | Ile | Asn | Ile | Ile | Thr | Gln | Leu | Ala | Asn | Lys | Leu | Thr | Gln | 20 | 25 | 30 | |
| Val | Lys | Asn | Leu | Asn | Phe | Phe | Glu | Asn | Lys | Asp | His | Thr | Ile | Lys | Leu | 35 | 40 | 45 | |
| Asn | Thr | Ile | His | Asn | Gly | Leu | His | Ile | Arg | Pro | Leu | Asn | Tyr | Val | Ser | 50 | 55 | 60 | |
| Asn | Leu | Phe | Phe | Asn | Leu | Gln | Arg | Ile | Ile | Gly | Leu | Ile | Ser | Leu | Phe | 65 | 70 | 75 | 80 |
| Gly | Ile | Leu | Phe | Ser | Ile | Ser | Ile | Tyr | Leu | Pro | Phe | Ile | Met | Ile | Phe | 85 | 90 | 95 | |
| Ala | Thr | Val | Pro | Cys | Ile | Leu | Ile | Ser | Asn | His | Ile | Ala | Lys | Lys | His | 100 | 105 | 110 | |
| Ser | Ala | Ser | Ile | Asp | Lys | Leu | Gln | Asp | Gln | Lys | Glu | Ser | Met | Gln | Asn | 115 | 120 | 125 | |
| Tyr | Leu | Tyr | Ser | Gly | Leu | Asp | Asn | Gln | Lys | Asn | Lys | Asp | Asn | Leu | Leu | 130 | 135 | 140 | |
| Phe | Asn | Phe | Met | Leu | Asn | Phe | His | His | Lys | Phe | Ile | Glu | Thr | Lys | Glu | 145 | 150 | 155 | 160 |
| Leu | Tyr | Leu | Asn | Asn | Phe | Val | Lys | Val | Ala | Gln | Lys | Asn | Leu | Ile | Phe | 165 | 170 | 175 | |
| Thr | Ile | Tyr | Ala | Asp | Val | Leu | Ile | Thr | Thr | Leu | Ser | Ile | Ala | Leu | Phe | 180 | 185 | 190 | |
| Phe | Leu | Met | Val | Phe | Ile | Ile | Leu | Ser | Lys | Leu | Ile | Gly | Val | Gly | Ala | 195 | 200 | 205 | |
| Ile | Ala | Gly | Tyr | Ile | Gln | Ala | Phe | Ser | Ser | Thr | Gln | Gln | Gln | Leu | Gln | 210 | 215 | 220 | |
| Asp | Leu | Ser | Phe | Tyr | Gly | Lys | Trp | Phe | Phe | Ala | Ile | Asn | Lys | Tyr | Phe | 225 | 230 | 235 | 240 |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Glu | Asn | Tyr | Phe | Cys | Ile | Leu | Asp | Tyr | Lys | Ile | Pro | Lys | Pro | Glu | Thr | |
| | | | | 245 | | | | | 250 | | | | | 255 | | |
| Gln | Ile | Lys | Leu | Glu | Glu | Lys | Ile | His | Ser | Ile | Thr | Phe | Glu | Asn | Ile | |
| | | | 260 | | | | | 265 | | | | | 270 | | | |
| Ser | Phe | Ser | Tyr | Pro | Asn | Ser | Lys | Leu | Ile | Phe | Glu | Asn | Phe | Asn | Leu | |
| | | 275 | | | | | 280 | | | | | 285 | | | | |
| Ser | Leu | His | Ser | Asn | Lys | Ile | Tyr | Ala | Leu | Val | Gly | Lys | Asn | Ala | Ser | |
| | 290 | | | | | 295 | | | | | 300 | | | | | |
| Gly | Lys | Ser | Thr | Leu | Ile | Asn | Leu | Leu | Leu | Gly | Phe | Tyr | Thr | Pro | Asn | |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 | |
| Ser | Gly | Gln | Ile | Ile | Ile | Asn | Asn | Lys | Tyr | Pro | Leu | Gln | Asp | Leu | Glu | |
| | | | | 325 | | | | | 330 | | | | | 335 | | |
| Leu | Asn | Ser | Tyr | His | Gln | Gln | Met | Ser | Ala | Ile | Phe | Gln | Asp | Phe | Ser | |
| | | | 340 | | | | | 345 | | | | | 350 | | | |
| Leu | Tyr | Ala | Gly | Tyr | Ser | Ile | Asp | Asp | Asn | Leu | Phe | Met | Gln | Asn | Asn | |
| | | 355 | | | | | 360 | | | | | 365 | | | | |
| Ile | Thr | Lys | Glu | Gln | Leu | Lys | Gln | Lys | Arg | Glu | Ile | Leu | Lys | Ser | Phe | |
| | 370 | | | | | 375 | | | | | 380 | | | | | |
| Asp | Glu | Asn | Phe | Gln | Asn | Cys | Leu | Asn | Asp | Cys | Asn | Asn | Thr | Leu | Phe | |
| 385 | | | | | 390 | | | | | 395 | | | | | 400 | |
| Gly | Ala | Gln | Tyr | Asn | Gly | Val | Asp | Phe | Ser | Leu | Gly | Gln | Lys | Gln | Arg | |
| | | | | 405 | | | | | 410 | | | | | 415 | | |
| Ile | Ala | Thr | Met | Arg | Ala | Phe | Leu | Lys | Pro | Ser | Asn | Cys | Ile | Val | Leu | |
| | | | 420 | | | | | 425 | | | | | 430 | | | |
| Asp | Glu | Pro | Ser | Ser | Ala | Ile | Asp | Pro | Ile | Met | Glu | Lys | Glu | Phe | Leu | |
| | | 435 | | | | | 440 | | | | | 445 | | | | |
| Asp | Phe | Ile | Phe | Lys | Lys | Ser | Gln | Ser | Lys | Met | Ala | Leu | Ile | Ile | Thr | |
| | 450 | | | | | 455 | | | | | 460 | | | | | |
| His | Arg | Met | Asn | Ser | Val | Lys | Gln | Ala | Asn | Glu | Ile | Ile | Val | Leu | Asp | |
| 465 | | | | | 470 | | | | | 475 | | | | | 480 | |
| Gln | Gly | Lys | Leu | Ile | Glu | Gln | Gly | Asn | Phe | Glu | Thr | Leu | Met | Lys | Lys | |
| | | | | 485 | | | | | 490 | | | | | 495 | | |
| Gln | Gly | Leu | Phe | Cys | Glu | Leu | Phe | Leu | Lys | Gln | Gln | Tyr | | | | |
| | | | 500 | | | | | 505 | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:10181942_c1_11 - AA

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 77 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

HPP3

Figure 3A - page 4

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ile | Gly | Gly | Tyr | Met | Ala | Met | Asn | Ile | Gly | Ala | Asn | Asp | Val | Tyr |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Asn | Asn | Val | Gly | Pro | Tyr | Val | Gly | Ser | Lys | Ala | Ile | Ser | Met | Gly | Gly |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Ala | Ile | Leu | Ile | Ala | Ala | Val | Cys | Glu | Met | Leu | Gly | Ala | Ile | Ile | Ala |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Gly | Gly | Glu | Val | Val | Ser | Thr | Ile | Lys | Gly | Arg | Ile | Val | Ser | Pro | Glu |
| | | 50 | | | | 55 | | | | | 60 | | | | |
| Phe | Ile | Asn | Asp | Ala | Gln | Val | Phe | Ile | Asn | Val | Met | Leu | Gly | | |
| 65 | | | | | 70 | | | | | 75 | | | | | |

Figure 4A-page 5

HPP4

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 204 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori
- (xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Unk | Unk | Thr | Phe | Asn | Lys | Gln | Ile | Gln | Gly | Ile | Trp | Arg | Phe | Trp | |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | | |
| Val | Leu | Unk | Thr | Ala | Ile | Leu | Trp | Ser | Leu | Met | Gly | Phe | Cys | Ala | Gly | |
| | | | 20 | | | | | 25 | | | | | 30 | | | |
| Leu | Ser | Ala | Leu | Asp | Tyr | Asp | Thr | Leu | Asp | Pro | Lys | Tyr | Tyr | Lys | Tyr | |
| | | 35 | | | | | 40 | | | | | 45 | | | | |
| Ile | Lys | Tyr | Tyr | Lys | Ala | Tyr | Glu | Asp | Lys | Glu | Val | Glu | Glu | Leu | Ile | |
| | 50 | | | | | 55 | | | | | 60 | | | | | |
| Arg | Asp | Leu | Lys | Arg | Ala | Asn | Ala | Lys | Ser | Gly | Leu | Ile | Leu | Gly | Ile | |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 | |
| Asn | Thr | Gly | Phe | Phe | Tyr | Asn | His | Glu | Ile | Met | Val | Lys | Thr | Asn | Ser | |
| | | | | 85 | | | | | 90 | | | | | 95 | | |
| Ser | Ser | Ile | Thr | Gly | Asn | Ile | Leu | Asn | Tyr | Leu | Phe | Ala | Tyr | Gly | Cys | |
| | | | 100 | | | | | 105 | | | | | 110 | | | |
| Val | Leu | Ala | Ile | Lys | Leu | Ser | Gly | Arg | Arg | Phe | Leu | Arg | Ala | Trp | Leu | |
| | | 115 | | | | | 120 | | | | | 125 | | | | |
| Ser | Pro | Ile | Ser | Leu | Ala | Gly | Arg | Thr | Ile | Ile | Gln | Tyr | Tyr | Gly | Gly | |
| | 130 | | | | | 135 | | | | | 140 | | | | | |
| Ala | Pro | Lys | Lys | Thr | Gly | Phe | Gly | Ser | Val | Gly | Phe | Gln | Ser | Ala | Met | |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 | |
| Leu | Asn | Gly | Asp | Phe | Leu | Leu | Asp | Phe | Pro | Leu | Pro | Phe | Val | Gly | Lys | |
| | | | | 165 | | | | | 170 | | | | | 175 | | |
| Tyr | Leu | Tyr | Met | Gly | Gly | Val | Tyr | Gly | Phe | Arg | Leu | Gly | Gly | Cys | Gly | |
| | | 180 | | | | | | 185 | | | | | 190 | | | |
| Ala | Trp | Gly | Glu | Leu | Tyr | Gly | Gly | Met | Gly | Asp | Val | Phe | | | | |
| | | 195 | | | | | 200 | | | | | 205 | | | | |

(2) INFORMATION FOR SEQ ID NO:10353192_c1_7-AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

Figure 5A-page 6

(ii) MOLECULE TYPE: protein

HPP5

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: biopolymer transport exbB protein

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Arg | Lys | Thr | Leu | Gln | Ser | Ile | Leu | Cys | Leu | Ile | Lys | Lys | Glu |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Met | Met | Arg | Pro | Lys | Gly | Ile | Leu | Met | Asn | Cys | Cys | Arg | Thr | Trp | Lys |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| His | Gln | Val | Leu | Lys | Gln | Ser | Thr | Thr | Gly | Leu | Val | Val | Leu | Ser | Ile |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Ile | Ser | Ser | Thr | Ala | Pro | Phe | Ile | Gly | Leu | Phe | Gly | Thr | Val | Val | Glu |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Ile | Leu | Glu | Ala | Phe | Asn | Asn | Leu | Gly | Ala | Leu | Gly | Gln | Ala | Ser | Phe |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 |
| Gly | Val | Ile | Ala | Pro | Ile | Ile | Ser | Lys | Ala | Leu | Ile | Ala | Thr | Ala | Ala |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| Gly | Ile | Leu | Ala | Ala | Ile | Pro | Ala | Tyr | Ser | Phe | Tyr | Leu | Ile | Leu | Lys |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Arg | Lys | Val | Tyr | Asp | Leu | Ser | Val | Tyr | Val | Gln | Met | Gln | Val | Asp | Ile |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| Leu | Ser | Ser | Lys | Lys | | | | | | | | | | | |
| | | | 130 | | | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:10407625_f2_11-AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

Figure 7 - page 8

HPP7

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Pro | Gly | Val | Tyr | Gln | Met | Ser | Ile | Glu | Pro | Leu | Leu | Lys | Glu | Cys |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Glu | Glu | Leu | Val | Gly | Leu | Gly | Ile | Lys | Ala | Val | Leu | Leu | Phe | Gly | Ile |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Pro | Lys | His | Lys | Asp | Ala | Thr | Gly | Ser | His | Ala | Leu | Asn | Lys | Asp | His |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Ile | Val | Ala | Lys | Ala | Thr | Arg | Glu | Ile | Lys | Lys | Arg | Phe | Lys | Asp | Leu |
| | | 50 | | | | 55 | | | | | 60 | | | | |
| Ile | Val | Ile | Ala | Asp | Leu | Cys | Phe | Cys | Glu | Tyr | Thr | Asp | His | Gly | His |
| | | 65 | | | 70 | | | | 75 | | | | | 80 | |
| Cys | Gly | Ile | Leu | Glu | Asn | Ala | Ser | Val | Ser | Asn | Asp | Lys | Thr | Leu | Lys |
| | | | 85 | | | | | | 90 | | | | | 95 | |
| Ile | Leu | Asn | Leu | Gln | Gly | Leu | Ile | Leu | Leu | Lys | Ala | Val | Trp | Ile | Phe |
| | | | 100 | | | | | 105 | | | | | 110 | | |

(2) INFORMATION FOR SEQ ID NO:104792_f1_1-AA

Figure 8A-page 9

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 64 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

HPP8

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: FLAGELLAR HOOK-ASSOCIATED PROTEIN 1 HAP1

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Glu | Asn | Asn | Lys | Ser | Leu | Lys | His | Ala | Asn | Glu | Leu | Arg | Asp | Lys |
| 1 | | | | 5 | | | | 10 | | | | | | 15 | |
| Arg | Asp | Glu | Leu | Glu | Phe | His | Leu | Arg | Glu | Leu | Phe | Gly | Gly | Asn | Val |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Phe | Lys | Ser | Ser | Ile | Lys | Thr | His | Ser | Leu | Thr | Asp | Lys | Asp | Ser | Ala |
| | | | 35 | | | | 40 | | | | | 45 | | | |
| Asp | Phe | Asp | Glu | Ser | Tyr | Asn | Leu | Asn | Ile | Gly | His | Gly | Unk | Asn | Unk |
| | 50 | | | | | 55 | | | | 60 | | | | | |
| Ile | | | | | | | | | | | | | | | |
| 65 | | | | | | | | | | | | | | | |

Figure 9A - page 10

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPD9

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Met Gln Glu Phe Ser Leu Trp Cys Asp Phe Ile Glu Arg Asp Phe Leu
1 5 10 15

Glu Asn Asp Phe Leu Lys Leu Ile Asn Lys Gly Ala Ile Cys Gly Unk
20 25 30

Thr Ser Asn Pro Ser Leu Phe Cys Glu Ala Ile Thr Lys Ser Ala Phe
35 40 45

Tyr Gln Asp Glu Ile Ala Lys Leu Lys Gly Lys Lys Ala Lys Glu Ile
50 55 60

Tyr Glu Thr Leu Ala Leu Lys Asp Ile Leu Gln Ala Ser Ser Ala Leu
65 70 75 80

Met Pro Leu Tyr Glu Lys Asp Pro Asn Asn Gly Tyr Ile Ser Leu Glu
85 90 95

Ile Asp Pro Phe Leu Glu Asp Asp Ala Ile Lys Ser Ile Asp Glu Ala
100 105 110

Lys Arg Leu Phe Lys Thr Leu Asn Arg Pro Asn Val Met Ile Lys Val
115 120 125

Pro Ala Ser Glu Ser Ala Phe Glu Val Ile Ser Ala Leu Ala Gln Ala
130 135 140

Ser Ile Pro Ile Asn Val Thr Leu Val Phe Ser Pro Lys Ile Ala Gly
145 150 155 160

Glu Ile Ala Gln Ile Leu Ala Lys Glu Ala Arg Lys Arg Ala Val Ile
165 170 175

Ser Val Phe Val Ser Arg Phe Asp Lys Glu Ile Asp Pro Leu Val Pro
180 185 190

Gln Unk Leu Gln Ala Gln Ser Gly Ile Met Lys
195 200

Figure 10A - page 11

(ii) MOLECULE TYPE: protein

HPP10

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: INVOLVED IN F PILUS ASSEMBLY

Val Phe Val Ala Ser Lys Gln Ala Asp Glu Gln Lys Lys Leu Val Ile
1 5 10 15

Glu Gln Glu Val Gln Lys Arg Gln Phe Gln Lys Ile Glu Glu Leu Lys
20 25 30

Ala Asp Met Gln Lys Gly Val Asn Pro Phe Phe Lys Val Leu Phe Asp
35 40 45

Gly Gly Asn Arg Leu Phe Gly Phe Pro Glu Thr Phe Ile Tyr Ser Ser
50 55 60

Ile Phe Ile Leu Phe Val Thr Ile Val Leu Ser Val Ile Leu Phe Gln
65 70 75 80

Ala Tyr Glu Pro Val Leu Ile Val Ala Ile Val Ile Val Leu Val Ala
85 90 95

Leu Gly Phe Lys Lys Asp Tyr Arg Leu Tyr Gln Arg Met Glu Arg Ala
100 105 110

Met Lys Phe Lys Lys Pro Phe Leu Phe Lys Gly Val Lys Asn Lys Ala
115 120 125

Phe Met Ser Ile Phe Ser Met Lys Pro Ser Lys Glu Met Ala Asn Asp
130 135 140

Ile His Leu Asn Pro Asn Arg Glu Asp Arg Leu Val Ser Ala Ala Asn
145 150 155 160

Ser Tyr Leu Ala Asn Asn Tyr Glu Cys Phe Leu Asp Asp Gly Val Ile
165 170 175

Leu Thr Asn Asn Tyr Ser Leu Leu Gly Thr Ile Lys Leu Gly Gly Ile
180 185 190

Asp Phe Leu Thr Thr Ser Lys Lys Asp Leu Ile Glu Leu His Ala Ser
195 200 205

Ile Tyr Ser Val Phe Arg Asn Phe Val Thr Pro Glu Phe Lys Phe Tyr
210 215 220

Phe His Thr Val Lys Lys Lys Ile Val Ile Asp Glu Thr Asn Arg Asp
225 230 235 240

| | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Gly | Leu | Ile | Phe | Ser | Asn | Asp | Phe | Met | Arg | Ala | Tyr | Asn | Glu | Lys | 245 | 250 | 255 |
| Gln | Lys | Arg | Glu | Ser | Phe | Tyr | Asp | Ile | Ser | Phe | Tyr | Leu | Thr | Ile | Glu | 260 | 265 | 270 |
| Gln | Asp | Leu | Leu | Asp | Thr | Leu | Asn | Glu | Pro | Val | Met | Asn | Lys | Lys | His | 275 | 280 | 285 |
| Phe | Ala | Asp | Asn | Asn | Phe | Glu | Glu | Phe | Gln | Arg | Ile | Ile | Arg | Ala | Lys | 290 | 295 | 300 |
| Leu | Glu | Asn | Phe | Lys | Asp | Arg | Ile | Glu | Leu | Ile | Glu | Glu | Leu | Leu | Ser | 305 | 310 | 315 |
| Lys | Tyr | His | Pro | Thr | Arg | Leu | Lys | Glu | Tyr | Thr | Lys | Asp | Gly | Ile | Ile | 325 | 330 | 335 |
| Tyr | Ser | Lys | Gln | Cys | Glu | Phe | Tyr | Asn | Phe | Leu | Val | Gly | Met | Asn | Glu | 340 | 345 | 350 |
| Ala | Pro | Phe | Ile | Cys | Asn | Arg | Lys | Asp | Leu | Tyr | Leu | Lys | Glu | Lys | Met | 355 | 360 | 365 |
| His | Gly | Gly | Val | Lys | Glu | Val | Tyr | Phe | Ala | Asn | Lys | His | Gly | Lys | Ile | 370 | 375 | 380 |
| Leu | Asn | Asp | Asp | Leu | Ser | Glu | Lys | Tyr | Phe | Ser | Ala | Ile | Glu | Ile | Ser | 385 | 390 | 395 |
| Glu | Tyr | Ala | Pro | Lys | Ser | Gln | Ser | Asp | Leu | Phe | Asp | Lys | Ile | Asn | Ala | 405 | 410 | 415 |
| Leu | Asp | Ser | Glu | Phe | Ile | Phe | Met | His | Ala | Tyr | Ser | Pro | Lys | Asn | Ser | 420 | 425 | 430 |
| Gln | Val | Leu | Lys | Asp | Lys | Leu | Ala | Phe | Thr | Ser | Arg | Arg | Ile | Ile | Ile | 435 | 440 | 445 |
| Ser | Gly | Gly | Ser | Lys | Glu | Gln | Gly | Met | Thr | Leu | Gly | Cys | Leu | Ser | Glu | 450 | 455 | 460 |
| Leu | Val | Gly | Asn | Gly | Asp | Ile | Thr | Leu | Gly | Ser | Tyr | Gly | Asn | Ser | Leu | 465 | 470 | 475 |
| Val | Leu | Phe | Ala | Asp | Ser | Phe | Glu | Lys | Met | Lys | Gln | Ser | Val | Lys | Glu | 485 | 490 | 495 |
| Cys | Val | Ser | Ser | Leu | Asn | Ala | Lys | Gly | Phe | Leu | Ala | Asn | Ala | Ala | Thr | 500 | 505 | 510 |
| Phe | Ser | Met | Glu | Asn | Tyr | Phe | Phe | Ala | Lys | His | Cys | Ser | Phe | Ile | Thr | 515 | 520 | 525 |
| Leu | Pro | Phe | Ile | Phe | Asp | Val | Thr | Ser | Asn | Asn | Phe | Ala | Asp | Phe | Ile | 530 | 535 | 540 |
| Ala | Met | Arg | Ala | Met | Ser | Phe | Asp | Gly | Lys | Glu | Asp | Asn | Asn | Ala | Trp | 545 | 550 | 555 |

Figure 10 A-
page 13

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Asn | Ser | Val | Met | Thr | Leu | Lys | Ser | Glu | Ile | Asn | Ser | Pro | Phe | Tyr |
| | | | | 565 | | | | | 570 | | | | | 575 | |
| Leu | Asn | Phe | His | Met | Pro | Thr | Asp | Phe | Gly | Ser | Ala | Ser | Ala | Gly | His |
| | | | 580 | | | | | 585 | | | | | 590 | | |
| Thr | Leu | Ile | Leu | Gly | Ser | Thr | Gly | Ser | Gly | Lys | Asn | Ser | Val | Tyr | Val |
| | | 595 | | | | | 600 | | | | | 605 | | | |
| His | Asp | Ser | Lys | Arg | Tyr | Gly | Ala | Ile | Cys | Leu | | | | | |
| | 610 | | | | | 615 | | | | | | | | | |

Figure 11A-page 14

(B) TYPE: amino acid

(D) TOPOLOGY: linear

HPP 11

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Phe | Ala | Lys | Glu | Arg | Gly | Ser | Ser | Trp | Ala | Lys | His | Leu |
| | | | 100 | | | | | 105 | | | | | 110 |

(2) INFORMATION FOR SEQ ID NO:10675632_f2_3 - AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

Figure 12A - page 15

(ii) MOLECULE TYPE: protein

HPP12

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: H⁺-transporting ATP synthase alpha chain homolog

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ala | Lys | Asp | Ile | Ile | Ser | Glu | Ser | Gln | Asn | Leu | Cys | Ala | Arg | Lys |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Phe | Arg | Arg | Leu | Tyr | Ala | Leu | Leu | Lys | Glu | Asn | Glu | Met | Leu | Ile | Arg |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Ile | Gly | Ser | Tyr | Gln | Met | Gly | Asn | Asp | Lys | Glu | Leu | Asp | Glu | Ala | Ile |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Lys | Lys | Lys | Ala | Leu | Met | Glu | Gln | Phe | Leu | Val | Gln | Asp | Glu | Asn | Ala |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Leu | Unk | Ala | Phe | | | | | | | | | | | | |
| 65 | | | | | | | | | | | | | | | |

Figure 13A - page 16

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 445 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

HPP 13

- ```
(ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: YES
(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori
(xi) SEQUENCE DESCRIPTION:
```

|            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Met<br>1   | Lys        | Ser        | Arg        | Pro<br>5   | Ile        | Leu        | Ala        | Gln        | Ala<br>10  | Tyr        | Ala        | Leu        | Gln        | Met<br>15  | Met        |
| Val        | Lys        | Gln        | Ile<br>20  | Ala        | Phe        | Leu        | Glu        | Thr<br>25  | Ile        | Leu        | Val        | Glu        | Asn<br>30  | Glu        | Gln        |
| Asp        | Ala        | Leu<br>35  | Ile        | Leu        | Glu        | Asn        | Ser<br>40  | Leu        | Ile        | Lys        | Gln        | Leu<br>45  | Lys        | Pro        | Lys        |
| Tyr        | Asn<br>50  | Ile        | Leu        | Leu        | Arg        | Asp<br>55  | Asp        | Lys        | Thr        | Tyr        | Pro<br>60  | Tyr        | Ile        | Tyr        | Met        |
| Asp<br>65  | Phe        | Ser        | Ile        | Asp        | Phe<br>70  | Pro        | Ile        | Pro        | Leu        | Ile<br>75  | Thr        | Arg        | Lys        | Ile        | Leu<br>80  |
| Lys        | Gln        | Pro        | Gly        | Val<br>85  | Lys        | Tyr        | Phe        | Gly        | Pro<br>90  | Phe        | Thr        | Ser        | Gly        | Ala<br>95  | Lys        |
| Asp        | Ile        | Leu        | Asp<br>100 | Ser        | Leu        | Tyr        | Glu        | Leu<br>105 | Leu        | Pro        | Leu        | Val        | Gln<br>110 | Lys        | Lys        |
| Asn        | Cys        | Ile<br>115 | Lys        | Asp        | Lys        | Lys        | Ala<br>120 | Cys        | Met        | Phe        | Tyr        | Gln<br>125 | Ile        | Glu        | Arg        |
| Cys        | Lys<br>130 | Ala        | Pro        | Cys        | Glu        | Asp<br>135 | Lys        | Ile        | Thr        | Lys        | Glu<br>140 | Glu        | Tyr        | Leu        | Lys        |
| Ile<br>145 | Ala        | Lys        | Glu        | Cys        | Leu<br>150 | Glu        | Met        | Ile        | Glu        | Asn<br>155 | Lys        | Asp        | Arg        | Leu        | Ile<br>160 |
| Lys        | Glu        | Leu        | Glu        | Leu<br>165 | Lys        | Met        | Glu        | Arg        | Leu<br>170 | Ser        | Ser        | Asn        | Leu        | Arg<br>175 | Phe        |
| Glu        | Glu        | Ala        | Leu<br>180 | Ile        | Tyr        | Arg        | Asp        | Arg<br>185 | Ile        | Ala        | Lys        | Ile        | Gln<br>190 | Lys        | Ile        |
| Ala        | Pro        | Phe<br>195 | Thr        | Cys        | Met        | Asp        | Leu<br>200 | Ala        | Lys        | Leu        | Tyr        | Asp<br>205 | Leu        | Asp        | Ile        |
| Phe        | Ala<br>210 | Phe        | Tyr        | Gly        | Gly        | Asn<br>215 | Asn        | Lys        | Ala        | Val        | Leu<br>220 | Val        | Lys        | Met        | Phe        |
| Met<br>225 | Arg        | Gly        | Gly        | Lys        | Ile<br>230 | Ile        | Ser        | Ser        | Ala        | Phe<br>235 | Glu        | Lys        | Ile        | His        | Ser<br>240 |

Figure 13A - page 17

|     |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |
|-----|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Leu | Asn        | Gly        | Phe        | Asp<br>245 | Thr        | Asp        | Glu        | Ala        | Met<br>250 | Lys        | Gln        | Ala        | Ile        | Ile        | Asn<br>255 |
| His | Tyr        | Gln        | Ser<br>260 | His        | Leu        | Pro        | Leu        | Met<br>265 | Pro        | Glu        | Gln        | Ile        | Leu        | Leu        | Ser<br>270 |
| Ala | Cys        | Ser<br>275 | Asn        | Glu        | Thr        | Leu        | Lys<br>280 | Glu        | Leu        | Gln        | Glu        | Phe<br>285 | Ile        | Ser        | His        |
| Gln | Tyr<br>290 | Ser        | Lys        | Lys        | Ile        | Ala<br>295 | Leu        | Ser        | Ile        | Pro        | Lys<br>300 | Lys        | Gly        | Asp        | Lys        |
| Leu | Ala        | Leu        | Ile        | Glu        | Ile<br>310 | Ala        | Met        | Lys        | Asn        | Ala<br>315 | Gln        | Glu        | Ile        | Phe        | Ser<br>320 |
| Gln | Glu        | Lys        | Thr        | Ser<br>325 | Asn        | Glu        | Asp        | Arg        | Ile<br>330 | Leu        | Glu        | Glu        | Ala        | Arg        | Ser<br>335 |
| Leu | Phe        | Asn        | Leu<br>340 | Glu        | Cys        | Val        | Pro        | Tyr<br>345 | Arg        | Val        | Glu        | Ile        | Phe<br>350 | Asp        | Thr        |
| Ser | His        | His<br>355 | Ser        | Asn        | Ser        | Gln        | Cys<br>360 | Val        | Gly        | Gly        | Met        | Val<br>365 | Val        | Tyr        | Glu        |
| Asn | Asn        | Ala<br>370 | Phe        | Gln        | Lys        | Asp<br>375 | Ser        | Tyr        | Arg        | Arg        | Tyr<br>380 | His        | Leu        | Lys        | Gly        |
| Ser | Asn        | Glu        | Tyr        | Asp        | Gln<br>390 | Met        | Ser        | Glu        | Leu        | Leu<br>395 | Thr        | Arg        | Arg        | Ala        | Leu<br>400 |
| Asp | Phe        | Ala        | Lys        | Glu<br>405 | Pro        | Pro        | Pro        | Asn        | Leu<br>410 | Trp        | Val        | Ile        | Asp        | Gly<br>415 | Gly        |
| Arg | Ala        | Gln        | Leu<br>420 | Asn        | Ile        | Ala        | Leu        | Glu<br>425 | Ile        | Leu        | Lys        | Ser        | Ser<br>430 | Gly        | Ser        |
| Phe | Val        | Glu<br>435 | Val        | Ile        | Ala        | Ile        | Ser<br>440 | Lys        | Glu        | Lys        | Arg        | Gly<br>445 | Phe        |            |            |

(2) INFORMATION FOR SEQ ID NO:1071890\_f3\_3 - AA

Figure 14A - page 18

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 83 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

HPP 14

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: oligopeptide permease membrane protein

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ser | Leu | Gly | Ala | Phe | Gln | Gly | Tyr | Tyr | Gly | Gly | Leu | Val | Asp | Leu |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Val | Gly | Gln | Arg | Leu | Ser | Glu | Ile | Trp | Ser | Ala | Ile | Pro | Met | Leu | Phe |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Leu | Ile | Val | Ile | Ser | Ser | Ala | Phe | Asn | Ser | Asn | Phe | Trp | Ile | Ile |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Phe | Leu | Val | Leu | Leu | Phe | Ser | Trp | Met | Gly | Leu | Ser | Gln | Val | Val |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Arg | Thr | Glu | Phe | Leu | Lys | Ala | Arg | Asn | Met | Asp | Tyr | Thr | Lys | Ala | Ala |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Arg | Ala | Leu | Gly |     |     |     |     |     |     |     |     |     |     |     |     |



(2) INFORMATION FOR SEQ ID NO:10723412\_f2\_2 - AA

Figure 15A - page 19

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 15

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: hypothetical abc transporter in bcr 5' region

Met Ser Glu Ala Tyr Phe Leu His His Lys Asn Ala Ser Gln Val Ser  
1 5 10 15

Leu Asn Glu Gln Val Leu Asn Val Met Lys Gln Val Gln Leu Asp Glu  
20 25 30

Asn Phe Trp Asn Val Ser Leu Met  
35 40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 299 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

Figure 16A - page 20

(ii) MOLECULE TYPE: protein

HPP 16

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Val Ile Leu Ile Phe Ile Ile Val Val Glu Asp Gln Lys Gly Ile Phe  
1 5 10 15

Pro Ile Ala Ala Ser Lys Arg Lys Ser Gln Ser Ser Val Ile Ile Glu  
20 25 30

Asp Val Cys Phe Ser Lys Glu Asp Phe Val Glu Gly Ala Lys Ala Ile  
35 40 45

Glu Gly Leu Leu Lys Lys His Gly Phe Lys Asp Asn Gly Ile Ile Phe  
50 55 60

Gly His Ala Leu Ser Gly Asn Leu His Phe Val Val Thr Pro Ile Leu  
65 70 75 80

Glu Asn Glu Ala Glu Arg Lys Ala Phe Glu Asn Leu Val Ser Glu Met  
85 90 95

Phe Leu Met Val Ser Lys Ser Ser Gly Ser Ile Lys Ala Glu His Gly  
100 105 110

Thr Gly Arg Met Val Ala Pro Phe Val Glu Met Glu Trp Gly Glu Lys  
115 120 125

Ala Tyr Lys Ile His Lys Gln Ile Lys Glu Leu Phe Asp Pro Asn Gly  
130 135 140

Leu Leu Asn Pro Asp Val Ile Ile Thr Asn Asp Lys Glu Ile His Thr  
145 150 155 160

Lys Asn Leu Lys Ser Ile Tyr Pro Ile Glu Glu His Leu Asp Met Cys  
165 170 175

Met Glu Cys Gly Phe Cys Glu Arg Ile Cys Pro Ser Lys Asp Leu Ser  
180 185 190

Leu Thr Pro Arg Gln Arg Ile Val Ile His Arg Glu Val Glu Arg Leu  
195 200 205

Lys Glu Arg Val Ser His Gly His Asp Glu Asp Gln Val Leu Leu Asp  
210 215 220

Glu Leu Leu Lys Glu Ser Glu Tyr Leu Ala His Ala Thr Cys Ala Val  
225 230 235 240

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Cys | His | Met | Cys | Ser | Thr | Leu | Cys | Pro | Leu | Gly | Ile | Asp | Thr | Gly | Unk |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Ile | Ala | Leu | Asn | His | Tyr | Gln | Lys | Asn | Pro | Lys | Gly | Glu | Lys | Ile | Ala |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Ser | Lys | Ile | Leu | Lys | Ser | His | Ala | Asn | Asp | His | Lys | Arg | Gly | Ser | Phe |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Phe | Phe | Lys | Unk | Arg | Phe | Arg | Gly | Phe | Lys | Asn | Ser |     |     |     |     |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |

Figure 16A - page 21

(2) INFORMATION FOR SEQ ID NO:10742963\_c1\_8 - AA

Figure 17A - page 22

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP17

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Glu | Lys | Asn | Phe | Trp | Pro | Leu | Gly | Ile | Met | Ser | Val | Leu | Ile | 1   | 5   | 10  | 15  |
| Phe | Gly | Leu | Gly | Ile | Val | Val | Phe | Leu | Val | Val | Phe | Ala | Leu | Lys | Asn | 20  | 25  | 30  |     |
| Ser | Pro | Lys | Asn | Asp | Leu | Val | Tyr | Phe | Lys | Gly | His | Asn | Glu | Val | Asp | 35  | 40  | 45  |     |
| Leu | Asn | Phe | Asn | Ala | Met | Leu | Lys | Thr | Tyr | Glu | Asn | Phe | Lys | Ser | Asn | 50  | 55  | 60  |     |
| Tyr | Arg | Phe | Ser | Val | Gly | Leu | Lys | Pro | Leu | Thr | Glu | Ser | Pro | Lys | Thr | 65  | 70  | 75  | 80  |
| Pro | Ile | Leu | Pro | Tyr | Phe | Ser | Lys | Gly | Thr | His | Gly | Asp | Lys | Lys | Ile | 85  | 90  | 95  |     |
| Gln | Glu | Asn | Leu | Leu | Asn | Asn | Ala | Leu | Ile | Leu | Glu | Lys | Ser | Asn | Thr | 100 | 105 | 110 |     |
| Leu | Tyr | Ala | Gln | Leu | Gln | Pro | Leu | Lys | Pro | Ala | Leu | Asp | Ser | Pro | Asn | 115 | 120 | 125 |     |
| Ile | Gln | Val | Tyr | Leu | Ala | Phe | Tyr | Pro | Ser | Gln | Ser | Gln | Pro | Arg | Leu | 130 | 135 | 140 |     |
| Leu | Gly | Thr | Leu | Asp | Cys | Lys | Asn | Ala | Cys | Glu | Pro | Leu | Lys | Phe | Asp | 145 | 150 | 155 | 160 |
| Leu | Leu | Glu | Gly | Asp | Lys | Val | Gly | Arg | Tyr | Lys | Ile | Leu | Phe | Lys | Phe | 165 | 170 | 175 |     |
| Val | Phe | Lys | Asn | Lys | Glu | Glu | Leu | Ile | Leu | Glu | Gln | Leu | Leu | Phe | Leu | 180 | 185 | 190 |     |
| Ser | Ser | Met | Ala | Cys | Met | Gly | Ile | Ser | Ile | Leu | Lys | Asn | Ala | Lys | Ala | 195 | 200 | 205 |     |
| Phe | Phe | Lys | Tyr | Lys | Ile |     |     |     |     |     |     |     |     |     |     | 210 |     |     |     |

(2) INFORMATION FOR SEQ ID NO:10745275\_f3\_8 - AA

Figure 18A - page 23

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP18

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| Met | Pro | Ile | Lys | Gly | Ser | Phe | Leu | Ala | Arg | Asn | Arg | Leu | Val | Ile | Ala | 1   | 5   | 10  | 15 |
| Leu | Thr | Asp | Ala | Val | Ile | Ile | Pro | Gln | Ala | Asp | Leu | Lys | Ser | Gly | Ser | 20  | 25  | 30  |    |
| Met | Ser | Ser | Ala | Arg | Leu | Ala | Gln | Lys | Tyr | Gln | Lys | Pro | Leu | Phe | Val | 35  | 40  | 45  |    |
| Leu | Pro | Gln | Arg | Leu | Asn | Glu | Ser | Asp | Gly | Thr | Asn | Glu | Leu | Leu | Glu | 50  | 55  | 60  |    |
| Lys | Gly | Gln | Ala | Gln | Gly | Ile | Phe | Asn | Ile | Gln | Asn | Phe | Ile | Asn | Thr | 65  | 70  | 75  | 80 |
| Leu | Leu | Lys | Asp | Tyr | His | Leu | Lys | Glu | Met | Pro | Glu | Met | Lys | Asp | Glu | 85  | 90  | 95  |    |
| Phe | Leu | Glu | Tyr | Cys | Ala | Lys | Asn | Pro | Ser | Tyr | Glu | Glu | Ala | Tyr | Leu | 100 | 105 | 110 |    |
| Lys | Phe | Gly | Asp | Lys | Leu | Leu | Glu | Tyr | Glu | Leu | Leu | Gly | Lys | Ile | Lys | 115 | 120 | 125 |    |
| Arg | Ile | Asn | His | Leu | Val | Val | Leu | Ala | 130 | 135 |     |     |     |     |     |     |     |     |    |

(2) INFORMATION FOR SEQ ID NO:11132778\_f1\_4 - AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 271 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

Figure 19A - page 24

(ii) MOLECULE TYPE: protein

HPP19

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: ATP-BINDING PROTEIN ABC

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Val | Glu | Leu | Lys | Asn | Ile | Glu | Lys | Ile | Tyr | Glu | Asn | Gly | Phe | 1   | 5   | 10  | 15  |
| His | Ala | Leu | Lys | Gly | Val | Asn | Leu | Glu | Leu | Lys | Lys | Gly | Asp | Ile | Leu | 20  | 25  | 30  |     |
| Gly | Val | Ile | Gly | Tyr | Ser | Gly | Ala | Gly | Lys | Ser | Thr | Leu | Ile | Arg | Leu | 35  | 40  | 45  |     |
| Ile | Asn | Cys | Leu | Glu | Arg | Pro | Ser | Ser | Gly | Glu | Val | Leu | Val | Asn | Gly | 50  | 55  | 60  |     |
| Val | Asn | Leu | Leu | Asn | Leu | Lys | Pro | Lys | Glu | Leu | Gln | Lys | Ala | Arg | Gln | 65  | 70  | 75  | 80  |
| Lys | Ile | Gly | Met | Ile | Phe | Gln | His | Phe | Asn | Leu | Leu | Ser | Ala | Lys | Asn | 85  | 90  | 95  |     |
| Val | Phe | Glu | Asn | Val | Ala | Phe | Ala | Leu | Glu | Ile | Ala | Arg | Trp | Glu | Lys | 100 | 105 | 110 |     |
| Thr | Lys | Ile | Lys | Ser | Arg | Val | His | Glu | Leu | Leu | Glu | Leu | Val | Gly | Leu | 115 | 120 | 125 |     |
| Glu | Asp | Lys | Val | His | Phe | Tyr | Pro | Lys | Gln | Leu | Ser | Gly | Gly | Gln | Lys | 130 | 135 | 140 |     |
| Gln | Arg | Val | Ala | Ile | Ala | Arg | Ser | Leu | Ala | Asn | Cys | Pro | Asn | Leu | Leu | 145 | 150 | 155 | 160 |
| Leu | Cys | Asp | Glu | Ala | Thr | Ser | Ala | Leu | Asp | Ser | Lys | Thr | Thr | His | Ser | 165 | 170 | 175 |     |
| Ile | Leu | Thr | Leu | Leu | Ser | Gly | Ile | Gln | Lys | Lys | Phe | Asp | Leu | Ser | Ile | 180 | 185 | 190 |     |
| Val | Phe | Ile | Thr | His | Gln | Ile | Glu | Val | Val | Lys | Glu | Leu | Cys | Asn | Gln | 195 | 200 | 205 |     |
| Met | Cys | Val | Ile | Ser | Ser | Gly | Glu | Ile | Val | Glu | Arg | Gly | Ser | Val | Glu | 210 | 215 | 220 |     |
| Glu | Ile | Phe | Ala | Asn | Pro | Lys | His | Ala | Val | Thr | Lys | Glu | Leu | Leu | Gly | 225 | 230 | 235 | 240 |

Figure 19A - page 25

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Lys | Asn | Glu | His | Ala | Asp | Gln | Lys | Ser | Gln | Asp | Ile | Tyr | Arg | Ile |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Val | Phe | Leu | Gly | Glu | His | Leu | Asp | Glu | Pro | Ile | Ile | Ser | Unk | Phe | Unk |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |

(2) INFORMATION FOR SEQ ID NO:11253 f1 1-AA

Figure 20A - page 26

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 20

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xii) SEQUENCE DESCRIPTION: N-ACETYLMURAMATE--ALANINE LIGASE

Met Lys Val Ile Gln Val Phe Leu Phe Ser Asn Pro Phe Cys Ala Ile  
1 5 10 15

Val Pro Asn Thr Glu Pro Glu His Leu Glu His Tyr Asp His Asp Leu  
20 25 30

Glu Arg Phe Phe Phe Ala Tyr Lys Tyr Phe Leu Asp His Ala Gln Lys  
35 40 45

Arg Val Ile Tyr Lys Glu Asp Pro Phe Leu Lys Asn Tyr Ser Lys Asp  
50 55 60

Ala Ile Val Leu Glu Lys Lys Asp Ile Tyr Asn Ile Gln Tyr Ile Leu  
65 70 75 80

Lys Asp Gly Glu Pro Tyr Thr Ser Phe Glu Leu Lys Asn Leu Gly Ala  
85 90 95

Phe Leu Val Trp Gly Leu Gly Glu His Asn Ala Thr Asn Ala Ser Leu  
100 105 110

Ala Ile Leu Ser Ala Leu Asp Glu Leu Asn Leu Glu Glu Ile Arg Asn  
115 120 125

Asn Unk Leu Asn Phe Lys Gly Ile Lys Lys Arg Phe Asp Ile Leu Gln  
130 135 140

Lys Asn Asn Leu Ile Leu Ile Asp Asp Tyr Ala His His Pro Thr Glu  
145 150 155 160

Ile Gly Unk Thr Leu Lys Ser Ala Arg Ile Tyr Ala Asn Leu Leu Asn  
165 170 175

Thr Gln Glu Lys Ile Ile Val Ile Trp Gln Ala His Lys Tyr Ser Arg  
180 185 190

Leu Met Asp Asn Leu Glu Glu Phe Lys Lys Cys Phe Leu Glu His Cys  
195 200 205

Asp Arg Leu Ile Ile Leu Pro Val Tyr Ser Ala Ser Glu Val Lys Arg  
210 215 220

Asp Ile Asp Leu Lys Ala His Phe Lys His Tyr Asn Pro Thr Phe Ile  
225 230 235 240



Asp Arg Val Arg

(2) INFORMATION FOR SEQ ID NO:114505\_c1\_12 - AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

Figure 21A - page 28

(ii) MOLECULE TYPE: protein

HPP21

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Ala | Leu | Ile | Ala | Met | Phe | Phe | Leu | Met | Leu | Ile | Lys | Lys | Thr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ile | Ala | Tyr | Lys | Glu | Asp | Lys | Lys | Ser | Ala | Ala | Leu | Lys | Val | Val | Pro |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Tyr | Leu | Val | Ala | Leu | Met | Ser | Leu | Ala | Phe | Ser | Trp | Tyr | Leu | Ile | Val |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Lys | Val | Leu | Lys | Arg | Leu | Tyr | Ala | Val | Ser | Phe | Glu | Ile | Gln | Leu | Ala |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Cys | Gly | Cys | Val | Leu | Ala | Leu | Leu | Ile | Phe | Ile | Leu | Phe | Lys | Arg | Phe |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Val | Leu | Lys | Lys | Ala | Pro | Gln | Leu | Glu | Asn | Ser | His | Glu | Ser | Val | Asn |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Glu | Leu | Phe | Asn | Val | Pro | Leu | Ile | Phe | Ala |     |     |     |     |     |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     |     |     |

Figure 22- page 29

HPP 22

- ```
(i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 156 amino acids
      (B) TYPE: amino acid
      (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
      (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:
```

| | | | | | | | | | | | | | | | |
|------------|------------|------------|------------|-----------|------------|------------|------------|------------|-----------|------------|------------|------------|------------|-----------|-----------|
| Met 1 | Ile | Lys | Arg | Ile 5 | Ala | Cys | Ile | Leu | Ser 10 | Leu | Ser | Ala | Ser | Leu 15 | Ala |
| Leu | Ala | Gly | Glu 20 | Val | Asn | Gly | Phe | Phe 25 | Met | Gly | Ala | Gly | Tyr 30 | Gln | Gln |
| Gly | Arg | Tyr 35 | Gly | Pro | Tyr | Asn | Ser 40 | Asn | Tyr | Ser | Asp | Trp 45 | Arg | His | Gly |
| Asn | Asp 50 | Leu | Tyr | Gly | Leu | Asn 55 | Phe | Lys | Leu | Gly | Phe 60 | Val | Gly | Phe | Ala |
| Asn 65 | Lys | Trp | Phe | Gly | Ala 70 | Arg | Val | Tyr | Gly | Phe 75 | Leu | Asp | Trp | Phe | Asn 80 |
| Thr | Ser | Gly | Thr | Glu 85 | His | Thr | Lys | Thr | Asn 90 | Leu | Leu | Thr | Tyr | Gly 95 | Gly |
| Gly | Gly | Asp | Leu 100 | Ile | Val | Asn | Leu | Ile 105 | Pro | Leu | Asp | Lys | Phe 110 | Ala | Leu |
| Gly | Leu | Ile 115 | Gly | Gly | Val | Gln | Leu 120 | Ala | Gly | Asn | Thr | Trp 125 | Met | Phe | Pro |
| Tyr | Asp 130 | Val | Asn | Gln | Thr | Arg 135 | Phe | Gln | Phe | Leu | Trp 140 | Asn | Leu | Gly | Gly |
| Arg 145 | Met | Arg | Val | Gly | Asp 150 | Thr | Val | Arg | Leu | Lys 155 | Arg | Ala | | | |

(2) INFORMATION FOR SEQ ID NO:1171928_f3_10 - AA

Figure 23A - page 30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 277 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP23

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: FLAGELLAR BIOSYNTHETIC PROTEIN FLHB

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Tyr | Arg | His | Val | Leu | Lys | Asp | Phe | Ser | Leu | Asp | Phe | Ser | Lys | Glu | 1 | 5 | 10 | 15 |
| Ser | Val | Gln | Glu | Leu | Phe | Asn | Gln | Leu | Ala | Lys | Asp | Thr | Phe | Leu | Leu | 20 | 25 | 30 | |
| Leu | Leu | Pro | Val | Leu | Ile | Ile | Leu | Met | Val | Val | Ala | Phe | Leu | Ser | Asn | 35 | 40 | 45 | |
| Val | Leu | Gln | Phe | Gly | Trp | Leu | Phe | Ala | Pro | Lys | Val | Ile | Glu | Pro | Lys | 50 | 55 | 60 | |
| Phe | Ser | Lys | Ile | Asn | Pro | Ile | Asn | Gly | Val | Lys | Asn | Leu | Phe | Ser | Leu | 65 | 70 | 75 | 80 |
| Lys | Lys | Ile | Leu | Asp | Gly | Ser | Leu | Ile | Thr | Leu | Lys | Val | Phe | Leu | Ala | 85 | 90 | 95 | |
| Phe | Phe | Leu | Gly | Phe | Phe | Ile | Phe | Ser | Leu | Phe | Leu | Gly | Glu | Leu | Asn | 100 | 105 | 110 | |
| His | Ala | Ala | Leu | Leu | Asn | Leu | Gln | Gly | Gln | Leu | Leu | Trp | Phe | Lys | Ser | 115 | 120 | 125 | |
| Lys | Ala | Leu | Trp | Leu | Ile | Ser | Ser | Leu | Leu | Phe | Leu | Phe | Phe | Val | Leu | 130 | 135 | 140 | |
| Ala | Phe | Val | Asp | Leu | Ile | Ile | Lys | Arg | Arg | Gln | Tyr | Thr | Asn | Ser | Leu | 145 | 150 | 155 | 160 |
| Lys | Met | Thr | Lys | Gln | Glu | Val | Lys | Asp | Glu | Tyr | Lys | Gln | Gln | Glu | Gly | 165 | 170 | 175 | |
| Asn | Pro | Glu | Ile | Lys | Ala | Lys | Ile | Arg | Gln | Met | Met | Val | Lys | Asn | Ala | 180 | 185 | 190 | |
| Thr | Asn | Lys | Met | Met | Gln | Glu | Ile | Pro | Lys | Ser | Asn | Val | Val | Val | Thr | 195 | 200 | 205 | |
| Asn | Pro | Thr | His | Tyr | Ala | Val | Ala | Leu | Lys | Phe | Asp | Glu | Glu | His | Pro | 210 | 215 | 220 | |
| Val | Pro | Val | Val | Val | Ala | Lys | Gly | Thr | Asp | Tyr | Leu | Ala | Ile | Arg | Ile | 225 | 230 | 235 | 240 |

Lys Gly Ile Ala Arg Glu His Asp Ile Glu Ile Ile Glu Asn Lys Thr
245 250 255
Leu Ala Arg Glu Leu Tyr Arg Asp Val Lys Leu Asn Ala Thr Ile Pro
260 265 270
Glu Glu Leu Phe Glu Arg
275

Figure 23A-page 31

(2) INFORMATION FOR SEQ ID NO:11719687_f3_4 - AA

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 119 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

Figure 24A-page 32

(ii) MOLECULE TYPE: protein

HPP 24

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Met Asn Thr Unk Pro Leu Ile Ala Thr Leu Leu Gln Ala Pro Leu His
1 5 10 15

Val Leu Gly Ile Arg Glu Pro Val Ser Phe Gln Pro Phe Tyr Pro Lys
20 25 30

Thr Glu Lys Pro Asn Arg Pro Gln Lys Phe Ala His Val Ser Ser Met
35 40 45

Pro Ser Leu Glu Phe Leu Glu Lys Leu Val Ile Arg Tyr Leu Leu Glu
50 55 60

Asp Arg Ser Leu Leu Asp Leu Ala Val Gly Tyr Ile His Ser Gly Val
65 70 75 80

Phe Leu His Lys Lys Gln Glu Phe Asp Ala Leu Cys Gln Glu Lys Leu
85 90 95

Asp Asp Pro Lys Leu Val Ala Leu Leu Leu Asp Ala Asn Leu Pro Leu
100 105 110

Lys Lys Gly Gly Phe Glu Lys Glu
115 120

Figure 25A-page 33

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 225 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 25

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

[illegible]

(2) INFORMATION FOR SEQ ID NO:1181418_c3_12-AA

Figure 26A-page 34

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 26

(iii) HYPOTHETICAL: YES

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Leu | Ala | Leu | Val | Met | Gly | Ser | Ser | Thr | Gly | Leu | Glu | Glu | Phe | Cys |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| | | | | | | | | | | | | | | | |
| Val | Leu | Glu | Glu | Leu | Ile | Asn | Ser | Gly | Leu | Ser | Val | | | | |
| | | | | 20 | | | | 25 | | | | | | | |

Figure 27A - page 35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 49 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 27

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: homology to NITROGEN FIXATION; TRANSMEMBRANE [Rhi

Met Asn Thr Glu Ile Leu Thr Ile Met Leu Val Val Ser Val Leu Met
1 5 10 15

Gly Leu Val Gly Leu Ile Ala Phe Leu Trp Gly Val Lys Ser Gly Gln
20 25 30

Phe Asp Asp Glu Lys Arg Met Leu Glu Ser Val Leu Tyr Asp Ala Arg
35 40 45

Ala Thr
50

(2) INFORMATION FOR SEQ ID NO:11878127_c3_10: AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

Figure 28A - page 316

(ii) MOLECULE TYPE: protein

HPP 28

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Met 1 | Gly | Phe | Leu | Lys 5 | Val | Leu | Lys | His | Asp 10 | Ala | Leu | Gly | Gln | Val 15 | Gly |
| Asn | Ile | Val | Ile 20 | Gly | Asn | Phe | Leu | Ile 25 | Thr | Leu | Thr | Val | Leu 30 | Ala | Val |
| Cys | Phe | Ser 35 | Ser | Gln | Ser | Ala | Glu 40 | Glu | Thr | Thr | Met | Leu 45 | Thr | Leu | Ser |
| Tyr | Thr 50 | Leu | Phe | Phe | Ile | Leu 55 | Gly | Ala | Phe | Leu | Leu 60 | Val | Ala | Ile | Ser |
| Val 65 | Gly | Ala | Ile | Lys | Asn 70 | Leu | Asn | Ala | Leu | Phe 75 | Ser | Lys | Arg | Gly | Val 80 |
| Leu | Ser | Phe | Ser | Leu 85 | Pro | Ile | Ser | Leu | Glu 90 | Ser | Leu | Leu | Leu | Pro 95 | Lys |
| Ile | Leu | Leu | Pro 100 | Arg | Cys | Phe | Phe | Ile 105 | Phe | Ser | Leu | Phe | Trp 110 | Phe | Val |
| Ala | Ser | Val 115 | Arg | Leu | Gly | Tyr | Tyr 120 | Leu | Phe | Asn | Ala | Gln 125 | Ser | Ser | Val |
| Leu | Phe 130 | Ile | Leu | His | Thr | Ala 135 | Leu | Lys | Thr | Phe | Ala 140 | Leu | Lys | Pro | Thr |
| Lys 145 | Thr | Ile | Gly | Val | Ala 150 | Leu | Phe | Leu | Gly | Leu 155 | Val | Leu | Met | Lys | Phe 160 |
| Leu | Phe | Val | Leu | Ser 165 | Val | Leu | Asn | Ala | Thr 170 | Arg | Ile | Lys | Lys | Ala 175 | Arg |
| Phe | Leu | Leu | Gly 180 | Gly | Leu | Leu | Phe | Ile 185 | Leu | Val | Gly | Val | Val 190 | Leu | Glu |
| Leu | Ala | Phe 195 | Asn | Ser | Leu | Leu | Pro 200 | Leu | Met | Ser | Ser | Ser 205 | Leu | Ser | Ile |
| Asn | Glu 210 | Gly | Phe | Tyr | Tyr | Phe 215 | Leu | Gln | Gln | Gln | Glu 220 | Leu | Gln | Glu | Asn |
| Lys 225 | Tyr | Tyr | Leu | Leu | Trp 230 | Gly | Val | Asp | Phe | Leu 235 | Lys | Ile | Leu | Leu | Leu 240 |

Tyr Gly Val Ile Arg Tyr Leu Leu Thr His Lys Leu Glu Leu Asp
245 250 255

Figure 28A - page 37

(2) INFORMATION FOR SEQ ID NO:11924177_f1_1 - AA

Figure 29A - page 38

HPP 29

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 73 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*
- (xi) SEQUENCE DESCRIPTION:

[illegible]

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 129 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Met Phe Val Ala Ala Gly Leu Gly Ala Tyr Ala Ile Ala Leu Phe His
1 5 10 15

Leu Phe Thr His Ala Phe Phe Lys Ser Leu Leu Phe Leu Gly Ser Gly
20 25 30

Asn Val Met His Ala Met Glu Asp Asn Leu Asp Ile Thr Lys Met Gly
35 40 45

Ala Leu Tyr Lys Pro Met Arg Ile Thr Ala Val Phe Met Ile Ile Gly
50 55 60

Ser Val Ala Leu Cys Gly Ile Tyr Pro Phe Ala Gly Tyr Phe Ser Lys
65 70 75 80

Asp Lys Ile Leu Glu Val Ala Phe Gly Met His His His Ile Leu Trp
85 90 95

Phe Val Leu Leu Ile Gly Ala Ile Phe Thr Ala Phe Tyr Ser Phe Arg
100 105 110

Leu Ile Met Leu Val Phe Phe Ala Pro Lys Gln His Glu Ile Asn His
115 120 125

Pro Pro
130

(2) INFORMATION FOR SEQ ID NO:1206675_c1_17 - AA

Figure 31A - page 40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP31

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Phe | Ile | Ser | Ser | Ser | Tyr | Thr | Leu | Ser | Phe | Val | Trp | Leu | Phe | Leu | 1 | 5 | 10 | 15 |
| Ile | Phe | Phe | Phe | Phe | Lys | Asn | Lys | Pro | Leu | Gly | Leu | Arg | Phe | Ser | Leu | 20 | 25 | 30 | |
| Ser | Leu | Ile | Ser | Val | Ile | Leu | Ser | Asn | Ile | Ala | Leu | Lys | Asp | Ser | Leu | 35 | 40 | 45 | |
| Ser | Leu | Asn | Glu | Phe | Leu | Ser | Ser | Phe | Thr | Ala | Pro | Leu | Ser | Pro | Phe | 50 | 55 | 60 | |
| Ser | Cys | Leu | Leu | Ile | Leu | Ala | Tyr | Ala | Ser | Phe | Ser | Cys | His | Ile | Leu | 65 | 70 | 75 | 80 |
| Lys | Lys | Pro | Pro | Leu | Glu | Thr | Leu | Gln | Ser | Tyr | Ser | Val | Met | Leu | Phe | 85 | 90 | 95 | |
| Phe | Asn | Leu | Leu | Leu | Leu | Thr | Asp | Ile | Leu | Gly | Phe | Leu | Pro | Phe | Ser | 100 | 105 | 110 | |
| Ile | Tyr | His | His | Phe | Met | Ala | Ser | Leu | Ile | Phe | Ser | Ala | Leu | Phe | Cys | 115 | 120 | 125 | |
| Ser | Ser | Leu | Phe | Leu | Ser | Ser | Pro | Leu | Leu | Gly | Val | Ile | Ala | Leu | Val | 130 | 135 | 140 | |
| Ala | Leu | Ser | Ser | Ser | Leu | Leu | Met | Arg | Ser | Asn | Phe | Gln | Ile | Leu | Asp | 145 | 150 | 155 | 160 |
| Ser | Leu | Leu | Asp | Phe | Pro | Leu | Phe | Leu | Phe | Val | Phe | Phe | Lys | Thr | Leu | 165 | 170 | 175 | |
| Tyr | Leu | Ala | Lys | Lys | Arg | Leu | 180 | | | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:12120938 f3_10: AA

Figure 32A - page 41

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 32

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Met Ala Met Pro Ile Phe Met Asp Thr Val Val Val Phe Pro Met Leu
1 5 10 15

Asp Gly Arg Leu Leu Val Val Asp Tyr Val His Gly Asn Pro Thr Pro
20 25 30

Ile Arg Asn Ile Val Ile Ser Ser Asp Lys Phe Phe Asn Asn Ile Pro
35 40 45

Thr Leu Ser
50

(2) INFORMATION FOR SEQ ID NO:1218751_c2_13 - AA

Figure 33A - page 42

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP33

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Phe | Asn | Ser | Thr | Trp | Lys | Leu | Cys | Cys | Phe | Arg | Ile | Ser | Glu | Met | 1 | 5 | 10 | 15 |
| Ile | Leu | Pro | Asn | Cys | Phe | Leu | Leu | Lys | Thr | Cys | Tyr | Asp | Phe | Ile | Ile | 20 | 25 | 30 | |
| Lys | Leu | Asp | Tyr | Leu | Gly | Leu | Ile | Gly | Val | Ser | Ser | Ile | Tyr | Leu | Leu | 35 | 40 | 45 | |
| Ala | Leu | Ile | Leu | Lys | Pro | Phe | Thr | Leu | Thr | Arg | Gln | Lys | Cys | Ala | Cys | 50 | 55 | 60 | |
| Ile | Gly | Ile | Leu | Cys | Leu | Ser | Phe | Tyr | Ala | Trp | Asn | Phe | Pro | Ile | Lys | 65 | 70 | 75 | 80 |
| Asn | Ser | Ser | Ile | Ala | Leu | Tyr | Val | Phe | Tyr | Phe | Ala | Leu | Leu | Gly | Thr | 85 | 90 | 95 | |
| Leu | Leu | Trp | Arg | Phe | Leu | Gly | Ala | Ser | Met | Lys | Gln | Ser | Phe | Leu | Pro | 100 | 105 | 110 | |
| Ser | Met | Asn | Ile | Cys | Val | Val | Trp | Val | Phe | Ala | Ser | Ser | Leu | Gln | Ser | 115 | 120 | 125 | |
| Phe | Arg | Phe | Leu | Ser | Val | Ser | Asp | Cys | Val | Asp | Phe | Ser | Leu | Phe | Ile | 130 | 135 | 140 | |
| Leu | Ala | Leu | Phe | Leu | Leu | Ile | Leu | Val | Leu | Ile | Tyr | His | Lys | Arg | Leu | 145 | 150 | 155 | 160 |
| Phe | Gly | Leu | Tyr | Glu | Tyr | Ala | Asn | Thr | Leu | Ile | Leu | Ile | Val | Gly | Leu | 165 | 170 | 175 | |
| Cys | Val | Val | Val | Leu | Cys | Ser | Ser | Met | Phe | Ile | Gln | Thr | Lys | Glu | Tyr | 180 | 185 | 190 | |
| Tyr | Gly | Met | Arg | Leu | Gly | Phe | Tyr | Phe | Leu | Gly | Leu | Leu | Gly | Trp | Leu | 195 | 200 | 205 | |
| Leu | Glu | Tyr | Ile | His | Asn | Thr | Leu | Arg | Arg | Leu | Glu | His | Lys | Ile | 210 | 215 | 220 | | |

(2) INFORMATION FOR SEQ ID NO:12343763_f3_15:-AA

Figure 34A -page 43

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP34

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Val Gly Ser Phe Leu Phe Val Gly Pro Ser Gly Val Gly Lys Thr Glu
1 5 10 15

Leu Ala Lys Glu Leu Ala Leu Asn Leu Ile Cys Ile Leu Asn Ala Leu
20 25 30

Thr

(2) INFORMATION FOR SEQ ID NO:12400007_c2_9- AA

Figure 35A-page 44

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 35

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Thr | Tyr | Thr | Asn | Thr | Trp | Pro | Thr | Thr | Thr | Gly | Trp | Ile | Thr | Leu | 1 | 5 | 10 | 15 |
| Leu | Leu | Leu | Val | Ile | Ile | Thr | Leu | Thr | Leu | Cys | Gly | Arg | Asp | Leu | Ala | 20 | 25 | 30 | |
| Gln | Phe | Arg | Asn | Pro | Ala | Pro | Ser | Lys | Val | Ile | Arg | Thr | Ile | Leu | Leu | 35 | 40 | 45 | |
| Glu | Leu | Asn | Arg | Met | Ile | Ser | His | Ile | Phe | Phe | Ile | Ser | Val | His | Ala | 50 | 55 | 60 | |
| Leu | Asp | Val | Gly | Ala | Met | Ser | Val | Phe | Leu | Tyr | Ala | Phe | Lys | Thr | Arg | 65 | 70 | 75 | 80 |
| Glu | Tyr | Gly | Leu | Asp | Leu | Met | Glu | Asp | Tyr | Cys | Gly | Ala | Arg | Leu | Thr | 85 | 90 | 95 | |
| His | Asn | Ala | Ile | Arg | Ile | Gly | Gly | Val | Pro | Leu | Asp | Leu | Pro | Pro | Asn | 100 | 105 | 110 | |
| Trp | Leu | Glu | Gly | Leu | Lys | Lys | Phe | Leu | Gly | Glu | Met | Arg | Glu | Cys | Lys | 115 | 120 | 125 | |
| Lys | Leu | Ile | Gln | Gly | Leu | Leu | Asp | Lys | Asn | Arg | Ile | Trp | Arg | Asn | Ala | 130 | 135 | 140 | |
| Phe | Gly | Lys | Cys | Gly | Arg | Cys | Asn | Ala | Lys | Met | Ala | Gln | Ser | Trp | Gly | 145 | 150 | 155 | 160 |
| Met | Ser | Gly | Ile | Met | Leu | Arg | Gly | Thr | Gly | Ile | Ala | Tyr | Asp | Ile | Arg | 165 | 170 | 175 | |
| Lys | Glu | Glu | Pro | Tyr | Glu | Leu | Tyr | Lys | Glu | Leu | Asp | Phe | Asp | Val | Pro | 180 | 185 | 190 | |
| Val | Gly | Asn | Tyr | Gly | Asp | Ser | Tyr | Asp | Arg | Tyr | Cys | Leu | Tyr | Met | Leu | 195 | 200 | 205 | |
| Glu | Ile | Asp | Glu | Ser | Ile | Arg | Ile | Ile | Glu | Gln | Leu | Ile | Pro | Met | Tyr | 210 | 215 | 220 | |
| Ala | Lys | Thr | Asp | Thr | Pro | Ile | Met | Ala | Gln | Asn | Pro | His | Tyr | Ile | Ser | 225 | 230 | 235 | 240 |

Ala Pro Lys Glu Asp Ile Met Thr Gln Asn Tyr Ala Leu Met Gln His
245 250 255

Phe Val Leu Val Ala Gln Gly Met Arg Pro Pro Leu Gly Ser Val Cys
260 265 270

Pro His Arg Lys Pro
275

Figure 35A-page 45

(2) INFORMATION FOR SEQ ID NO:12505125_c3_10 - AA

Figure 36A - page 46

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 234 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP36

(iii) HYPOTHETICAL: YES

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Arg | Leu | Asp | Tyr | Ala | Leu | Phe | Asn | Gln | His | Leu | Ala | Asn | Ser | Arg |
| 1 | | | | 5 | | | | 10 | | | | | | 15 | |
| Glu | Lys | Ala | Lys | Ala | Leu | Val | Leu | Lys | Lys | Gln | Val | Leu | Val | Asn | Lys |
| | | | 20 | | | | | 25 | | | | | | 30 | |
| Met | Val | Val | Ser | Lys | Pro | Ser | Phe | Ile | Val | Lys | Glu | Gly | Asp | Gln | Ile |
| | | | 35 | | | | | 40 | | | | | 45 | | |
| Glu | Leu | Ile | Ala | Pro | Asn | Leu | Phe | Val | Ser | Arg | Ala | Gly | Glu | Lys | Leu |
| | | | 50 | | | | | 55 | | | | | 60 | | |
| Gly | Ala | Phe | Leu | Glu | Asp | His | Phe | Ile | Asp | Phe | Lys | Glu | Lys | Val | Val |
| | | | | | 70 | | | | | 75 | | | | | 80 |
| Leu | Asp | Val | Gly | Ala | Ser | Lys | Gly | Gly | Phe | Ser | Gln | Val | Ala | Leu | Leu |
| | | | | | 85 | | | | | 90 | | | | 95 | |
| Lys | Gly | Ala | Lys | Lys | Val | Leu | Cys | Val | Asp | Val | Gly | Lys | Met | Gln | Leu |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Asp | Glu | Ser | Leu | Lys | Asn | Asp | Gln | Arg | Ile | Glu | Cys | Tyr | Glu | Glu | Cys |
| | | | 115 | | | | | 120 | | | | | 125 | | |
| Asp | Ile | Arg | Gly | Phe | Lys | Thr | Pro | Glu | Lys | Ile | Asp | Leu | Ala | Leu | Cys |
| | | | 130 | | | | | 135 | | | | 140 | | | |
| Asp | Val | Ser | Phe | Ile | Ser | Leu | Tyr | Cys | Ile | Leu | Glu | Ala | Ile | Leu | Pro |
| | | | | | 150 | | | | | 155 | | | | | 160 |
| Leu | Ser | Gly | Glu | Phe | Leu | Thr | Leu | Phe | Lys | Pro | Gln | Phe | Glu | Val | Gly |
| | | | | 165 | | | | | 170 | | | | | 175 | |
| Arg | Thr | Ile | Lys | Arg | Asn | Lys | Lys | Gly | Val | Val | Met | Asp | Lys | Glu | Ala |
| | | | 180 | | | | | 185 | | | | | 190 | | |
| Ile | Leu | Asn | Ala | Leu | Glu | Asn | Phe | Lys | Asn | His | Leu | Lys | Thr | Lys | Asp |
| | | | 195 | | | | | 200 | | | | | 205 | | |
| Phe | Gln | Ile | Leu | Thr | Ile | Gln | Glu | Ser | Leu | Val | Lys | Gly | Lys | Asn | Gly |
| | | | 210 | | | | | 215 | | | | 220 | | | |
| Asn | Val | Glu | Phe | Phe | Ile | His | Phe | Lys | Arg | Ala | | | | | |
| | | | | | 230 | | | | | 235 | | | | | |

Lys Phe Leu Ala Leu Glu Leu Lys
85

(2) INFORMATION FOR SEQ ID NO:1256885_f3_4-AA

Figure 38A - page 48

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 38

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Met Gln Asn Arg Ser His Glu Ile Gln Gly Val Ser His Ile Lys Asn
1 5 10 15

Asn Tyr Lys Phe Phe Thr Lys Glu Leu Asp Asn Tyr Ile Ser Lys Gly
20 25 30

Tyr Arg Ile Glu Glu Ile Tyr Gly Ala Phe Leu Trp Leu Lys Ile Val
35 40 45

Ala Ile Gly Leu Glu Leu Gly Glu Asp Asp Pro Gln Val Val Phe Glu
50 55 60

Ser Ile Asn Ala Thr Gly Val Gln Leu Lys Gly Leu Asp Leu Ile Arg
65 70 75 80

Asn Tyr Leu Met Met Gly Glu Asn Unk Asp Asn Gln Asn Arg Leu Tyr
85 90 95

Asn Thr Tyr Trp Val Pro Leu Glu Asn Trp Leu Gly Glu
100 105

(2) INFORMATION FOR SEQ ID NO:12617677_f3_5 - AA

Figure 39A- page 49

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 106 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 39

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asp | Thr | Ile | Lys | Ser | Ile | Pro | Ile | Arg | Thr | Phe | Ile | Leu | Leu | Tyr |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Lys | Ser | Ser | Pro | Lys | Cys | Val | Val | Leu | Ala | Ser | Ile | Thr | Val | Leu | Phe |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Val | Gly | Ile | Leu | Unk | Ser | Leu | Asn | Ile | Leu | Val | Met | Ile | Lys | Leu | Ile |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Asp | Ile | Val | Val | Asn | Leu | Leu | Gln | Lys | His | Thr | His | Phe | Glu | Tyr | Ser |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Leu | Leu | Leu | Pro | Thr | Leu | Leu | Leu | Trp | Gly | Ala | Leu | Leu | Phe | Leu | Thr |
| 65 | | | | | 70 | | | | 75 | | | | | 80 | |
| His | Val | Phe | Ser | Gly | Asn | Phe | Ile | Lys | Leu | Ala | Asn | His | Tyr | Cys | Arg |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| Thr | Ile | Phe | Tyr | Lys | Tyr | His | His | Ser | Ala | Cys | | | | | |
| | | | 100 | | | | | 105 | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:12694087_f1_2 - AA

Figure 40A - page 50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP40

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| Met | Ile | Phe | Tyr | Thr | Thr | Ile | Lys | Glu | Pro | Leu | Lys | Asn | Leu | Gln | Tyr | 1 | 5 | 10 | 15 |
| Arg | Tyr | Ala | Gln | Phe | Phe | Gly | Lys | Ile | Lys | Pro | Cys | Ser | Phe | Leu | Glu | 20 | 25 | 30 | |
| Ser | Leu | Lys | Ser | Cys | Phe | Phe | Gln | Thr | Tyr | Ser | Phe | Ser | Leu | Thr | Arg | 35 | 40 | 45 | |
| Lys | Gln | Asp | Phe | Lys | Ser | His | Leu | Arg | His | Phe | Ile | Asp | Ser | Ala | His | 50 | 55 | 60 | |
| Ser | Asn | Ala | Leu | Val | Gly | Asn | Leu | Tyr | Arg | Ala | Leu | Phe | Ile | Gly | Asp | 65 | 70 | 75 | 80 |
| Ser | Leu | Asn | Lys | Asp | Leu | Arg | Asp | Arg | Ala | Asn | Ala | Leu | Gly | Ile | Asn | 85 | 90 | 95 | |
| His | Leu | Leu | Ala | Ile | Ser | Gly | Phe | His | Leu | Gly | Ile | Leu | Ser | Ala | Ser | 100 | 105 | 110 | |
| Val | Tyr | Phe | Leu | Phe | Ser | Leu | Phe | Tyr | Thr | Pro | Leu | Gln | Lys | Arg | Tyr | 115 | 120 | 125 | |
| Phe | Pro | Tyr | Arg | Asn | Ala | Phe | Unk | | | | | | | | | 130 | 135 | | |

Figure 41A - page 51

(2) INFORMATION FOR SEQ ID NO:12697338_c2_16 - AA

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 68 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 41

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: rod shape-determining protein envB

Val Lys Pro Asp Leu Val Arg Asp Ile Val Gln Asn Gly Val Val Leu
1 5 10 15

Thr Gly Gly Gly Ala Leu Ile Lys Gly Leu Asp Lys Tyr Leu Ser Asp
20 25 30

Met Val Lys Leu Pro Val Tyr Val Gly Asp Glu Pro Leu Leu Ala Val
35 40 45

Ala Lys Gly Thr Gly Glu Ala Ile Gln Asp Leu Asp Leu Leu Ser Arg
50 55 60

Val Gly Phe Ser Glu
65

(2) INFORMATION FOR SEQ ID NO:12698442_f3_9-AA

Figure 42A - page 52

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 42

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Met Asn Lys Pro Phe Leu Ile Leu Leu Ile Ala Leu Ile Ala Phe Ser
1 5 10 15

Gly Cys Asn Met Arg Lys Tyr Phe Lys Pro Ala Lys His Gln Ile Lys
20 25 30

Ala Lys Arg Ile Ser Leu Thr Ile Cys Lys Lys Ala Ser Phe Arg Leu
35 40 45

Ile Val Met Glu Pro Phe
50

(2) INFORMATION FOR SEQ ID NO:12897656_f1_1 - AA

Figure 43A - page 53

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 43

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Ala | Trp | Asn | Thr | Leu | Val | Glu | Lys | Ile | Ile | Ala | Pro | Lys | His |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Lys | Val | Lys | Ile | Gly | Phe | Val | Gly | Lys | Tyr | Leu | Ser | Leu | Lys | Glu | Ser |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Tyr | Lys | Ser | Leu | Ile | Glu | Ala | Leu | Ile | His | Ala | Gly | Ala | His | Leu | Asp |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Thr | Gln | Val | Asn | Ile | Glu | Trp | Leu | Asp | Ser | Glu | Asn | Phe | Asn | Glu | Lys |
| | | 50 | | | | 55 | | | | | 60 | | | | |
| Thr | Asp | Leu | Glu | Gly | Val | Asp | Ala | Ile | Leu | Val | Pro | Gly | Gly | Phe | Gly |
| | | 65 | | | 70 | | | | 75 | | | | | 80 | |
| Glu | Arg | Gly | Ile | Glu | Gly | Lys | Ile | Cys | Ala | Ile | Gln | Arg | Ala | Arg | Leu |
| | | | 85 | | | | | 90 | | | | | | 95 | |
| Glu | Lys | Leu | Pro | Phe | Leu | Gly | Ile | Cys | Leu | Gly | Met | Gln | Leu | Ala | Ile |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Val | Glu | Phe | Cys | Arg | Lys | Cys | Phe | Arg | Leu | Glu | Arg | Gly | | | |
| | | 115 | | | | | 120 | | | | | 125 | | | |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 44

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Met Thr Lys Ala Phe Val Pro Leu Ser Leu Leu Val Ser Ala Ile Leu
1 5 10 15

Leu Ala Phe Ser Leu Ile Leu Ile Pro Thr Ser Lys Ser Ala Tyr Tyr
20 25 30

Gly Phe Leu Arg Gln Lys Lys Asp Lys Ile Asp Ile Asn Ile Arg Ala
35 40 45

Gly Glu Phe Gly Gln Lys Leu Gly Asp Trp Leu Val Tyr Val Asp Lys
50 55 60

Thr Glu Asn Asn Ser Tyr Asp Asn Leu Val Leu Phe Ser Asn Lys Ser
65 70 75 80

Leu Ser Gln Glu Ser Phe Ile Leu Ala Gln Lys Gly Asn Ile Asn Asn
85 90 95

Gln Asn Gly Val Phe Glu Leu Asn Leu Tyr Asn Gly His Ala Tyr Phe
100 105 110

Thr Gln Gly Asp Lys Met Arg Lys Val Asp Phe Glu Glu Leu His Leu
115 120 125

Arg Asn Lys Leu Lys Ser Phe Asn Ser Asn Asp Ala Ala Tyr Leu Gln
130 135 140

Gly Thr Asp Tyr Leu Gly Tyr Trp Lys Lys Ala Phe Gly Lys Asn Ala
145 150 155 160

Asn Lys Asn Gln Lys Arg Arg Phe Ser Gln Ala Ile Leu Val Ser Leu
165 170 175

Phe Pro Leu Ala Ser Val Phe Leu Ile Pro Leu Phe Gly Ile Ala Asn
180 185 190

Pro Arg Phe Lys Thr Asn Trp Ser Tyr Phe Unk Val Leu Gly Ala Val
195 200 205

Gly Val Tyr Phe Leu Met Val His Val Ile Ser Thr Asp Leu Phe Leu
210 215 220

Met Thr Phe Phe Phe Pro Phe Ile Trp Ala Phe Ile Ser Tyr Leu Leu
225 230 235 240

Phe Arg Lys Phe Ile Leu Lys Arg Tyr
245

Figure 44A - page 55

Figure 45A - page 56

(2) INFORMATION FOR SEQ ID NO:13178562_c3_14 - AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 45

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

[illegible]

(2) INFORMATION FOR SEQ ID NO:134666_c3_6 - AA

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

Figure 46A - page 57

(ii) MOLECULE TYPE: protein

HPP 46

(iii) HYPOTHETICAL: YES

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Leu | Phe | Leu | Ile | Phe | Met | Gly | Met | Ile | Ile | Gly | Leu | Ile | Leu |
| 1 | | | | 5 | | | | 10 | | | | | 15 | | |
| Glu | Pro | Val | Pro | Ser | Gly | Leu | Ile | Ala | Leu | Ser | Ala | Leu | Val | Leu | Cys |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Ile | Ala | Leu | Lys | Ile | Gly | Ala | Ser | Ser | Glu | Val | Ala | Ser | Ala | Asn | Lys |
| | | 35 | | | | | 40 | | | | | 45 | | | |

Ala

Figure 47A - page 58

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

HPP 47

Val Met Ala Gln Ser Leu Leu Val His Ala Phe Phe Ala Ala Leu Leu
1 5 10 15

Ala Leu Ala Phe Met Ile Asn Leu Tyr Thr Leu Phe Lys Glu Lys Asn
20 25 30

Phe Ile Gln Leu Asn Arg Lys Ile Tyr Leu Val Met Pro Ala Ile Tyr
35 40 45

Ile Leu Leu Ser Ile Ala Leu Leu Ser Gly Val Phe Ile Trp Ala Met
50 55 60

Gln Gln Phe Glu Phe Ser Phe Ser Ala Val Val Met Leu Leu Gly Leu
65 70 75 80

Leu Leu Met Leu Ile Ala Glu Ile Lys Arg His Lys Ser Val Lys Phe
85 90 95

Ala Ile Thr Lys Lys Glu Arg Met Lys Ala Tyr Ile Lys Lys Ala Lys
100 105 110

Ile Leu Tyr Phe Leu Glu Thr Ile Leu Ile Ile Val Leu Met Gly Ile
115 120 125

(2) INFORMATION FOR SEQ ID NO:1365943_f1_1-AA

Figure 48A - page 59

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 48

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Val Arg Asn Val Val Leu Phe Ile Leu Thr Ala Ile Phe Leu Ala Phe
1 5 10 15

Met Leu Leu Val Ser Tyr Cys Met Pro His Tyr Ser Val Ala Val Ile
20 25 30

Ser Gly Val Glu Val Lys Arg Met Asn Glu Asn Glu Asn Thr Pro Asn
35 40 45

Asn Lys Glu Val Lys Thr Leu Ala Arg Asp Val Tyr Phe Val Gln Thr
50 55 60

Tyr Asp Pro Lys Asp Gln Lys Ser Val Thr Val Tyr Arg Asn Glu Asp
65 70 75 80

Thr Arg Phe Gly Phe Pro Phe Tyr Phe Lys Phe Asn Ser
85 90

(2) INFORMATION FOR SEQ ID NO:13673328_f1_3-AA

Figure 50A - page 61

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 50

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| Val | His | Phe | Thr | Cys | Ile | Phe | Leu | Thr | Leu | Leu | Lys | Trp | Ile | Leu | Pro | 1 | 5 | 10 | 15 |
| Ala | Lys | Asn | Lys | Gln | Ala | Cys | Lys | Lys | Ala | Thr | Asn | Gln | Ile | His | Ser | 20 | 25 | 30 | |
| Arg | Unk | Ala | Lys | His | Pro | Ala | Lys | Tyr | Pro | Pro | Ser | Ser | Ile | Asn | Pro | 35 | 40 | 45 | |
| Ser | Ile | Gln | Ala | Gly | Ile | Gln | Gly | Val | Met | Gln | Gly | Phe | Gly | Ala | Leu | 50 | 55 | 60 | |
| Ser | Ser | Unk | Leu | Glu | Unk | Pro | Unk | Phe | Val | Unk | Unk | Ala | Lys | Cys | Gly | 65 | 70 | 75 | 80 |
| Trp | Ile | Gly | Gly | Phe | Glu | His | Tyr | Leu | Ser | Pro | Leu | Tyr | Gly | Trp | Gly | 85 | 90 | 95 | |
| Lys | Ile | His | Asp | Gly | Ala | His | Cys | Asp | Leu | Met | Gln | Lys | Asp | Ala | Asn | 100 | 105 | 110 | |
| Gly | Arg | Gly | Ile | Gly | Leu | Glu | Lys | Gly | Leu | Pro | Pro | Phe | Lys | Gly | Leu | 115 | 120 | 125 | |

(2) INFORMATION FOR SEQ ID NO:1370202 c3 6-11

Figure 51A - page 62

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 51

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | |
|-----------|-----|-----------|------------|-----------|-----------|-----------|-----------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| Met 1 | Gln | Lys | Phe 5 | Phe | Ser | Arg | Phe | Arg 10 | Arg | Trp | Ala | Leu | Pro | Phe 15 | Tyr |
| Phe | Val | Ser | Ala 20 | Leu | Ala | Ala | Ile | Asp 25 | Ile | Asp | Glu | Val | Thr 30 | Glu | Ala |
| Gln | Ala | Asn 35 | Ser | Ile | Lys | Leu | Ser 40 | Asp | Gln | Leu | Val | Ser 45 | Leu | Ser | Asp |
| Lys 50 | Leu | Leu | Glu | Lys | Ala | Val 55 | Asp | Arg | Gly | Arg | Asn 60 | Thr | Asp | His | Leu |
| Lys 65 | Asp | Leu | Asn | Asp | Leu 70 | His | Glu | Lys | Ile | Lys 75 | His | Leu | Arg | Leu | Ile 80 |
| Leu | Glu | Pro | Lys | Pro 85 | Lys | Gly | Lys | Glu | Asp 90 | Ser | Pro | Asn | Leu | Gly 95 | Gly |
| Asn | Lys | Asp | Met 100 | Lys | Thr | Val | Glu | Ile 105 | Gly | Ser | Gly | | | | |

(2) INFORMATION FOR SEQ ID NO:13704718 f1 1- AA

Figure 52A - page 63

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 117 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP52

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

[illegible]

(2) INFORMATION FOR SEQ ID NO:13723593_f1_1- AA

Figure 53A - page 64

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 53

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Met Ile Tyr Leu Gly Lys Lys Asn Phe Asn Ala Leu Leu Lys Gly Ala
1 5 10 15

Tyr Leu Met Asp Glu His Phe Arg Asn Ala Pro Phe Glu Ser Asn Leu
20 25 30

Pro Val Leu Met Gly Leu Ile Trp Arg Val Val Tyr Leu Thr Phe Phe
35 40 45

Pro Ile Gln Lys Ala Thr
50

(2) INFORMATION FOR SEQ ID NO:13726562_f1_1 - AA

Figure 54A - page 65

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 287 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 54

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: HYPOTHETICAL ABC TRANSPORTER

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Ala | Lys | Ser | Lys | Ala | Unk | Thr | Leu | Lys | Val | Phe | Ser | Lys | Phe |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Phe | Ser | Asn | Phe | Lys | Ile | Thr | Lys | Leu | Lys | Asp | Asn | His | Glu | Glu | Ala |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| His | Lys | Leu | Phe | Gly | Glu | Asn | Ser | Arg | Lys | Ala | His | Asp | Thr | Glu | Ile |
| | | | 35 | | | | 40 | | | | | 45 | | | |
| Ile | Tyr | Ser | Thr | Leu | Gln | Val | Val | Pro | Arg | Tyr | Ser | Ile | Glu | Thr | Val |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Gly | Phe | Ser | Leu | Leu | Ile | Leu | Ala | Val | Ala | Tyr | Ile | Leu | Phe | Lys | Tyr |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 |
| Gly | Glu | Ala | Arg | Met | Val | Leu | Pro | Thr | Ile | Ser | Met | Tyr | Ala | Leu | Ala |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| Leu | Tyr | Arg | Ile | Leu | Pro | Ser | Val | Thr | Gly | Val | Ile | Ser | Tyr | Tyr | Asn |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Glu | Ile | Ala | Tyr | Asn | Gln | Leu | Ala | Thr | Asn | Val | Val | Phe | Lys | Ser | Leu |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| Ser | Lys | Thr | Ile | Val | Glu | Glu | Asp | Leu | Val | Pro | Leu | Asp | Phe | Asn | Glu |
| | 130 | | | | | 135 | | | | | 140 | | | | |
| Lys | Ile | Thr | Leu | Gln | Asn | Ile | Ser | Phe | Ala | Tyr | Lys | Ser | Lys | His | Pro |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 |
| Val | Leu | Lys | Asn | Phe | Asn | Leu | Thr | Ile | Gln | Lys | Gly | Gln | Lys | Ile | Ala |
| | | | | 165 | | | | | 170 | | | | | 175 | |
| Leu | Ile | Gly | His | Ser | Gly | Cys | Gly | Lys | Ser | Thr | Leu | Ala | Asp | Ile | Ile |
| | | | 180 | | | | | 185 | | | | | 190 | | |
| Met | Gly | Leu | Thr | Tyr | Pro | Lys | Ser | Gly | Glu | Ile | Phe | Ile | Asp | Asn | Thr |
| | | 195 | | | | 200 | | | | | | 205 | | | |
| Leu | Leu | Thr | Ser | Glu | Asn | Arg | Arg | Ser | Trp | Arg | Lys | Lys | Ile | Gly | Tyr |
| | 210 | | | | | 215 | | | | | 220 | | | | |
| Ile | Pro | Gln | Asn | Ile | Tyr | Leu | Phe | Asp | Gly | Thr | Val | Gly | Asp | Asn | Ile |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 |

Ala Phe Gly Ser Ala Ile Asp Glu Lys Arg Leu Ile Lys Val Cys Lys Figure 54A-page 66
245 250 255

Met Ala His Ile Tyr Asp Phe Leu Cys Glu His Glu Gly Leu Lys Thr
260 265 270

Gln Val Gly Glu Gly Ala Leu Ser Leu Ala Ala Val Lys Asn Ser Ala
275 280 285

(2) INFORMATION FOR SEQ ID NO:13727311_c3_16-AA

Figure 55A -page 67

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 272 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 55

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: flagellin

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Ala | Phe | Gln | Val | Asn | Thr | Asn | Ile | Asn | Ala | Met | Asn | Ala | His | Val | |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | | |
| Gln | Ser | Ala | Leu | Thr | Gln | Asn | Ala | Leu | Lys | Thr | Ser | Leu | Glu | Arg | Leu | |
| | | | 20 | | | | | 25 | | | | | 30 | | | |
| Ser | Ser | Gly | Leu | Arg | Ile | Asn | Lys | Ala | Ala | Asp | Asp | Ala | Ser | Gly | Met | |
| | | 35 | | | | | 40 | | | | | 45 | | | | |
| Thr | Val | Ala | Asp | Ser | Leu | Arg | Ser | Gln | Ala | Ser | Ser | Leu | Gly | Gln | Ala | |
| | 50 | | | | | 55 | | | | | 60 | | | | | |
| Ile | Ala | Asn | Thr | Asn | Asp | Gly | Met | Gly | Ile | Ile | Gln | Val | Ala | Asp | Lys | |
| 65 | | | | | 70 | | | | 75 | | | | | 80 | | |
| Ala | Met | Asp | Glu | Gln | Leu | Lys | Ile | Leu | Asp | Thr | Val | Lys | Val | Lys | Ala | |
| | | | | 85 | | | | | 90 | | | | | 95 | | |
| Thr | Gln | Ala | Ala | Gln | Asp | Gly | Gln | Thr | Thr | Glu | Ser | Arg | Lys | Ala | Ile | |
| | | | 100 | | | | | 105 | | | | | 110 | | | |
| Gln | Ser | Asp | Ile | Val | Arg | Leu | Ile | Gln | Gly | Leu | Asp | Asn | Ile | Gly | Asn | |
| | | 115 | | | | | 120 | | | | | 125 | | | | |
| Thr | Thr | Thr | Tyr | Asn | Gly | Gln | Ala | Leu | Leu | Ser | Gly | Gln | Phe | Thr | Asn | |
| | | 130 | | | | 135 | | | | | 140 | | | | | |
| Lys | Glu | Phe | Gln | Val | Gly | Ala | Tyr | Ser | Asn | Gln | Ser | Ile | Lys | Ala | Ser | |
| 145 | | | | | 150 | | | | 155 | | | | | 160 | | |
| Ile | Gly | Ser | Thr | Thr | Ser | Asp | Lys | Ile | Gly | Gln | Val | Arg | Ile | Ala | Thr | |
| | | | | 165 | | | | | 170 | | | | | 175 | | |
| Gly | Ala | Leu | Ile | Thr | Ala | Ser | Gly | Asp | Ile | Ser | Leu | Thr | Phe | Lys | Gln | |
| | | | 180 | | | | | 185 | | | | | 190 | | | |
| Val | Asp | Gly | Val | Asn | Asp | Val | Thr | Leu | Glu | Ser | Val | Lys | Val | Ser | Ser | |
| | | 195 | | | | | 200 | | | | | 205 | | | | |
| Ser | Ala | Gly | Thr | Gly | Ile | Gly | Val | Leu | Ala | Glu | Val | Ile | Asn | Lys | Asn | |
| | | 210 | | | | 215 | | | | | 220 | | | | | |
| Ser | Asn | Arg | Thr | Gly | Val | Lys | Ala | Tyr | Ala | Ser | Val | Ile | Thr | Thr | Ser | |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Val | Ala | Val | Gln | Ser | Gly | Ser | Leu | Ser | Asn | Leu | Thr | Leu | Asn | Gly |
| | | | | 245 | | | | | 250 | | | | | 255 | |
| Ile | His | Leu | Gly | Asn | Ile | Ala | Asp | Ile | Lys | Lys | Thr | Thr | Gln | Thr | Glu |
| | | | 260 | | | | | 265 | | | | | 270 | | |

Gly

(2) INFORMATION FOR SEQ ID NO:1385937_f1_3 - AA

Figure 56A - page 69

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP56

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Asp | Ile | Trp | Ile | Asp | Met | Ile | Ile | Cys | Ile | Phe | Tyr | Leu | Leu | 1 | 5 | 10 | 15 |
| Phe | Phe | Thr | Thr | Pro | Tyr | Ile | Val | Gly | Asp | Ile | Leu | Gln | Leu | Lys | Phe | 20 | 25 | 30 | |
| Ile | Arg | Gln | Lys | Leu | Cys | Glu | Lys | Pro | Val | Leu | Leu | Pro | Gln | Lys | Asp | 35 | 40 | 45 | |
| Tyr | Glu | Glu | Ala | Gly | Asn | Tyr | Ala | Ile | Arg | Lys | Met | Gln | Leu | Ser | Ile | 50 | 55 | 60 | |
| Ile | Ser | Gln | Ile | Leu | Asp | Gly | Val | Ile | Phe | Ala | Gly | Trp | Val | Phe | Phe | 65 | 70 | 75 | 80 |
| Gly | Leu | Thr | His | Leu | Glu | Asp | Leu | Thr | His | Tyr | Leu | Asn | Leu | Pro | Glu | 85 | 90 | 95 | |
| Thr | Leu | Gly | Tyr | Leu | Val | Phe | Ala | Leu | Leu | Phe | Leu | Ala | Ile | Gln | Ser | 100 | 105 | 110 | |
| Val | Leu | Ala | Leu | Pro | Ile | Ser | Tyr | Tyr | Thr | Thr | Met | His | Leu | Asp | Lys | 115 | 120 | 125 | |
| Glu | Phe | Gly | Phe | Ser | Lys | Val | Ser | Leu | Ser | Leu | Phe | Phe | Lys | Asp | Phe | 130 | 135 | 140 | |
| Phe | Lys | Gly | Leu | Leu | Leu | Thr | Leu | Gly | Val | Gly | Leu | Leu | Leu | Ile | Tyr | 145 | 150 | 155 | 160 |
| Thr | Leu | Ile | Met | Ile | Ile | Glu | His | Val | Glu | His | Trp | Glu | Ile | Ser | Ser | 165 | 170 | 175 | |
| Phe | Phe | Val | Val | Phe | Val | Phe | Met | Ile | Leu | Ala | Asn | Leu | Phe | Leu | Pro | 180 | 185 | 190 | |

(2) INFORMATION FOR SEQ ID NO:13865928_f2_7-AA

Figure 57 - page 70

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 57

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: VIRULENCE FACTOR MVIN

| | | | | | | | | | | | | | | | |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|-----------|------------|------------|------------|------------|-----------|------------|
| Met 1 | Leu | Lys | Lys | Ile 5 | Phe | Leu | Thr | Asn | Ser 10 | Leu | Gly | Ile | Leu | Cys 15 | Ser |
| Arg | Ile | Phe | Gly 20 | Phe | Leu | Arg | Asp | Leu 25 | Met | Met | Ala | Asn | Ile 30 | Leu | Gly |
| Ala | Gly | Val 35 | Tyr | Ser | Asp | Ile | Phe 40 | Phe | Val | Ala | Phe | Lys 45 | Leu | Pro | Asn |
| Leu | Phe 50 | Arg | Arg | Ile | Phe | Ala 55 | Glu | Gly | Ser | Phe | Ser 60 | Gln | Ser | Phe | Leu |
| Pro 65 | Ser | Phe | Ile | Arg | Ser 70 | Ser | Ile | Lys | Gly | Gly 75 | Phe | Ala | Ser | Leu | Val 80 |
| Gly | Leu | Ile | Phe | Cys 85 | Gly | Val | Leu | Phe | Met 90 | Trp | Cys | Leu | Leu | Val 95 | Ala |
| Leu | Asn | Pro | Leu 100 | Trp | Leu | Thr | Lys | Leu 105 | Leu | Ala | Tyr | Gly | Phe 110 | Asp | Glu |
| Glu | Thr | Leu 115 | Lys | Leu | Cys | Thr | Pro 120 | Ile | Val | Ala | Ile | Asn 125 | Phe | Trp | Tyr |
| Leu | Leu 130 | Leu | Val | Phe | Ile | Thr 135 | Thr | Phe | Leu | Gly | Ala 140 | Leu | Leu | Gln | Tyr |
| Lys 145 | His | Ser | Phe | Phe | Ala 150 | Ala | Leu | Met | Arg | Lys 155 | Leu | Thr | Gln | Phe | Met 160 |
| His | Asp | Phe | Ser | Pro 165 | Phe | Asp | Phe | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:14063518_c1_23-AA

Figure 58A - page 71

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 123 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPD58

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: flagellar basal-body rod proteins

Met Asn Val Lys Arg Arg Asp Met Leu Met Pro Asn Ala Glu Ile Glu
1 5 10 15

Val Asp Gln Asn Gly Gly Ile Thr Phe Arg Asp Asn Glu Ala Gln Ile
20 25 30

Gln Ala Gly Ala Leu Ala Leu Val Ser Phe Ser Glu Pro Lys Asn Leu
35 40 45

Lys Lys Ile Gly Gln Asn Leu Tyr Thr Tyr Gln Gly Glu Gly Val His
50 55 60

Gln Val Ser Asp Ser Gly Ala Leu Arg Gln Ser Met Leu Glu Lys Ser
65 70 75 80

Asn Val Asn Ala Val Arg Glu Met Ser Thr Leu Ile Glu Ile Asn Arg
85 90 95

Phe Leu Asp Met Tyr Ser Lys Val Leu Lys Thr His Gln Asp Asp Met
100 105 110

```

Asn Ala Glu Ala Ile Asn Lys Leu Ala Thr Lys Ala
      115                      120

```

(2) INFORMATION FOR SEQ ID NO:1408_c3_19: - AA

Figure 59A - page 72

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 59

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | |
|------------|------------|------------|------------|-----------|------------|------------|------------|------------|-----------|-----------|------------|------------|------------|-----------|-----------|
| Met 1 | Asn | Leu | Glu | Val 5 | Ala | Leu | Lys | Ala | Phe 10 | Glu | Thr | Leu | Leu | Pro 15 | Cys |
| Asn | Lys | Gln | Glu 20 | Val | Leu | Lys | Asn | Leu 25 | Lys | Pro | Leu | Asp | Leu 30 | Ile | Gly |
| Arg | Cys | Glu 35 | Leu | Leu | Ser | Pro | Asn 40 | Ile | Leu | Ile | Asp | Val 45 | Gly | His | Asn |
| Pro | His 50 | Ser | Ala | Lys | Ala | Leu 55 | Lys | Glu | Glu | Ile | Lys 60 | Arg | Ile | Phe | Asn |
| Ala 65 | Pro | Ile | Val | Leu | Ile 70 | Tyr | Asn | Cys | Tyr | Gln 75 | Asp | Lys | Asp | Ala | Phe 80 |
| Leu | Val | Leu | Glu | Ile 85 | Leu | Lys | Ser | Val | Val 90 | Lys | Lys | Val | Leu | Ile 95 | Leu |
| Glu | Leu | His | Asn 100 | Glu | Arg | Ile | Ile | Gln 105 | Leu | Glu | Lys | Leu | Lys 110 | Gly | Ile |
| Leu | Glu | Thr 115 | Leu | Gly | Leu | Glu | His 120 | Ala | Leu | Phe | Glu | Glu 125 | Leu | Lys | Glu |
| Asn | Glu 130 | Asn | Tyr | Leu | Val | Tyr 135 | Gly | Ser | Phe | Leu | Val 140 | Ala | Asn | Ala | Phe |
| Tyr 145 | Glu | Arg | Tyr | Pro | Lys 150 | Lys | Arg | Asp | | | | | | | |

[illegible]

(2) INFORMATION FOR SEQ ID NO:1411681 f2 1 -AA

Figure: 61A - page 74

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 58 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 61

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: beginning of protein???

Met Ala Ile Gly Phe Pro Leu Val Phe Gly Ile Leu Leu Thr Leu Phe
1 5 10 15

Ser Arg Ser Tyr Trp Arg Glu Phe Gly Gly Val Ser Gly Val Leu Trp
20 25 30

Arg Ala Ser Gly Phe Ser Gly Ala Lys Val Glu Arg Asn Leu Glu Arg
35 40 45

Asp Pro His Ala Phe Phe Thr His Cys Asp Phe
50 55

(2) INFORMATION FOR SEQ ID NO:1416312_c1_10 - AA

Figure 62A - page 75

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 221 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP62

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Lys | Lys | Ala | Lys | Val | Phe | Trp | Cys | Cys | Phe | Lys | Met | Ile | Arg | 1 | 5 | 10 | 15 |
| Trp | Leu | Tyr | Leu | Ala | Val | Phe | Phe | Leu | Leu | Ser | Val | Ser | Asp | Ala | Lys | 20 | 25 | 30 | |
| Glu | Ile | Ala | Met | Gln | Arg | Phe | Asp | Lys | Gln | Asn | His | Lys | Ile | Phe | Glu | 35 | 40 | 45 | |
| Ile | Leu | Ala | Asp | Lys | Val | Ser | Ala | Lys | Asp | Asn | Val | Ile | Thr | Ala | Ser | 50 | 55 | 60 | |
| Gly | Asn | Ala | Ile | Leu | Leu | Asn | Tyr | Asp | Val | Tyr | Ile | Leu | Ala | Asp | Lys | 65 | 70 | 75 | 80 |
| Val | Arg | Tyr | Asp | Thr | Lys | Thr | Lys | Glu | Ala | Leu | Leu | Glu | Gly | Asn | Ile | 85 | 90 | 95 | |
| Lys | Val | Tyr | Arg | Gly | Glu | Gly | Leu | Leu | Val | Lys | Thr | Asp | Tyr | Val | Lys | 100 | 105 | 110 | |
| Leu | Ser | Leu | Asn | Glu | Lys | Tyr | Glu | Ile | Ile | Phe | Pro | Phe | Tyr | Val | Gln | 115 | 120 | 125 | |
| Asp | Ser | Val | Ser | Gly | Ile | Trp | Val | Ser | Ala | Asp | Ile | Ala | Ser | Gly | Lys | 130 | 135 | 140 | |
| Asp | Gln | Lys | Tyr | Lys | Ile | Lys | Asn | Met | Ser | Ala | Ser | Gly | Cys | Ser | Ile | 145 | 150 | 155 | 160 |
| Asp | Asn | Pro | Ile | Trp | His | Val | Asn | Ala | Thr | Ser | Gly | Ser | Phe | Asn | Met | 165 | 170 | 175 | |
| Gln | Lys | Ser | His | Leu | Ser | Met | Trp | Asn | Pro | Lys | Ile | Tyr | Val | Gly | Asp | 180 | 185 | 190 | |
| Ile | Pro | Val | Leu | Tyr | Leu | Pro | Tyr | Ile | Phe | Met | Ser | Thr | Ser | Asn | Lys | 195 | 200 | 205 | |
| Arg | Thr | Thr | Gly | Phe | Leu | Tyr | Pro | Glu | Phe | Gly | Thr | Ser | Thr | 210 | 215 | 220 | | | |

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Met Leu Asp Phe Asp Leu Val Leu Phe Gly Ala Thr Gly Asp Leu Ala
1 5 10 15

Met Arg Lys Leu Phe Val Ser Leu Tyr Glu Ile Tyr Ile Ser Phe Met
20 25 30

Val Leu Lys Thr Ile Leu Gly Leu Ser His Arg Gly Val Arg Ser Tyr
35 40 45

Pro Met Lys Ser Phe
50

(2) INFORMATION FOR SEQ ID NO:14313885_c3_11: - AA

Figure 64 A -page 77

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP64

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: alkylphosphonate uptake genes A through Q

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gln | Asp | Leu | Pro | Pro | Cys | Pro | Lys | Arg | Asn | Asp | Ala | Tyr | Thr | Tyr |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| His | Asp | Gly | Thr | Gln | Phe | Val | Cys | Ser | Ser | Cys | Leu | Tyr | Glu | Trp | Asn |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Gly | Asn | Glu | Ile | Ser | Asn | Glu | Glu | Leu | Ile | Val | Lys | Asp | Cys | His | Asn |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Asn | Leu | Leu | Gln | Asn | Gly | Asp | Ser | Val | Ile | Leu | Ile | Lys | Asp | Leu | Lys |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Val | Lys | Gly | Ser | Ser | Leu | Val | Leu | Lys | Lys | Gly | Thr | Lys | Ile | Lys | Asn |
| 65 | | | | | 70 | | | | | 75 | | | | 80 | |
| Ile | Lys | Leu | Val | Asn | Ser | Asp | His | Asn | Val | Asp | Cys | Lys | Val | Glu | Gly |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| Gln | Ser | Leu | Ser | Leu | Lys | Ser | Glu | Phe | Leu | Lys | Lys | Ala | | | |
| | | | 100 | | | | | 105 | | | | | | | |

Figure 65A - page 78

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 65

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: outer membrane 30.2K protein

Val Asp Gly Ala Ile Ile Thr Gly Asn Tyr Ala Leu Gln Ala Lys Leu
1 5 10 15

Thr Gly Ala Leu Phe Ser Glu Asp Lys Asp Ser Pro Tyr Ala Asn Leu
20 25 30

Val Ala Ser Arg Glu Asp Asn Ala Gln Asp Glu Ala Ile Lys Ala Leu
35 40 45

Ile Glu Ala Leu Gln Ser Glu Lys Thr Arg Lys Phe Ile Leu Asp Thr
50 55 60

Tyr Lys Gly Ala Ile Ile Pro Ala Phe
65 70

(2) INFORMATION FOR SEQ ID NO:14344378_f1_1-AA

Figure 66A - page 79

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 66

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| Met | Ser | Ile | Gly | Ile | Met | Met | Leu | Asn | Gln | Leu | Ala | Phe | Leu | Thr | Ser | 1 | 5 | 10 | 15 |
| Leu | Lys | Leu | Lys | Asp | Ala | Asp | Ile | Glu | Ile | Val | Glu | Thr | His | His | Asn | 20 | 25 | 30 | |
| Leu | Lys | Lys | Asp | Ala | Pro | Ser | Gly | Thr | Ala | Leu | Ser | Leu | Tyr | Glu | Thr | 35 | 40 | 45 | |
| Cys | Unk | Lys | Ala | Arg | Gly | Tyr | Asp | Glu | Lys | Asn | Ala | Leu | Ile | Thr | His | 50 | 55 | 60 | |
| Arg | Glu | Gly | Leu | Arg | Ser | Lys | Glu | Ser | Ile | Gly | Ile | Ala | Thr | Leu | Arg | 65 | 70 | 75 | 80 |
| Gly | Gly | Asp | Val | Ala | Gly | Lys | His | Thr | Ile | Gly | Phe | Tyr | Leu | Glu | Gly | 85 | 90 | 95 | |
| Glu | Tyr | Ile | Glu | Leu | Ser | His | Thr | Ala | Thr | Asn | Arg | Ser | Ile | Phe | Ala | 100 | 105 | 110 | |
| Lys | Gly | Ala | Leu | Glu | Val | Ala | Leu | Trp | Leu | Lys | Asp | Lys | Ala | Ala | Lys | 115 | 120 | 125 | |
| Lys | Tyr | Glu | Ile | Ser | Glu | Met | Phe | Gly | | | | | | | | 130 | 135 | | |

Figure 67A - page 80

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 236 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 67

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Val 1 | Phe | Thr | Met | Leu 5 | Val | Leu | Val | Leu | Ser 10 | Asp | Asn | Phe | Leu | Gly 15 | Leu |
| Phe | Ile | Gly | Trp 20 | Glu | Gly | Val | Gly | Leu 25 | Cys | Ser | Tyr | Leu | Leu 30 | Ile | Gly |
| Phe | Trp | Tyr 35 | His | Lys | Lys | Ser | Ala 40 | Asn | Asn | Ala | Ser | Ile 45 | Glu | Ala | Phe |
| Val | Met 50 | Asn | Arg | Ile | Thr | Asp 55 | Leu | Gly | Met | Leu | Met 60 | Gly | Ile | Ile | Leu |
| Ile 65 | Phe | Trp | Asn | Phe | Gly 70 | Thr | Leu | Gln | Tyr | Lys 75 | Glu | Val | Phe | Ser | Met 80 |
| Leu | Asn | Asn | Ala | Asp 85 | Tyr | Ser | Met | Leu | Phe 90 | Tyr | Ile | Ser | Val | Phe 95 | Leu |
| Phe | Ile | Gly | Ala 100 | Met | Gly | Lys | Ser | Ala 105 | Gln | Phe | Pro | Met | His 110 | Thr | Trp |
| Leu | Ala | Asn 115 | Ala | Met | Glu | Gly | Pro 120 | Thr | Pro | Val | Ser | Ala 125 | Leu | Ile | His |
| Ala | Thr 130 | Thr | Met | Val | Thr | Ala 135 | Gly | Val | Tyr | Leu | Ile 140 | Ile | Arg | Ala | Asn |
| Pro 145 | Leu | Tyr | Ser | Ala | Val 150 | Phe | Glu | Val | Gly | Tyr 155 | Phe | Ile | Ala | Cys | Leu 160 |
| Gly | Ala | Phe | Val | Ala 165 | Leu | Phe | Gly | Ala | Ser 170 | Met | Ala | Leu | Val | Asn 175 | Lys |
| Asp | Leu | Lys | Arg 180 | Ile | Val | Glu | Tyr | Ser 185 | Thr | Leu | Ser | Gln | Leu 190 | Gly | Leu |
| Tyr | Val | Cys 195 | Ser | Gly | Arg | Ala | Trp 200 | Gly | Leu | Cys | Asp | Arg 205 | Ala | Phe | Pro |
| Pro | Leu 210 | Tyr | Ala | Cys | Val | Leu 215 | Gln | Ile | Pro | Pro | Phe 220 | Leu | Arg | Leu | Arg |
| Gln 225 | Cys | His | Ala | Cys | Asp 230 | Gly | Arg | Gln | Ser | Gly 235 | Tyr | Tyr | | | |

(2) INFORMATION FOR SEQ ID NO:14480927_c1_17 - AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

Figure 68A - page 81

(ii) MOLECULE TYPE: protein

HPP 68

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Cys | Leu | Gly | Leu | Ala | Asp | Val | Met | Val | Val | Leu | Ser | Leu | His | Leu |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Asn | Leu | Asn | Pro | Thr | Asn | Pro | Lys | Trp | Leu | Asn | Arg | Asp | Arg | Leu | Val |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Phe | Ser | Gly | Gly | His | Ala | Ser | Ala | Leu | Val | Tyr | Ser | Leu | Leu | His | Leu |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Trp | Gly | Phe | Asp | Leu | Ser | Leu | Asp | Asp | Leu | Lys | Arg | Phe | Arg | Gln | Leu |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| His | Ser | Lys | Thr | Pro | Gly | His | Pro | Glu | Leu | His | His | Thr | Glu | Gly | Ile |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 |
| Glu | Ile | Thr | Thr | Thr | Phe | Arg | Ala | Arg | Phe | Cys | | | | | |
| | | | | 85 | | | | | 90 | | | | | | |

Figure 69A-page 82

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 96 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 69

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: chloramphenicol resistance protein

Met Met Ile Thr Lys Gln Ser Tyr Gln Arg Phe Ala Leu Met Arg Val
1 5 10 15

Phe Val Phe Ser Leu Ser Ala Phe Ile Phe Asn Thr Thr Glu Phe Val
20 25 30

Pro Val Ala Leu Leu Ser Asp Ile Ala Lys Ser Phe Glu Met Glu Ser
35 40 45

Ala Thr Val Gly Leu Met Ile Thr Ala Tyr Ala Trp Val Val Ser Leu
50 55 60

Gly Ser Leu Pro Leu Met Leu Leu Ser Ala Lys Ile Glu Arg Lys Arg
65 70 75 80

Leu Leu Leu Phe Leu Phe Ala Leu Phe Ile Phe Ser His Ile Leu Ser
85 90 95

Arg

(2) INFORMATION FOR SEQ ID NO:14570443_f3_15 - AA

Figure 70A - page 83

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 70

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Leu | Arg | Ala | Ser | Val | Leu | Ile | Gly | Val | Ala | Ile | Leu | Cys | Leu | 1 | 5 | 10 | 15 |
| Ile | Leu | Ser | Ala | Cys | Ser | Asn | Tyr | Ala | Lys | Lys | Val | Val | Lys | Gln | Lys | 20 | 25 | 30 | |
| Asn | His | Val | Tyr | Thr | Pro | Val | Tyr | Asn | Glu | Leu | Ile | Glu | Lys | Tyr | Ser | 35 | 40 | 45 | |
| Glu | Ile | Pro | Leu | Asn | Asp | Lys | Leu | Lys | Asp | Thr | Pro | Phe | Met | Val | Gln | 50 | 55 | 60 | |
| Val | Lys | Leu | Pro | Asn | Tyr | Lys | Asp | Tyr | Leu | Leu | Asp | Asn | Lys | Gln | Val | 65 | 70 | 75 | 80 |
| Val | Leu | Thr | Phe | Lys | Leu | Val | His | His | Ser | Lys | Lys | Ile | Thr | Leu | Ile | 85 | 90 | 95 | |
| Gly | Asp | Ala | Asn | Lys | Ile | Leu | Gln | Tyr | Lys | Asn | Tyr | Phe | Gln | Ala | Asn | 100 | 105 | 110 | |
| Gly | Ala | Arg | Ser | Asp | Ile | Asp | Phe | Tyr | Leu | Gln | Pro | Thr | Leu | Asn | Gln | 115 | 120 | 125 | |
| Lys | Gly | Val | Val | Met | Ile | Ala | Ser | Asn | Tyr | Asn | Asp | Asn | Pro | Asn | Asn | 130 | 135 | 140 | |
| Lys | Glu | Lys | Pro | Gln | Thr | Phe | Asp | Val | Leu | Gln | Gly | Ser | Gln | Pro | Met | 145 | 150 | 155 | 160 |
| Leu | Gly | Ala | Asn | Thr | Lys | Asn | Leu | His | Gly | Tyr | Asp | Val | Ser | Gly | Ala | 165 | 170 | 175 | |
| Asn | Asn | Lys | Gln | Val | Ile | Asn | Glu | Val | Ala | Arg | Glu | Lys | Ala | Gln | Leu | 180 | 185 | 190 | |
| Glu | Lys | Ile | Asn | Gln | Tyr | Tyr | Lys | Thr | Leu | Leu | Gln | Asp | Lys | Glu | Gln | 195 | 200 | 205 | |
| Glu | Tyr | Thr | Thr | Arg | Lys | Asn | Asn | Gln | Arg | Glu | Ile | Leu | Glu | Thr | Leu | 210 | 215 | 220 | |
| Ser | Asn | Arg | Ala | Gly | Tyr | Gln | Met | Arg | Gln | Asn | Val | Ile | Ser | Ser | Glu | 225 | 230 | 235 | 240 |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Phe | Lys | Asn | Gly | Asn | Leu | Asn | Met | Gln | Ala | Lys | Glu | Glu | Glu | Val |
| | | | | 245 | | | | | 250 | | | | | 255 | |
| Arg | Glu | Lys | Leu | Gln | Glu | Glu | Arg | Glu | Asn | Glu | Tyr | Leu | Arg | Asn | Gln |
| | | | 260 | | | | | 265 | | | | | 270 | | |
| Ile | Arg | Ser | Leu | Leu | Ser | Gly | Lys | | | | | | | | |
| | | 275 | | | | | 280 | | | | | | | | |

Figure 70A-page 84

(2) INFORMATION FOR SEQ ID NO:14572133_f2_2 - AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 71

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Thr | Thr | Pro | Met | Ile | Ile | Ile | Ser | Leu | Glu | Met | Gly | Leu | Ser | Leu | 1 | 5 | 10 | 15 |
| Val | Pro | Met | Arg | Gln | Cys | Leu | Val | Cys | Gln | Ala | Leu | Ala | Arg | Ser | Ile | 20 | 25 | 30 | |
| Ser | Trp | Asn | Gly | Leu | Gly | Gly | Asn | Val | Arg | Asn | Thr | Lys | Val | Tyr | Gly | 35 | 40 | 45 | |
| Lys | Phe | Ala | Ala | Tyr | His | His | Leu | Gln | Lys | Tyr | Leu | Leu | Ile | Asp | Leu | 50 | 55 | 60 | |
| Ile | Ala | Arg | Phe | Lys | Thr | Gln | Gly | Gly | Tyr | Ile | Phe | Arg | Tyr | Asn | Thr | 65 | 70 | 75 | 80 |
| Asp | Asp | Tyr | Leu | Pro | Leu | Asn | Ser | Thr | Phe | Tyr | Met | Gly | Gly | Val | Thr | 85 | 90 | 95 | |
| Thr | Val | Arg | Gly | Phe | Arg | Asn | Gly | Ser | Ile | Thr | Pro | Lys | Asp | Glu | Phe | 100 | 105 | 110 | |
| Gly | Leu | Trp | Leu | Gly | Gly | Asp | Gly | Ile | Phe | Thr | Unk | Ser | Thr | Glu | Leu | 115 | 120 | 125 | |
| Ser | Tyr | Gly | Val | Leu | Lys | Ala | Ala | Lys | Met | Arg | Leu | Ala | Trp | Phe | Phe | 130 | 135 | 140 | |
| Asp | Phe | Gly | Phe | Leu | Thr | Phe | Lys | Pro | Gln | Leu | Gly | Gly | Val | Ser | Ser | 145 | 150 | 155 | 160 |
| Ile | Thr | Leu | Pro | Pro | Arg | Arg | Arg | Ile | Leu | Lys | Ile | Met | Unk | Leu | 165 | 170 | 175 | | |

(2) INFORMATION FOR SEQ ID NO:14574201_c3_19 - AA

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP72

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Met Trp Leu Asp His Ile Ala Lys Glu Ile Arg Ser Leu Val Glu Asn
1 5 10 15

Asp Ile Glu Val Gly Ile Val Ile Gly Gly Gly Asn Ile Ile Arg Gly
20 25 30

Val Ser Ala Ala Leu Gly Gly Ile Ile Arg Arg Thr Ser Gly Asp Tyr
35 40 45

Met Gly Met Leu Ala Thr Val Ile Lys Arg
50 55

Figure 73A - page 87

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 84 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 73

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: variable antigen from Treponema

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | His | Asn | Phe | His | Trp | Asn | Val | Lys | Gly | Thr | Asp | Phe | Phe | Asn | Val |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |

His Lys Ala Thr Glu Glu Ile Tyr Glu Gly Phe Ala Asp Met Phe Asp
20 25 30

Asp Leu Ala Glu Arg Ile Val Gln Leu Gly His His Pro Leu Val Thr
35 40 45

Leu Ser Glu Ala Ile Lys Leu Thr Arg Val Lys Glu Glu Thr Lys Thr
50 55 60

Ser Phe His Ser Lys Asp Ile Phe Lys Glu Ile Leu Glu Asp Tyr Lys
65 70 75 80

His Leu Glu Lys Glu
85

(2) INFORMATION FOR SEQ ID NO:14642202_f1_3 - AA

Figure 74A - page 88

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 74

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: HYPERSENSITIVITY RESPONSE SECRETION PROTEIN

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asn | Lys | Thr | Ile | Lys | Ala | Ala | Ala | Leu | Ala | Tyr | Asn | Met | Gly | Gln |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Asp | His | Ala | Pro | Lys | Val | Ile | Ala | Ser | Gly | Val | Gly | Glu | Val | Ala | Lys |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Arg | Ile | Ile | Gln | Lys | Ala | Lys | Glu | Tyr | Asp | Ile | Ala | Leu | Phe | Ser | Asn |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Pro | Met | Leu | Val | Asp | Ser | Leu | Leu | Lys | Val | Glu | Leu | Asp | Cys | Ala | Ile |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Pro | Glu | Glu | Leu | Tyr | Glu | Ser | Val | Val | Gln | Val | Phe | Leu | Trp | Leu | Asn |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 |
| Ser | Val | Glu | Asn | Asn | Ala | Gln | Met | Ser | Lys | | | | | | |
| | | | 85 | | | | | | 90 | | | | | | |

(2) INFORMATION FOR SEQ ID NO:14642217 f2 3 -AA

Figure 75A -- page 89

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 75

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | |
|-----------|-----------|------------|------------|-----------|-----------|-----------|-----------|------------|-----------|-----------|-----------|-----------|------------|-----------|-----------|
| Met 1 | Gln | Ala | Leu 5 | Lys | Ser | Leu | Leu | Glu 10 | Val | Ile | Thr | Lys | Leu 15 | Asn | |
| Leu | Gly | Gly 20 | Tyr | Leu | Met | His | Ile | Ala 25 | Ile | Phe | Ile | Ile | Phe 30 | Ile | Trp |
| Ile | Gly 35 | Gly | Leu | Lys | Phe | Val | Pro 40 | Tyr | Glu | Ala | Glu | Gly 45 | Ile | Ala | Pro |
| Phe 50 | Val | Unk | Asn | Ser | Pro | Phe 55 | Phe | Ser | Phe | Met | Tyr 60 | Lys | Phe | Glu | Lys |
| Pro 65 | Ala | Tyr | Lys | Gln | His 70 | Lys | Met | Ser | Glu | Ser 75 | Gln | Ser | Met | Gln | Glu 80 |
| Glu | Met | Gln | Asp | Asn 85 | Pro | Lys | Ile | Val | Glu 90 | Asn | Lys | Asn | Gly | Ile 95 | Lys |
| Lys | Thr | Ala | Leu 100 | His | Leu | Val | Ala | Glu 105 | Gly | Leu | Gly | Ile | Thr 110 | Ile | Met |
| Ile | Leu | Gly 115 | Ile | Leu | Val | Leu | Leu | Gly | Leu | | | | | | |

Figure 76A - page 90

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 171 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein HPP76

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: sensor protein

| | | | | | | | | | | | | | | | |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|-----------|------------|
| Met 1 | Gly | Lys | Ile | Ser 5 | Ala | His | Leu | Ala | His 10 | Glu | Ile | Arg | Asn | Pro 15 | Val |
| Gly | Ser | Ile | Ser 20 | Leu | Leu | Ala | Ser | Val 25 | Leu | Leu | Lys | His | Ala 30 | Asn | Glu |
| Lys | Thr | Lys 35 | Pro | Ile | Val | Val | Glu 40 | Leu | Gln | Lys | Ala | Leu 45 | Trp | Arg | Val |
| Glu | Arg 50 | Ile | Ile | Lys | Ala | Thr 55 | Leu | Leu | Phe | Ser | Lys 60 | Gly | Ile | Gln | Ala |
| Asn 65 | Arg | Thr | Lys | Gln | Ser 70 | Leu | Lys | Thr | Leu | Glu 75 | Ser | Asp | Leu | Lys | Glu 80 |
| Ala | Leu | Asn | Cys | Tyr 85 | Thr | Tyr | Ser | Lys | Asp 90 | Ile | Asp | Phe | Leu | Phe 95 | Asn |
| Phe | Ser | Asp | Glu 100 | Glu | Gly | Phe | Phe | Asp 105 | Phe | Asp | Leu | Met | Gly 110 | Ile | Val |
| Leu | Gln | Asn 115 | Phe | Leu | Tyr | Asn | Ala 120 | Ile | Asp | Ala | Ile | Glu 125 | Ala | Leu | Glu |
| Glu | Ser 130 | Glu | Gln | Gly | Gln | Val 135 | Lys | Ile | Glu | Ala | Phe 140 | Ile | Gln | Asn | Glu |
| Phe 145 | Ile | Val | Phe | Thr | Ile 150 | Ile | Asp | Asn | Gly | Lys 155 | Glu | Val | Glu | Asn | Lys 160 |
| Ser | Ala | Leu | Phe | Glu 165 | Pro | Phe | Glu | Thr | Thr 170 | Lys | Leu | | | | |

Figure 77A - page 91

(i) SEQUENCE CHARACTERISTICS:

(Å) LENGTH: 211 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 77

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: L-lactate permease

[illegible]

(2) INFORMATION FOR SEQ ID NO:14713512 f2 7-~~AA~~

Figure 78A - page 92

(i) SEQUENCE CHARACTERISTICS:

(Å) LENGTH: 181 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 78

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: INVOLVED IN PENICILLIN TOLERANCE-has signal pepti

Met Glu Ile Lys Met Ala Lys Asp Tyr Gly Phe Cys Phe Gly Val Lys
1 5 10 15

Arg Ala Ile Gln Ile Ala Glu Lys Asn Gln Asn Ser Leu Ile Phe Gly
20 25 30

Ser Leu Ile His Asn Ala Lys Glu Ile Asn Arg Leu Glu Lys Asn Phe
35 40 45

Asn Val Lys Ile Glu Glu Asp Pro Lys Lys Ile Pro Lys Asn Lys Ser
50 55 60

Val Ile Ile Arg Thr His Gly Ile Pro Lys Gln Asp Leu Glu Tyr Leu
65 70 75 80

Lys Asn Lys Gly Val Lys Ile Thr Asp Ala Thr Cys Pro Tyr Val Ile
85 90 95

Lys Pro Gln Gln Ile Val Glu Ser Met Ser Lys Glu Gly Tyr Gln Ile
100 105 110

Val Leu Phe Gly Asp Ile Asn His Pro Glu Val Lys Gly Val Ile Ser
115 120 125

Tyr Ala Thr Asn Gln Ala Leu Val Gly Asn Ser Leu Glu Glu Leu Gln
130 135 140

Glu Lys Lys Leu Gln Arg Lys Val Ala Leu Val Ser Gln Thr Thr Gln
145 150 155 160

Ala Asn Pro Lys Thr Leu Ala Asn Arg Phe Leu Phe Gly Gly Unk Cys
165 170 175

Thr Glu Val Arg Ile Phe
180

(2) INFORMATION FOR SEQ ID NO:14714687_f1_3 - AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

Figure 79A - page 93

(ii) MOLECULE TYPE: protein

HPP 79

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: molybdenum transport system permease

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asp | His | Glu | Phe | Leu | Ile | Thr | Met | Arg | Leu | Ser | Phe | Ser | Leu | Ala | 1 | 5 | 10 | 15 |
| Leu | Ile | Thr | Thr | Leu | Ile | Leu | Leu | Pro | Ile | Gly | Ile | Phe | Leu | Gly | Tyr | 20 | 25 | 30 | |
| Phe | Leu | Ser | Leu | Lys | Arg | Asn | Leu | Leu | Thr | Ser | Leu | Thr | Glu | Thr | Leu | 35 | 40 | 45 | |
| Val | Tyr | Met | Pro | Leu | Val | Leu | Pro | Pro | Ser | Val | Leu | Gly | Phe | Tyr | Leu | 50 | 55 | 60 | |
| Leu | Leu | Ile | Phe | Ser | Pro | Ser | Ser | Phe | Leu | Gly | Ala | Phe | Leu | Gln | Asp | 65 | 70 | 75 | 80 |
| Val | Leu | Asn | Val | Lys | Leu | Val | Phe | Ser | Phe | Gln | Gly | Leu | Ile | Leu | Gly | 85 | 90 | 95 | |
| Ser | Val | Ile | Phe | Ser | Leu | Pro | Phe | Met | Val | Ser | Pro | Ile | Lys | Ser | Ala | 100 | 105 | 110 | |
| Leu | Ile | Ser | Leu | Pro | Thr | Ser | Leu | Lys | Glu | Ala | Ser | Tyr | Ser | Leu | Gly | 115 | 120 | 125 | |
| Lys | Gly | Glu | Tyr | Tyr | Thr | Leu | Phe | Phe | Val | Leu | Leu | Pro | Asn | Ile | Lys | 130 | 135 | 140 | |
| Pro | Ser | Val | Leu | Met | Ala | Ile | Ile | Thr | Thr | Phe | Met | His | Thr | Ile | Gly | 145 | 150 | 155 | 160 |
| Glu | Phe | Gly | Val | Val | Met | Met | Leu | Gly | Gly | Asp | Ile | Leu | Gly | Glu | Thr | 165 | 170 | 175 | |
| Arg | Val | Ala | Ser | Ile | Thr | Ile | Phe | Asn | Glu | Ala | Glu | Ala | Leu | Asn | Tyr | 180 | 185 | 190 | |
| Ser | Lys | Ala | His | Gln | Tyr | Ala | Leu | Thr | Leu | Thr | Leu | Ile | Ser | Phe | Ser | 195 | 200 | 205 | |
| Leu | Leu | Phe | Val | Thr | Leu | Phe | Leu | Asn | Lys | Lys | Gln | Ser | Ser | Phe | Leu | 210 | 215 | 220 | |

(2) INFORMATION FOR SEQ ID NO:14726542_f3_30: -AA

Figure 80A - page 94

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 80

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Met His Pro Ile Met Phe Ala Tyr Ile Ala Asn Ala Leu Ala Gln Ala
1 5 10 15

Arg Lys Ile Asn Gly Thr Leu Cys Met Ala Phe Gln Lys Ile Ser Gln
20 25 30

Val Lys Glu Leu Gly Ile Asp Lys Ala Lys Ser Leu Ile Gly Asn Leu
35 40 45

Ser Gln Val Ile Ile Tyr Pro Thr Lys Asp Thr Asp Glu Leu Ile Glu
50 55 60

Cys Gly Val Pro Leu Ser Asp Ser Glu Ile Asn Phe Leu His Asn Thr
65 70 75 80

Asp Met Arg Ala Arg Gln Val Leu Val Lys Asn Ile Val Thr Asn Ala
85 90 95

Ser Ala Phe Ile Glu Ile Asp Leu Lys Lys Ile Cys Lys Asn Tyr Phe
100 105 110

Ile Phe Leu Ile Ala Met Leu Val Ile Glu Lys Ser Ser Met Ile Leu
115 120 125

Lys Lys Gln
130

Figure 81A-page 95

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPD 81

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | |
|-----------|-----------|-----------|-----------|----------|-----------|-----------|-----------|-----------|-----------|-----|-----------|-----------|-----------|-----------|-----|
| Met 1 | Cys | Leu | Thr | Gly 5 | Gly | Leu | Met | Arg | Trp 10 | Leu | Lys | Ser | Val | Lys 15 | Pro |
| Glu | Arg | Ile | Leu 20 | His | Ser | Val | Val | Glu 25 | Phe | Val | Asp | Ile | Ala 30 | Gly | Leu |
| Ile | Lys | Gly 35 | Ala | Ser | Lys | Gly | Glu 40 | Gly | Leu | Gly | Asn | Gln 45 | Phe | Leu | Ala |
| Asn | Ile 50 | Lys | Glu | Cys | Glu | Val 55 | Ile | Leu | Gln | Val | Val 60 | Arg | Cys | Phe | Glu |
| Asp 65 | Asp | Asn | Asn | His | Ala 70 | Cys | Glu | Arg | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:15039062_f3_15 -AA

Figure 82A - page 96

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 91 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 82

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|----|----|----|
| Met | His | Val | Ala | Cys | Leu | Leu | Ala | Leu | Gly | Asp | Asn | Leu | Ile | Thr | Leu | 1 | 5 | 10 | 15 |
| Ser | Leu | Leu | Lys | Glu | Ile | Ala | Ser | Lys | Gln | Gln | Gln | Ser | Leu | Lys | Ile | 20 | 25 | 30 | |
| Leu | Gly | Thr | His | Leu | Thr | Leu | Lys | Ile | Ala | Lys | Leu | Leu | Glu | Cys | Glu | 35 | 40 | 45 | |
| Lys | His | Phe | Glu | Ile | Ile | Pro | Val | Phe | Glu | Asn | Ile | Pro | Ala | Phe | Tyr | 50 | 55 | 60 | |
| Asp | Leu | Lys | Lys | Gln | Gly | Val | Phe | Trp | Ala | Met | Lys | Asp | Phe | Leu | Trp | 65 | 70 | 75 | 80 |
| Leu | Leu | Lys | Gln | Leu | Lys | Asn | Ile | Lys | Ser | Asn | Val | 85 | 90 | | | | | | |

Figure 83A - page 97

(2) INFORMATION FOR SEQ ID NO:15126875_c3_21: - AA

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 204 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPD 83

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Met 1 | Lys | Lys | Lys | Pro 5 | Leu | Met | Trp | Arg | Ile 10 | Cys | Ala | Leu | Arg | Arg 15 | Leu |
| Leu | Leu | Gly | Phe 20 | Lys | Arg | Glu | Arg | Glu 25 | Leu | Leu | Ser | Phe | Ala 30 | Lys | His |
| Trp | Asn | Ile 35 | Pro | Thr | Ile | Val | Val 40 | Phe | Thr | His | Thr | Gln 45 | Ala | Glu | Ala |
| Gly | Asp 50 | Ala | Phe | Val | Gln | Glu 55 | Thr | Lys | Gly | Ile | Ile 60 | Asp | Glu | Glu | Trp |
| Gly 65 | Phe | Lys | Gly | Phe | Val 70 | Arg | Ala | Tyr | Val | Arg 75 | Val | Asn | Ser | Val | Ala 80 |
| Phe | Ser | Phe | Arg | Gly 85 | Leu | Lys | Val | Pro | Val 90 | Glu | Gly | Leu | Glu | Glu 95 | Leu |
| Val | Asp | Glu | Thr 100 | Lys | Lys | Cys | Leu | Ser 105 | Asp | Ala | Glu | Lys | Asn 110 | Lys | Lys |
| Arg | His | Phe 115 | Leu | Ser | Ile | Gln | Arg 120 | Val | Lys | Ile | Gln | Glu 125 | Arg | Lys | Gln |
| Ala | Met 130 | Ile | Glu | Glu | Cys | Lys 135 | Thr | Ile | Ile | His | Val 140 | Ala | Ser | Gly | Ala |
| Ala 145 | Gly | Val | Ala | Gly | Leu 150 | Ile | Pro | Ile | Pro | Phe 155 | Ser | Asp | Ala | Leu | Ala 160 |
| Ile | Ala | Pro | Ile | Gln 165 | Ala | Gly | Met | Ile | Tyr 170 | Lys | Met | Asn | Asp | Ala 175 | Phe |
| Gly | Met | Asp | Leu 180 | Asp | Lys | Ser | Val | Gly 185 | Ala | Ser | Leu | Val | Ala 190 | Gly | Leu |
| Leu | Gly | Val 195 | Asn | Cys | Arg | Ala | Ser 200 | Gly | Glu | Asp | Ser | Arg 205 | | | |

(2) INFORMATION FOR SEQ ID NO:156587_f2_3- AA

Figure 84A - page 98

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 84

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: chemotaxis protein cheW

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Leu | Gly | Val | Unk | Asn | Leu | Arg | Gly | Asn | Val | Phe | Pro | Leu | Ile | Ser |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Arg | Leu | Lys | Phe | Gly | Leu | Lys | Ala | Glu | Lys | Gln | Asn | Lys | Asp | Thr |
| | | | 20 | | | | | 25 | | | | | 30 | | |

| | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Tyr | Leu | Val | Val | Arg | His | Asn | Asp |
| | | 35 | | | | | 40 | |

(2) INFORMATION FOR SEQ ID NO:15807794_c1_2 - AA

Figure 85A - page 99

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 218 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPD85

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Val 1 | Lys | Ser | Val | Phe 5 | Ser | Glu | Glu | Lys | Glu 10 | Thr | Pro | Val | Thr | Lys 15 | Glu |
| Asn | Gly | Ser | Tyr 20 | Leu | Ile | Ala | Tyr | Asp 25 | Pro | Leu | Asp | Gly | Ser 30 | Ser | Val |
| Met | Glu | Ala 35 | Asn | Phe | Leu | Val | Gly 40 | Thr | Ile | Ile | Gly | Val 45 | Tyr | Glu | Lys |
| Asp | Tyr 50 | Lys | Ala | Gln | Asn | Leu 55 | Val | Ala | Ser | Leu | Tyr 60 | Val | Val | Phe | Gly |
| His 65 | Lys | Ile | Glu | Leu | Val 70 | Val | Ala | Leu | Glu | Glu 75 | Val | Tyr | Arg | Tyr | Ala 80 |
| Phe | Tyr | Gln | Asn | Lys 85 | Phe | His | Phe | Ile | Glu 90 | Thr | Ile | Val | Leu | Glu 95 | Asn |
| Lys | Gly | Lys | Ile 100 | Ile | Ala | Ser | Gly | Gly 105 | Asn | Gln | Lys | Asp | Phe 110 | Ser | Leu |
| Gly | Leu | Lys 115 | Lys | Ala | Leu | Glu | Gly 120 | Phe | Phe | Ala | Glu | Asn 125 | Tyr | Arg | Leu |
| Arg | Tyr 130 | Ser | Gly | Ser | Met | Val 135 | Ala | Asp | Val | His | His 140 | Val | Leu | Val | Lys |
| Lys 145 | Gly | Gly | Met | Phe | Ser 150 | Tyr | Pro | Gln | Lys | Lys 155 | Leu | Arg | Lys | Leu | Phe 160 |
| Glu | Val | Phe | Pro | Leu 165 | Ala | Leu | Met | Val | Glu 170 | Lys | Ala | Lys | Gly | Glu 175 | Ala |
| Phe | Tyr | Phe | Asp 180 | Lys | Gly | Val | Lys | Lys 185 | Arg | Leu | Leu | Asp | Gln 190 | Ser | Val |
| Glu | Ser | Tyr 195 | His | Glu | Lys | Ser | Glu 200 | Cys | Tyr | Leu | Ala | Ser 205 | Pro | His | Glu |
| Ala | Gln 210 | Ile | Leu | Glu | Lys | His 215 | Leu | Lys | Gly | Glu | | | | | |

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 187 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

Figure 86A - page 100

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 86

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Met Lys Ser Ile Gly Glu Val Met Ala Ile Gly Gly Asn Phe Leu Glu
1 5 10 15

Ala Leu Gln Lys Ala Leu Cys Ser Leu Glu Asn Asn Trp Leu Gly Phe
20 25 30

Glu Ser Leu Ser Lys Asp Leu Glu Ala Ile Lys Lys Glu Ile Arg Arg
35 40 45

Pro Asn Pro Lys Arg Leu Leu Tyr Ile Ala Asp Ala Phe Arg Leu Gly
50 55 60

Val Ser Val Asp Glu Val Phe Glu Leu Cys Gln Ile Asp Arg Trp Phe
65 70 75 80

Leu Ser Gln Ile Gln Lys Leu Val Lys Ala Glu Glu Gly Ile Asn Ser
85 90 95

Ser Val Leu Thr Asp Ala Lys Lys Leu Arg Gly Leu Lys Asn Leu Gly
100 105 110

Phe Ser Asp Ala Arg Ile Ala Thr Lys Ile Lys Glu Asn Glu Asn Leu
115 120 125

Glu Val Ser Pro Phe Glu Val Glu Leu Ala Arg Ser Asn Leu Gln Ile
130 135 140

Ala Pro His Phe Glu Glu Val Asp Thr Cys Ala Ala Glu Phe Leu Ser
145 150 155 160

Leu Thr Leu Ile Cys Ile Pro Pro Met Pro Leu Thr Leu Cys Pro Leu
165 170 175

Leu Glu Thr Asn Lys Lys Asn Lys Lys Arg Lys Ser
180 185

(2) INFORMATION FOR SEQ ID NO:15824052_f3_6 - AA

Figure 87A - page 101

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 230 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 87

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: transmembrane receptor

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| Met | Phe | Gly | Asn | Lys | Gln | Leu | Gln | Leu | Gln | Ile | Ser | Gln | Lys | Asp | Ser | 1 | 5 | 10 | 15 |
| Glu | Ile | Ala | Glu | Leu | Lys | Lys | Glu | Val | Asn | Leu | Tyr | Gln | Ser | Leu | Leu | 20 | 25 | 30 | |
| Asn | Leu | Cys | Leu | His | Glu | Gly | Phe | Val | Gly | Ile | Lys | Asn | Asn | Lys | Val | 35 | 40 | 45 | |
| Val | Phe | Lys | Ser | Gly | Asn | Leu | Ala | Ser | Leu | Asn | Asn | Leu | Glu | Glu | Gln | 50 | 55 | 60 | |
| Ser | Val | His | Phe | Lys | Glu | Asn | Ala | Glu | Ser | Val | Asn | Leu | Gln | Gly | Val | 65 | 70 | 75 | |
| Ser | Tyr | Ser | Leu | Lys | Ser | Gln | Asn | Ile | Asp | Gly | Val | Gln | Tyr | Phe | Ser | 85 | 90 | 95 | |
| Leu | Ala | Lys | Lys | Thr | Gly | Gly | Val | Gly | Glu | Tyr | His | Lys | Asn | Asp | Leu | 100 | 105 | 110 | |
| Phe | Lys | Thr | Phe | Cys | Thr | Ser | Leu | Lys | Glu | Gly | Leu | Glu | Asn | Ala | Gln | 115 | 120 | 125 | |
| Glu | Ser | Met | Gln | Tyr | Phe | His | Gln | Glu | Thr | Gly | Leu | Leu | Leu | Asn | Ala | 130 | 135 | 140 | |
| Ala | Lys | Asn | Gly | Glu | Glu | His | Ser | Asn | Glu | Gly | Leu | Ile | Thr | Val | Asn | 145 | 150 | 155 | |
| Lys | Thr | Gly | Gln | Asp | Ile | Glu | Ser | Leu | Tyr | Glu | Lys | Met | Gln | Asn | Ala | 165 | 170 | 175 | |
| Thr | Ser | Leu | Ala | Asp | Ser | Leu | Asn | Gln | Arg | Ser | Asn | Glu | Ile | Thr | Gln | 180 | 185 | 190 | |
| Val | Ile | Ser | Leu | Ile | Asp | Asp | Ile | Ala | Glu | Gln | Thr | Asn | Leu | Leu | Ala | 195 | 200 | 205 | |
| Leu | Asn | Ala | Ala | Ile | Glu | Ala | Ala | Arg | Ala | Val | Asn | Met | Ala | Glu | Gly | 210 | 215 | 220 | |
| Leu | Arg | Trp | Trp | Leu | Met | Arg | | | | | | | | | | 225 | 230 | | |

(2) INFORMATION FOR SEQ ID NO:16100038_c3_30-AA

Figure 88A - page 102

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 62 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 88

(iii) HYPOTHETICAL: YES

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Trp | Ile | Met | Ser | Ser | Leu | Ser | Ser | Ser | Phe | Phe | His | Ser | Leu | Phe |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Phe | Ile | Lys | Ser | Asn | Pro | Gly | Gln | Leu | Leu | Lys | Gly | Trp | Gly | Ser | Lys |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Ile | Phe | Phe | Ile | Asn | Arg | Lys | Phe | Val | Leu | Ala | Gln | Tyr | Asn | Pro | Ser |
| | | | 35 | | | | 40 | | | | | 45 | | | |
| Val | Ser | Ile | Phe | Ile | Leu | Leu | Asn | Arg | Val | Phe | Gly | Val | Gly | Val | |
| | 50 | | | | | 55 | | | | | 60 | | | | |

(2) INFORMATION FOR SEQ ID NO:16131887_c3_5 - AA

Figure 89A - page 103

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 89

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Gln | Phe | Glu | Glu | Met | Lys | Glu | Leu | Ala | His | Gln | Ile | Gly | Val | Phe | |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | | |
| Tyr | His | Val | Gly | Val | Asp | Gly | Ile | Ala | Leu | Phe | Leu | Leu | Leu | Leu | Asn | |
| | | | 20 | | | | | 25 | | | | | 30 | | | |
| Ala | Ile | Val | Val | Leu | Leu | Ser | Val | Val | Tyr | Val | Lys | Glu | Arg | Arg | Lys | |
| | | | 35 | | | | 40 | | | | | 45 | | | | |
| Asp | Phe | Val | Ile | Cys | Leu | Leu | Leu | Leu | Glu | Gly | Ser | | | | | |
| | 50 | | | | | 55 | | | | | 60 | | | | | |

(2) INFORMATION FOR SEQ ID NO:16219090_c2_5 - AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 202 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

Figure 90A - page 104

(ii) MOLECULE TYPE: protein

HPP 90

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: flagellar biosynthesis protein flha

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Lys | Lys | Tyr | Ala | Glu | Asp | Phe | Ile | Thr | Lys | Asp | Glu | Val | Lys | Ser | 1 | 5 | 10 | 15 |
| Leu | Leu | Glu | Arg | Leu | Ala | Lys | Asp | Tyr | Pro | Thr | Ile | Val | Glu | Glu | Ser | 20 | 25 | 30 | |
| Lys | Lys | Ile | Pro | Thr | Gly | Ala | Ile | Arg | Ser | Val | Leu | Gln | Ala | Leu | Leu | 35 | 40 | 45 | |
| His | Glu | Lys | Ile | Pro | Ile | Lys | Asp | Met | Leu | Thr | Ile | Leu | Glu | Thr | Ile | 50 | 55 | 60 | |
| Thr | Asp | Ile | Ala | Pro | Leu | Val | Gln | Asn | Asp | Val | Asn | Ile | Leu | Thr | Glu | 65 | 70 | 75 | 80 |
| Gln | Val | Arg | Ala | Arg | Leu | Ser | Arg | Val | Ile | Thr | Asn | Ala | Phe | Lys | Ser | 85 | 90 | 95 | |
| Glu | Asp | Gly | Arg | Leu | Lys | Phe | Leu | Thr | Phe | Ser | Thr | Asp | Ser | Glu | Gln | 100 | 105 | 110 | |
| Phe | Leu | Leu | Asn | Lys | Leu | Arg | Glu | Asn | Gly | Thr | Ser | Lys | Ser | Leu | Leu | 115 | 120 | 125 | |
| Leu | Asn | Val | Gly | Glu | Leu | Gln | Lys | Leu | Ile | Glu | Gly | Val | Ser | Glu | Glu | 130 | 135 | 140 | |
| Ala | Met | Lys | Val | Leu | Gln | Lys | Gly | Ile | Ala | Pro | Val | Ile | Leu | Ile | Val | 145 | 150 | 155 | 160 |
| Glu | Pro | Asn | Leu | Arg | Lys | Ala | Leu | Ser | Lys | Gln | Met | Glu | Gln | Ala | Arg | 165 | 170 | 175 | |
| Asn | Asp | Gly | Leu | Val | Leu | Ser | His | Ala | Glu | Leu | Asp | Pro | Asn | Ser | Asn | 180 | 185 | 190 | |
| Phe | Glu | Ala | Leu | Gly | Thr | Ile | His | Ile | Asn | Phe | | | | | | 195 | 200 | | |

(2) INFORMATION FOR SEQ ID NO:16225006_c2_6 - AA

Figure 91A - page 105

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 91

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: Outer membrane 30K protein

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| Val | Gly | Ala | Asn | Pro | Val | Pro | His | Ala | Gln | Ile | Leu | Gln | Ser | Val | Val | 1 | 5 | 10 | 15 |
| Asp | Asp | Leu | Lys | Glu | Lys | Gly | Ile | Lys | Leu | Val | Ile | Val | Ser | Phe | Thr | 20 | 25 | 30 | |
| Asp | Tyr | Val | Leu | Pro | Asn | Leu | Ala | Leu | Asn | Asp | Gly | Ser | Leu | Asp | Ala | 35 | 40 | 45 | |
| Asn | Tyr | Phe | Gln | His | Arg | Pro | Tyr | Leu | Asp | Arg | Phe | Asn | Leu | Asp | Arg | 50 | 55 | 60 | |
| Lys | Met | His | Leu | Val | Gly | Leu | Ala | Asn | Ile | His | Val | Glu | Pro | Leu | Arg | 65 | 70 | 75 | 80 |
| Phe | Tyr | Ser | Gln | Lys | Ile | Thr | Asp | Ile | Lys | Asn | Leu | Lys | Lys | Gly | Ser | 85 | 90 | 95 | |
| Val | Ile | Ala | Val | Pro | Asn | Asp | Pro | Ala | Asn | Gln | Gly | Arg | Ala | Leu | Ile | 100 | 105 | 110 | |
| Leu | Leu | His | Lys | Gln | Gly | Leu | Ile | Ala | Leu | Lys | Asp | Pro | Ser | Asn | Leu | 115 | 120 | 125 | |
| Tyr | Ala | Thr | Glu | Phe | Asp | Ile | Val | Lys | Asn | Pro | Tyr | Asn | Ile | Lys | Ile | 130 | 135 | 140 | |
| Lys | Pro | Leu | Glu | Ala | Ala | Val | Ile | Ala | | | | | | | | 145 | 150 | | |

(2) INFORMATION FOR SEQ ID NO:16281449_c1_3 -AA

Figure 93A - page 107

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 93

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: signal recognition particle protein

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Lys | Gln | Leu | Lys | Val | Leu | Gly | Glu | Gln | Val | Asp | Val | Lys | Val | Phe |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| His | Glu | Glu | Asn | Lys | Ser | Val | Lys | Glu | Ile | Ala | Asn | Asn | Ala | Leu | Lys |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Arg | Ala | Lys | Glu | Ala | Gln | Phe | Asp | Val | Leu | Ile | Val | Asp | Ser | Ala | Gly |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Arg | Leu | Ala | Ile | Asp | Lys | Glu | Leu | Met | Gln | Glu | Leu | Lys | Glu | Val | Lys |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Glu | Val | Leu | Asn | Pro | His | Glu | Val | Leu | Tyr | Val | Ala | Asp | Ala | Leu | Asn |
| 65 | | | | | 70 | | | | 75 | | | | | | 80 |
| Gly | Gln | Asp | Gly | Val | Lys | Ser | Ala | Asn | Thr | Phe | Asn | Glu | Glu | Ile | Ala |
| | | | | 85 | | | | | 90 | | | | | 95 | |

(2) INFORMATION FOR SEQ ID NO:16305252 c3_9 - AA

Figure 94A - page 108

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 94

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Met Met Lys Asn Lys Arg Ser Gln Asn Ser Pro Tyr Val Thr Pro Asp
1 5 10 15

Asn Pro Tyr Leu Thr Leu Glu Lys Ala Leu Gly Tyr Ser Phe Lys Asp
20 25 30

Lys Arg Leu Leu Glu Gln Ala Leu Thr His Lys Ser Cys Lys Leu Ala
35 40 45

Leu Asn Asn Glu Arg Leu Glu Phe Leu Gly Asp Ala Val Leu Gly Leu
50 55 60

Val Ile Gly Glu Leu Leu Tyr His Lys Phe Tyr Gln Tyr Asp Gly Gly
65 70 75 80

Lys Leu Ser Lys Leu Arg Ala Ser Ile Val Ser Ala His Gly Phe Thr
85 90 95

Lys Leu Ala Lys Ala Ile Ala Leu Gln Asp Tyr Leu Arg Val Ser Ser
100 105 110

Ser Glu Glu Ile Ser Lys Gly Arg Glu Lys Pro Ser Ile Leu Ser Ser
115 120 125

Ala Phe Glu Ala Leu Met Ala Gly Val Tyr Leu Glu Ala Gly Leu Ala
130 135 140

Lys Val Arg Lys Ile Ile Gln Asn Leu Leu Asn Arg Ala Tyr Lys Arg
145 150 155 160

Leu Asp Leu Glu His Leu Phe Met Asp Tyr Lys Thr Ala Leu Gln Glu
165 170 175

Leu Thr Gln Pro Val Leu Arg Asp Pro His Leu Pro Ile Thr Pro Arg
180 185 190

Lys Arg Pro Arg Ser Pro
195

Figure 95A - page 109

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 208 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 95

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: integral protein in inner membrane

Met Gly Phe Asn Arg Leu Val Asp Arg Asp Ile Asp Lys Asp Asn Pro
1 5 10 15

Arg Thr Lys Asn Arg Pro Ser Val Asp Gly Arg Ile Ser Val Lys Gly
20 25 30

Met Val Ile Phe Ser Val Ser Asn Ala Leu Leu Phe Val Gly Val Ser
35 40 45

Tyr Phe Ile Asn Pro Leu Ala Phe Lys Leu Ser Leu Pro Phe Leu Ile
50 55 60

Ile Leu Gly Gly Tyr Ser Tyr Phe Lys Arg Phe Ser Ser Leu Ala His
65 70 75 80

Phe Val Val Gly Leu Ala Leu Gly Leu Ala Pro Ile Ala Gly Ser Val
85 90 95

Ala Val Leu Gly Asp Ile Pro Leu Trp Asn Val Phe Leu Ala Leu Gly
100 105 110

Val Met Leu Trp Val Ala Gly Phe Asp Leu Leu Tyr Ser Leu Gln Asp
115 120 125

Met Glu Phe Asp Lys Glu Arg Gly Leu Phe Ser Ile Pro Ser Gln Leu
130 135 140

Gly Glu Lys Trp Cys Leu Asn Leu Ser Arg Leu Ser His Leu Val Ala
145 150 155 160

Leu Ile Cys Trp Leu Cys Phe Val Lys Cys Tyr His Gly Gly Leu Phe
165 170 175

Ala Tyr Leu Gly Leu Gly Val Ser Ala Leu Ile Leu Leu Tyr Glu Gln
180 185 190

Ile Leu Val Ala Arg Asp Tyr Lys Asn Ile Pro Lys Ser Leu Phe Cys
195 200 205

Glu

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 94 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: MAGNESIUM AND COBALT TRANSPORT PROTEIN

Val Glu Gln Asn Lys Ile Ile Lys Leu Phe Thr Val Ala Thr Met Ala
1 5 10 15

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Met | Pro | Pro | Thr | Leu | Ile | Gly | Thr | Ile | Asn | Gly | Met | Asn | Phe | Lys |
| | | | 20 | | | | | 25 | | | | | 30 | | |

Phe Met Pro Glu Leu Glu Trp Gln Tyr Gly Tyr Leu Phe Ala Leu Ile
35 40 45

Val Met Ala Ile Ser Thr Ile Leu Pro Val Ile Tyr Phe Lys Lys Lys
50 55 60

Gly Leu Val Val Ala Phe His Gly Ile Phe Ile Leu Thr Leu Arg Arg
65 70 75 80

Ser Phe Tyr Thr Ala Trp His Ser Leu Leu Gly Tyr Ala Thr Leu
85 90 95

111

Figure 97A - page 111

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

HPP 97

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Met Trp Pro Leu Asp Ile Ile Val Val Val Ala Trp Val Leu Trp Gly
1 5 10 15

Val Asn Met Phe Gly Ser Met Ser Val Arg Arg Glu Asn Thr Ile Tyr
20 25 30

Val Ser Leu Trp Tyr Tyr Ile Ala Thr Tyr Val Gly Ile Ala Val Met
35 40 45

Tyr Ile Phe Asn Asn Leu Ser Ile Pro Thr Tyr Phe Val Ala Asp Met
50 55 60

Gly Ser Val Trp His Leu Phe Leu Cys Ile Gln Ala Val Met Met Arg
65 70 75 80

Ser Phe Asn Gly Gly Gly Gly Ile Met Arg Ser Leu Leu Ser Leu Arg
85 90 95

Val Gly

(2) INFORMATION FOR SEQ ID NO:16422591_c3_13-AA

Figure 98A - page 112

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 91 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 98

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Phe | Asp | Ser | Ile | Val | Tyr | Phe | Phe | Asn | Lys | Ser | Gly | Phe | Val | Thr |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Thr | Leu | Val | Leu | Val | Trp | Ile | Ser | Leu | Tyr | Leu | Val | Met | Thr | Leu | Trp |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Val | Phe | Leu | Tyr | Lys | Ser | Ile | Val | Leu | Lys | Ile | Glu | Leu | Arg | Arg | Glu |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Met | Gln | Ser | Leu | Ser | Asn | Ile | Leu | Asn | Gly | Ala | Gln | Asp | Ala | Pro | Glu |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| His | Phe | Met | Phe | Asn | Lys | Lys | Arg | Asn | Asp | Glu | Thr | Lys | Arg | Tyr | Ser |
| 65 | | | | 70 | | | | | 75 | | | | | 80 | |
| Asn | Glu | Leu | Leu | Gln | Asp | Leu | Glu | Thr | Pro | Gly | Ser | | | | |
| | | | | 85 | | | | | 90 | | | | | | |

(2) INFORMATION FOR SEQ ID NO:16440842_c3_8-AA

Figure 99A - page 113

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 99

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Met | Leu | Tyr | Cys | Met | Arg | Leu | Leu | Met | Pro | Ile | Leu | Gly | Ala |
| 1 | | | | 5 | | | | 10 | | | | | 15 | | |
| Ile | Lys | Gly | Gly | Asp | Ile | Gly | Glu | Trp | Phe | Pro | Asp | Asn | Asp | Pro | Lys |
| | | 20 | | | | | 25 | | | | | 30 | | | |
| Tyr | Lys | Asn | Ala | Ser | Ser | Lys | Glu | Leu | Leu | Lys | Ile | Val | Leu | Asp | Phe |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Ser | Gln | Ser | Ile | Gly | Phe | Glu | Leu | Leu | Glu | Met | Gly | Ala | Thr | Ile | Phe |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Ser | Glu | Ile | Pro | Lys | Ile | Thr | Pro | Tyr | Lys | Pro | Ala | Ile | Leu | Glu | Asn |
| 65 | | | | | 70 | | | | 75 | | | | | 80 | |
| Leu | Ser | Gln | Leu | Leu | Gly | Leu | Glu | Lys | Ser | Gln | Ile | Ser | Leu | Lys | Ala |
| | | | 85 | | | | | | 90 | | | | | 95 | |

(2) INFORMATION FOR SEQ ID NO:16459375_f1_1-AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1177 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

Figure 100A-page 114

(ii) MOLECULE TYPE: protein

HPP 100

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: cytotoxicity associated immunodominant antigen [H

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ile | Pro | Asn | Leu | Asp | Ile | Glu | Gly | Glu | Thr | Met | Thr | Asn | Glu | Ala | 1 | 5 | 10 | 15 |
| Ile | Asn | Gln | Gln | Pro | Gln | Thr | Glu | Ala | Ala | Phe | Asn | Pro | Gln | Gln | Phe | 20 | 25 | 30 | |
| Ile | Asn | Asn | Leu | Gln | Val | Ala | Phe | Ile | Lys | Val | Asp | Asn | Val | Val | Ala | 35 | 40 | 45 | |
| Ser | Phe | Asp | Pro | Asn | Gln | Lys | Pro | Ile | Val | Asp | Lys | Asn | Asp | Arg | Asp | 50 | 55 | 60 | |
| Asn | Arg | Gln | Ala | Phe | Glu | Lys | Ile | Ser | Gln | Leu | Arg | Glu | Glu | Phe | Ala | 65 | 70 | 75 | 80 |
| Asn | Lys | Ala | Ile | Lys | Asn | Pro | Thr | Lys | Lys | Asn | Gln | Tyr | Phe | Ser | Ser | 85 | 90 | 95 | |
| Phe | Ile | Ser | Lys | Ser | Asn | Asp | Leu | Ile | Asp | Lys | Asp | Asn | Leu | Ile | Asp | 100 | 105 | 110 | |
| Thr | Gly | Ser | Ser | Ile | Lys | Ser | Phe | Gln | Lys | Phe | Gly | Thr | Gln | Arg | Tyr | 115 | 120 | 125 | |
| Gln | Ile | Phe | Met | Asn | Trp | Val | Ser | His | Gln | Asn | Asp | Pro | Ser | Lys | Ile | 130 | 135 | 140 | |
| Asn | Thr | Gln | Lys | Ile | Arg | Gly | Phe | Met | Glu | Asn | Ile | Ile | Gln | Pro | Pro | 145 | 150 | 155 | 160 |
| Ile | Ser | Asp | Asp | Lys | Glu | Lys | Ala | Glu | Phe | Leu | Arg | Ser | Ala | Lys | Gln | 165 | 170 | 175 | |
| Ala | Phe | Ala | Gly | Ile | Ile | Ile | Gly | Asn | Gln | Ile | Arg | Ser | Asp | Gln | Lys | 180 | 185 | 190 | |
| Phe | Met | Gly | Val | Phe | Asp | Glu | Ser | Leu | Lys | Glu | Arg | Gln | Glu | Ala | Glu | 195 | 200 | 205 | |
| Lys | Asn | Gly | Glu | Pro | Asn | Gly | Asp | Pro | Thr | Gly | Gly | Asp | Trp | Leu | Asp | 210 | 215 | 220 | |
| Ile | Phe | Leu | Ser | Phe | Val | Phe | Asn | Lys | Lys | Gln | Ser | Ser | Asp | Leu | Lys | 225 | 230 | 235 | 240 |

Figure 100A - page 115

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Thr | Leu | Asn | Gln | Glu | Pro | Val | Pro | His | Val | Gln | Pro | Asp | Val | Ala |
| | | | | 245 | | | | | 250 | | | | | 255 | |
| Thr | Thr | Thr | Thr | Asp | Ile | Gln | Ser | Leu | Pro | Pro | Glu | Ala | Arg | Asp | Leu |
| | | | | 260 | | | | 265 | | | | | 270 | | |
| Leu | Asp | Glu | Arg | Gly | Asn | Phe | Ser | Lys | Phe | Thr | Leu | Gly | Asp | Met | Asn |
| | | 275 | | | | | 280 | | | | | 285 | | | |
| Met | Leu | Asp | Val | Glu | Gly | Val | Ala | Asp | Ile | Asp | Pro | Asn | Tyr | Lys | Phe |
| | 290 | | | | | 295 | | | | | 300 | | | | |
| Asn | Gln | Leu | Leu | Ile | His | Asn | Asn | Ala | Leu | Ser | Ser | Val | Leu | Met | Gly |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 |
| Ser | His | Asn | Gly | Ile | Glu | Pro | Glu | Lys | Val | Ser | Leu | Leu | Tyr | Gly | Asn |
| | | | | 325 | | | | | 330 | | | | | 335 | |
| Asn | Gly | Gly | Pro | Glu | Ala | Arg | His | Asp | Trp | Asn | Ala | Thr | Val | Gly | Tyr |
| | | | 340 | | | | | 345 | | | | | 350 | | |
| Lys | Asn | Gln | Arg | Gly | Asp | Asn | Val | Ala | Thr | Leu | Ile | Asn | Val | His | Met |
| | | 355 | | | | | 360 | | | | | 365 | | | |
| Lys | Asn | Gly | Ser | Gly | Leu | Val | Ile | Ala | Gly | Gly | Glu | Lys | Gly | Ile | Asn |
| | 370 | | | | | 375 | | | | | 380 | | | | |
| Asn | Pro | Ser | Phe | Tyr | Leu | Tyr | Lys | Glu | Asp | Gln | Leu | Thr | Gly | Ser | Gln |
| 385 | | | | | 390 | | | | | 395 | | | | | 400 |
| Arg | Ala | Leu | Ser | Gln | Glu | Glu | Ile | Gln | Asn | Lys | Val | Asp | Phe | Met | Glu |
| | | | | 405 | | | | | 410 | | | | | 415 | |
| Phe | Leu | Ala | Gln | Asn | Asn | Ala | Lys | Leu | Asp | Asn | Leu | Ser | Lys | Lys | Glu |
| | | | 420 | | | | | 425 | | | | | 430 | | |
| Lys | Glu | Lys | Phe | Gln | Asn | Glu | Ile | Glu | Asp | Phe | Gln | Lys | Asp | Ser | Lys |
| | | 435 | | | | | 440 | | | | | 445 | | | |
| Ala | Tyr | Leu | Asp | Ala | Leu | Gly | Asn | Asp | His | Ile | Ala | Phe | Val | Ser | Lys |
| | 450 | | | | | 455 | | | | | 460 | | | | |
| Lys | Asp | Lys | Lys | His | Leu | Ala | Leu | Val | Ala | Glu | Phe | Gly | Asn | Gly | Glu |
| 465 | | | | | 470 | | | | | 475 | | | | | 480 |
| Leu | Ser | Tyr | Thr | Leu | Lys | Asp | Tyr | Gly | Lys | Lys | Ala | Asp | Lys | Ala | Leu |
| | | | | 485 | | | | | 490 | | | | | 495 | |
| Asp | Arg | Glu | Ala | Lys | Thr | Thr | Leu | Gln | Gly | Ser | Leu | Lys | His | Asp | Gly |
| | | | 500 | | | | | 505 | | | | | 510 | | |
| Val | Met | Phe | Val | Asp | Tyr | Ser | Asn | Phe | Lys | Tyr | Thr | Asn | Ala | Ser | Lys |
| | | 515 | | | | | 520 | | | | | 525 | | | |
| Ser | Pro | Asp | Lys | Gly | Val | Gly | Ala | Thr | Asn | Gly | Val | Ser | His | Leu | Glu |
| | 530 | | | | | 535 | | | | | 540 | | | | |
| Ala | Gly | Phe | Ser | Lys | Val | Ala | Val | Phe | Asn | Leu | Pro | Asn | Leu | Asn | Asn |
| 545 | | | | | 550 | | | | | 555 | | | | | 560 |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Ala | Ile | Thr | Ser | Val | Val | Arg | Gln | Asp | Leu | Glu | Asp | Lys | Leu | Ile |
| | | | | 565 | | | | | 570 | | | | | 575 | |
| Ala | Lys | Gly | Leu | Ser | Pro | Gln | Glu | Ala | Asn | Lys | Leu | Val | Lys | Asp | Phe |
| | | | 580 | | | | | 585 | | | | | 590 | | |
| Leu | Ser | Ser | Asn | Lys | Glu | Leu | Val | Gly | Lys | Ala | Leu | Asn | Phe | Asn | Lys |
| | | 595 | | | | | 600 | | | | | 605 | | | |
| Ala | Val | Ala | Glu | Ala | Lys | Asn | Thr | Gly | Asn | Tyr | Asp | Glu | Val | Lys | Gln |
| | 610 | | | | | 615 | | | | | 620 | | | | |
| Ala | Gln | Lys | Asp | Leu | Glu | Lys | Ser | Leu | Lys | Lys | Arg | Glu | Arg | Leu | Glu |
| 625 | | | | | 630 | | | | | 635 | | | | | 640 |
| Lys | Asp | Val | Ala | Lys | Asn | Leu | Glu | Ser | Lys | Ser | Gly | Asn | Lys | Asn | Lys |
| | | | | 645 | | | | | 650 | | | | | 655 | |
| Met | Glu | Ala | Lys | Ser | Gln | Ala | Asn | Ser | Gln | Lys | Asp | Glu | Ile | Phe | Ala |
| | | | 660 | | | | | 665 | | | | | 670 | | |
| Leu | Ile | Asn | Lys | Glu | Ala | Asn | Arg | Asp | Ala | Arg | Ala | Ile | Ala | Tyr | Ala |
| | | 675 | | | | | 680 | | | | | 685 | | | |
| Gln | Asn | Leu | Lys | Gly | Ile | Lys | Arg | Glu | Leu | Ser | Asp | Lys | Leu | Glu | Asn |
| | 690 | | | | | 695 | | | | | 700 | | | | |
| Ile | Asn | Lys | Asp | Leu | Lys | Asp | Phe | Ser | Lys | Ser | Phe | Asp | Glu | Phe | Lys |
| 705 | | | | | 710 | | | | | 715 | | | | | 720 |
| Asn | Gly | Lys | Asn | Lys | Asp | Phe | Ser | Lys | Ala | Glu | Glu | Thr | Leu | Lys | Ala |
| | | | | 725 | | | | | 730 | | | | | 735 | |
| Leu | Lys | Gly | Ser | Val | Lys | Asp | Leu | Gly | Ile | Asn | Pro | Glu | Trp | Ile | Ser |
| | | | 740 | | | | | 745 | | | | | 750 | | |
| Lys | Val | Glu | Asn | Leu | Asn | Ala | Ala | Leu | Asn | Glu | Phe | Lys | Asn | Gly | Lys |
| | | 755 | | | | | 760 | | | | | 765 | | | |
| Asn | Lys | Asp | Phe | Ser | Lys | Val | Thr | Gln | Ala | Lys | Ser | Asp | Leu | Glu | Asn |
| | 770 | | | | | 775 | | | | | 780 | | | | |
| Ser | Ile | Lys | Asp | Val | Ile | Ile | Asn | Gln | Lys | Ile | Thr | Asp | Lys | Val | Asp |
| 785 | | | | | 790 | | | | | 795 | | | | | 800 |
| Asn | Leu | Asn | Gln | Ala | Val | Ser | Val | Ala | Lys | Ala | Thr | Gly | Asp | Phe | Ser |
| | | | | 805 | | | | | 810 | | | | | 815 | |
| Gly | Val | Glu | Gln | Ala | Leu | Ala | Asp | Leu | Lys | Asn | Phe | Ser | Lys | Glu | Gln |
| | | | 820 | | | | | 825 | | | | | 830 | | |
| Leu | Ala | Gln | Gln | Ala | Gln | Lys | Asn | Glu | Asp | Phe | Asn | Thr | Gly | Lys | Asn |
| | | 835 | | | | | 840 | | | | | 845 | | | |
| Ser | Ala | Leu | Tyr | Gln | Ser | Val | Lys | Asn | Gly | Val | Asn | Gly | Thr | Leu | Val |
| | 850 | | | | | 855 | | | | | 860 | | | | |
| Gly | Asn | Gly | Leu | Ser | Lys | Ala | Glu | Ala | Thr | Thr | Leu | Ser | Lys | Asn | Phe |
| 865 | | | | | 870 | | | | 875 | | | | | | 880 |

| | | | | | | | | | | | | | | | |
|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|
| Ser | Asp | Ile | Lys | Lys | Glu | Leu | Asn | Ala | Lys | Leu | Gly | Asn | Phe | Asn | Asn |
| | | | | 885 | | | | | 890 | | | | | 895 | |
| Asn | Asn | Asn | Asn | Gly | Leu | Glu | Asn | Ser | Thr | Glu | Pro | Ile | Tyr | Thr | Gln |
| | | | 900 | | | | | 905 | | | | | 910 | | |
| Val | Ala | Lys | Lys | Val | Lys | Ala | Lys | Ile | Asp | Arg | Leu | Asp | Gln | Ile | Ala |
| | | 915 | | | | | 920 | | | | | 925 | | | |
| Ser | Gly | Leu | Gly | Asp | Val | Gly | Gln | Ala | Ala | Ser | Phe | Leu | Leu | Lys | Arg |
| | 930 | | | | | 935 | | | | | 940 | | | | |
| His | Asp | Lys | Val | Asp | Asp | Leu | Ser | Lys | Val | Gly | Leu | Ser | Ala | Asn | His |
| 945 | | | | | 950 | | | | | 955 | | | | | 960 |
| Glu | Pro | Ile | Tyr | Ala | Thr | Ile | Asp | Asp | Leu | Gly | Gly | Pro | Phe | Pro | Leu |
| | | | | 965 | | | | | 970 | | | | | 975 | |
| Lys | Arg | His | Asp | Lys | Val | Asp | Asp | Leu | Ser | Lys | Val | Gly | Leu | Ser | Arg |
| | | | 980 | | | | | 985 | | | | | 990 | | |
| Glu | Gln | Lys | Leu | Thr | Gln | Lys | Ile | Asp | Asn | Leu | Asn | Gln | Ala | Val | Ser |
| | | 995 | | | | | 1000 | | | | | 1005 | | | |
| Glu | Ala | Lys | Ala | Ser | His | Phe | Asp | Asn | Leu | Asp | Gln | Met | Ile | Asp | Lys |
| | 1010 | | | | | 1015 | | | | | 1020 | | | | |
| Leu | Lys | Asp | Ser | Thr | Lys | Lys | Asn | Val | Val | Asn | Leu | Tyr | Val | Glu | Ser |
| 1025 | | | | | 1030 | | | | | 1035 | | | | | 1040 |
| Ala | Lys | Lys | Val | Pro | Thr | Ser | Leu | Ser | Ala | Lys | Leu | Asp | Asn | Tyr | Ala |
| | | | | 1045 | | | | | 1050 | | | | | 1055 | |
| Thr | Asn | Ser | His | Thr | Arg | Ile | Asn | Ser | Asn | Val | Lys | Asn | Gly | Thr | Ile |
| | | | 1060 | | | | | 1065 | | | | | 1070 | | |
| Asn | Glu | Lys | Ala | Thr | Gly | Met | Leu | Thr | Gln | Lys | Asn | Ser | Glu | Trp | Leu |
| | | 1075 | | | | | 1080 | | | | | 1085 | | | |
| Lys | Leu | Val | Asn | Asp | Lys | Ile | Val | Ala | His | Asn | Val | Gly | Ser | Ala | Pro |
| | 1090 | | | | | 1095 | | | | | 1100 | | | | |
| Leu | Ser | Ala | Tyr | Asp | Lys | Ile | Gly | Phe | Asn | Gln | Lys | Asn | Met | Lys | Asp |
| 1105 | | | | | 1110 | | | | | 1115 | | | | | 1120 |
| Tyr | Ser | Asp | Ser | Phe | Lys | Phe | Ser | Thr | Arg | Leu | Ser | Asn | Ala | Val | Lys |
| | | | | 1125 | | | | | 1130 | | | | | 1135 | |
| Asp | Ile | Lys | Ser | Gly | Phe | Val | Gln | Phe | Leu | Thr | Asn | Ile | Phe | Ser | Met |
| | | | 1140 | | | | | 1145 | | | | | 1150 | | |
| Gly | Ser | Tyr | Ser | Leu | Met | Lys | Ala | Ser | Val | Glu | His | Gly | Val | Lys | Asn |
| | | 1155 | | | | | 1160 | | | | | 1165 | | | |
| Thr | Asn | Thr | Lys | Gly | Gly | Phe | Gln | Lys | Ser | | | | | | |
| | 1170 | | | | | 1175 | | | | | | | | | |

Figure 100A - page 117

(2) INFORMATION FOR SEQ ID NO:16603381_c2_9-AA

Figure 101 A - page 118

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP101

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Ala | Pro | Ser | Gln | Lys | Asp | Leu | Lys | Lys | Ile | Leu | Gly | Ile | Glu | 1 | 5 | 10 | 15 |
| Glu | Val | Ile | Ile | Ile | Ser | Thr | Ser | Pro | Met | Glu | Leu | Arg | Leu | Ala | Asn | 20 | 25 | 30 | |
| Gln | Lys | Leu | Gly | Asn | Arg | Phe | Ile | Lys | Thr | Leu | Gln | Ala | Met | Asn | Glu | 35 | 40 | 45 | |
| Leu | Asp | Met | Gly | Ala | Phe | Phe | Asn | Ala | Tyr | Ala | Gln | Thr | Thr | Lys | Asp | 50 | 55 | 60 | |
| Pro | Thr | His | Ala | Thr | Ser | Tyr | Gly | Val | Phe | Ala | Ala | Ser | Leu | Asn | Met | 65 | 70 | 75 | 80 |
| Glu | Leu | Lys | Lys | Ala | Leu | Arg | His | Tyr | Leu | Tyr | Ala | Gln | Thr | Ser | Asn | 85 | 90 | 95 | |
| Met | Val | Ile | Asn | Cys | Val | Lys | Ser | Val | Pro | Leu | Ser | Gln | Asn | Asp | Gly | 100 | 105 | 110 | |
| Gln | Lys | Ile | Leu | Leu | Ser | Leu | Gln | Ser | Pro | Phe | Asn | Gln | Leu | Ile | Glu | 115 | 120 | 125 | |
| Lys | Thr | Leu | Glu | Leu | Asp | Glu | Ser | His | Leu | Cys | Ala | Ala | Ser | Val | Gln | 130 | 135 | 140 | |
| Asn | Asp | Ile | Lys | Ala | Met | Gln | His | Glu | Ser | Leu | Tyr | Ser | Arg | Leu | Tyr | 145 | 150 | 155 | 160 |
| Met | Ser | | | | | | | | | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:16603418_c3_33-AA

Figure 102A - page 119

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 102

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Ala | Leu | Lys | Thr | Phe | Leu | Lys | Lys | Ser | Leu | Ile | Leu | Leu | Leu | 1 | 5 | 10 | 15 |
| Ala | Ile | Ala | Leu | Asn | His | Leu | Asn | Ala | Val | Ala | Met | Ile | Val | Asp | Asn | 20 | 25 | 30 | |
| Pro | Thr | Gln | Asn | Ala | Trp | Asn | Gly | Ala | Lys | Arg | Ala | Trp | Asp | Glu | Ser | 35 | 40 | 45 | |
| Lys | Trp | Ala | Lys | His | Leu | Ala | Thr | Ile | Thr | Glu | Arg | Ile | Lys | Leu | Ala | 50 | 55 | 60 | |
| Gln | Asp | Thr | Leu | Asp | Arg | Ala | Asn | Gln | Thr | Leu | Asn | Ser | Ile | Asn | Lys | 65 | 70 | 75 | 80 |
| Val | Asn | Asp | Val | Leu | Asn | Lys | Thr | Asn | Gln | Phe | Leu | Thr | Gly | Ser | Ile | 85 | 90 | 95 | |
| Leu | Ser | Ile | Pro | Asn | Pro | Met | Gln | Tyr | Val | Glu | Lys | Ile | Gln | Ser | Phe | 100 | 105 | 110 | |
| Ala | Lys | Gln | Val | Gln | Ala | Asn | Thr | Glu | Arg | Ile | Lys | Glu | Asn | Ala | Gln | 115 | 120 | 125 | |
| Asn | Tyr | Asp | Ile | Arg | Asn | Gln | Ile | Ala | Ala | Lys | Arg | Ile | Ser | Glu | Lys | 130 | 135 | 140 | |
| Cys | Pro | Glu | Leu | Asn | Trp | Asp | Val | Ser | Gln | Asp | Ala | Ser | Pro | Thr | Glu | 145 | 150 | 155 | 160 |
| Lys | Asn | Leu | His | Gln | Phe | Phe | Thr | Ser | Lys | Gly | Lys | Glu | Ser | Ala | Asn | 165 | 170 | 175 | |
| Thr | Lys | Ala | Leu | Lys | Asp | Phe | Ala | Asn | Ala | Ile | Gly | Asn | Thr | Gln | Ile | 180 | 185 | 190 | |
| Ser | Thr | Ala | Asn | Asp | Leu | Gly | Ala | Gly | Leu | Arg | Gly | Arg | Ala | Leu | Leu | 195 | 200 | 205 | |
| Glu | Tyr | Ile | Cys | Ile | Gln | Lys | Gly | Asn | Leu | Glu | Ala | Ala | Lys | Lys | Ile | 210 | 215 | 220 | |
| Gln | Leu | Leu | Asp | Ser | Gln | Met | Thr | Leu | Ala | Leu | Leu | Asn | Asn | Asp | Tyr | 225 | 230 | 235 | 240 |

[illegible]

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 58 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 103

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Met Ala Phe Ile Leu Thr Thr Asn Leu Phe Ile Lys Ser Phe Thr Asn
1 5 10 15

Ser Ile Arg Ile Thr Gly Cys Ile Ile Ser Pro Asn Val Phe Phe Ala
20 25 30

Tyr Glu Phe Cys Ala Leu Gly Phe Arg Lys Gly Gly Leu Ile Leu Asp
35 40 45

Asn Phe Ser Lys Phe Val Ser His Arg Leu Gln
50 55

(2) INFORMATION FOR SEQ ID NO:16984442_f1_1-AA

Figure 104A -page 122

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 247 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 104

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: flagellar biosynthetic protein flpP

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Arg | Phe | Phe | Ile | Phe | Leu | Ile | Leu | Ile | Cys | Pro | Leu | Ile | Cys | Pro | 1 | 5 | 10 | 15 |
| Leu | Met | Ser | Ala | Asp | Ser | Ala | Leu | Pro | Ser | Val | Asn | Leu | Ser | Leu | Asn | 20 | 25 | 30 | |
| Ala | Pro | Ser | Asp | Pro | Lys | Gln | Leu | Val | Thr | Thr | Leu | Asn | Val | Ile | Ala | 35 | 40 | 45 | |
| Leu | Leu | Thr | Leu | Leu | Val | Leu | Ala | Pro | Ser | Leu | Ile | Leu | Val | Met | Thr | 50 | 55 | 60 | |
| Ser | Phe | Thr | Arg | Leu | Ile | Val | Val | Phe | Ser | Phe | Leu | Arg | Thr | Ala | Leu | 65 | 70 | 75 | 80 |
| Gly | Thr | Gln | Gln | Thr | Pro | Pro | Thr | Gln | Ile | Leu | Val | Ser | Leu | Ser | Leu | 85 | 90 | 95 | |
| Ile | Leu | Thr | Phe | Phe | Ile | Met | Glu | Pro | Ser | Leu | Lys | Lys | Ala | Tyr | Asp | 100 | 105 | 110 | |
| Thr | Gly | Ile | Lys | Pro | Tyr | Met | Asp | Lys | Lys | Ile | Ser | Tyr | Thr | Glu | Ala | 115 | 120 | 125 | |
| Phe | Glu | Lys | Ser | Thr | Leu | Pro | Phe | Lys | Glu | Phe | Met | Leu | Lys | Asn | Thr | 130 | 135 | 140 | |
| Arg | Glu | Lys | Asp | Leu | Ala | Leu | Phe | Phe | Arg | Ile | Arg | Asn | Leu | Pro | Asn | 145 | 150 | 155 | 160 |
| Pro | Lys | Thr | Pro | Asp | Asp | Val | Ser | Leu | Ser | Val | Leu | Ile | Pro | Ala | Phe | 165 | 170 | 175 | |
| Met | Ile | Ser | Glu | Leu | Lys | Thr | Ala | Phe | Gln | Ile | Gly | Phe | Leu | Leu | Tyr | 180 | 185 | 190 | |
| Leu | Pro | Phe | Leu | Val | Ile | Asp | Met | Val | Ile | Ser | Ser | Ile | Leu | Met | Ala | 195 | 200 | 205 | |
| Met | Gly | Met | Met | Met | Leu | Pro | Pro | Val | Met | Ile | Ser | Leu | Pro | Phe | Lys | 210 | 215 | 220 | |
| Ile | Leu | Val | Phe | Ile | Leu | Val | Asp | Gly | Phe | Asn | Leu | Leu | Thr | Glu | Asn | 225 | 230 | 235 | 240 |

Leu Val Ala Ser Phe Lys Met Val
245

Figure 104A - page 123

Figure 105A - page 124

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 105

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: D-alanyl-D-alanine carboxypeptidase

Val Met Asp Ala Glu Asn Gly Glu Leu Leu Val Ala Gly Ser Tyr Pro
1 5 10 15

Glu Tyr Asn Leu Asn Asp Phe Val Gly Gly Ile Ser Gln Asp Lys Trp
20 25 30

Gln Lys Leu Gln Asp Asp Ile Tyr Asn Pro Leu Leu
35 40

(2) INFORMATION FOR SEQ ID NO:17089217_f3_38-AA

Figure 106A - page 125

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 106

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|---|----|-----|----|-----|----|----|--|-----|--|-----|--|
| Met | Asn | Phe | Phe | Asp | Thr | Leu | Met | Gly | Met | Phe | Val | Glu | Pro | Ser | Gln | 1 | | 5 | | 10 | | 15 | | | | | |
| Lys | Val | Ala | Lys | Ser | Leu | Ala | Glu | His | Val | Gly | Ser | Phe | Phe | His | Ala | | 20 | | 25 | | 30 | | | | | | |
| Gln | Leu | Ile | Leu | Asn | Thr | Ile | Ile | Thr | Ile | Leu | Phe | Met | Ile | Trp | Ala | | 35 | | 40 | | 45 | | | | | | |
| Tyr | Lys | Arg | Val | Lys | Glu | Gly | Asp | Met | Phe | Glu | Phe | Lys | Thr | Ala | Met | | 50 | | 55 | | 60 | | | | | | |
| Gly | Val | Val | Val | Phe | Ile | Ala | Phe | Val | Gly | Phe | Ile | Asn | Trp | Gly | Ile | | 65 | | 70 | | 75 | | | | | | |
| Lys | Asn | Pro | Asn | Asp | Phe | Asn | Thr | Tyr | Phe | Ile | Asn | Thr | Ile | Phe | Tyr | | | 85 | | 90 | | | | 95 | | | |
| Pro | Ser | Glu | Lys | Leu | Ala | Ile | Leu | Ile | Ala | Gln | Ser | Leu | Asn | Asp | Gly | | | 100 | | 105 | | | | 110 | | | |
| Leu | Glu | Ile | Pro | Thr | Asn | Thr | Asn | Leu | Ser | Pro | Ser | Glu | Ile | Phe | Ser | | | 115 | | 120 | | | | 125 | | | |
| Ile | Gly | Asn | Leu | Ala | Ser | Ser | Ala | Tyr | Ala | Met | Ile | Val | Asn | Leu | Trp | | | 130 | | 135 | | | | 140 | | | |
| Asp | Asn | Ala | Phe | Asp | Gly | Ile | Asn | Met | Phe | Asn | Trp | Leu | Thr | Met | Ile | | | 145 | | 150 | | | | 155 | | 160 | |
| Pro | Lys | Ile | Ile | Met | Phe | Phe | Leu | Val | Ile | Leu | Gly | Glu | Leu | Leu | Phe | | | 165 | | 170 | | | | 175 | | | |
| Leu | Gly | Leu | Leu | Leu | Ile | Ile | Val | Leu | Leu | Val | Thr | Ala | Glu | Ile | Phe | | | 180 | | 185 | | | | 190 | | | |
| Met | Trp | Ser | Ala | Leu | Gly | Leu | Ile | Val | Leu | Pro | Leu | Gly | Leu | Ile | Pro | | | 195 | | 200 | | | | 205 | | | |
| Gln | Thr | Lys | Gly | Met | Leu | Phe | Ser | Tyr | Leu | Lys | Lys | Leu | Ile | Ser | Leu | | | 210 | | 215 | | | | 220 | | | |
| Thr | Leu | Tyr | Lys | Pro | Cys | Met | Met | Leu | Val | Ala | Phe | Phe | Asn | Tyr | Gly | | | 225 | | 230 | | | | 235 | | 240 | |

[illegible]

Figure 107A - page 127

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

HPP 107

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

[illegible]

(2) INFORMATION FOR SEQ ID NO:17787558_c3_18-AA

Figure 108A - page 128

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP108

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: ARGININE TRANSPORT ATP-BINDING [E.coli] & homolog

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|----|----|----|
| Met | Asp | Glu | Pro | Glu | Thr | Ser | Leu | Glu | Gln | Asn | Ala | Leu | Ile | Arg | Leu | 1 | 5 | 10 | 15 |
| Ser | Asn | Leu | Ile | Ser | Leu | Arg | Asn | Thr | Gln | Gln | Leu | Thr | Ser | Ile | Ile | 20 | 25 | 30 | |
| Ala | Thr | His | Asp | Pro | Ile | Val | Leu | Asp | Ser | Cys | Glu | Trp | Val | Leu | Leu | 35 | 40 | 45 | |
| Leu | Lys | Asn | Gly | Asn | Ile | Ala | Gln | Tyr | Lys | Pro | Leu | Asn | Ser | Ile | Leu | 50 | 55 | 60 | |
| Lys | Ser | Val | Ala | Lys | Thr | Phe | Asn | Phe | Lys | Glu | Lys | Pro | Thr | Thr | Lys | 65 | 70 | 75 | 80 |
| Asp | Leu | Leu | Ala | Leu | Leu | Lys | Asp | Ile | | | | | | | | 85 | | | |

(2) INFORMATION FOR SEQ ID NO:179677_c3_22 - AA

Figure 109A - page 129

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 236 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 109

(iii) HYPOTHETICAL: YES

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: proline/betaine transport protein

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Lys | Thr | Leu | Gly | Leu | Ser | Ser | Leu | Gly | Gly | Thr | Leu | Glu | Phe | Tyr | 1 | 5 | 10 | 15 |
| Asp | Phe | Ile | Ile | Phe | Val | Phe | Phe | Thr | Ser | Ile | Ile | Ala | Lys | His | Phe | 20 | 25 | 30 | |
| Phe | Pro | Asn | Thr | Leu | Ser | Pro | Ile | Trp | Ser | Glu | Ile | Asn | Thr | Tyr | Gly | 35 | 40 | 45 | |
| Ile | Phe | Ala | Ala | Gly | Tyr | Leu | Ala | Arg | Pro | Leu | Gly | Gly | Ile | Val | Met | 50 | 55 | 60 | |
| Ala | His | Phe | Gly | Asp | Lys | Phe | Gly | Arg | Lys | Asn | Met | Phe | Met | Leu | Ser | 65 | 70 | 75 | 80 |
| Ile | Leu | Leu | Met | Val | Ile | Pro | Thr | Phe | Ala | Leu | Ala | Leu | Met | Pro | Thr | 85 | 90 | 95 | |
| Phe | Asn | Asp | Leu | Val | Gly | Phe | Gly | Val | Asp | Ser | Met | Gly | Leu | Thr | Pro | 100 | 105 | 110 | |
| Lys | Asn | Ala | His | Tyr | Leu | Gly | Tyr | Ile | Ala | Pro | Val | Phe | Leu | Val | Leu | 115 | 120 | 125 | |
| Val | Arg | Ile | Cys | Gln | Gly | Val | Ala | Val | Gly | Gly | Glu | Leu | Pro | Gly | Ala | 130 | 135 | 140 | |
| Trp | Val | Phe | Val | His | Glu | His | Ala | Pro | Gln | Gly | Gln | Lys | Asn | Thr | Tyr | 145 | 150 | 155 | 160 |
| Ile | Gly | Phe | Leu | Thr | Ala | Ser | Val | Val | Ser | Gly | Ile | Leu | Leu | Gly | Ser | 165 | 170 | 175 | |
| Leu | Val | Tyr | Ile | Gly | Ile | Tyr | Met | Val | Phe | Asp | Lys | Pro | Val | Val | Glu | 180 | 185 | 190 | |
| Asp | Trp | Ala | Trp | Arg | Val | Ala | Phe | Gly | Leu | Gly | Gly | Ile | Phe | Gly | Ile | 195 | 200 | 205 | |
| Ile | Ser | Val | Tyr | Leu | Arg | Arg | Phe | Leu | Glu | Glu | Thr | Pro | Val | Phe | Gln | 210 | 215 | 220 | |
| Gln | Met | Lys | Gln | Gly | Arg | Cys | Leu | Ser | Gln | Ile | Pro | Ala | 225 | 230 | 235 | | | | |

(2) INFORMATION FOR SEQ ID NO:186752_c3_10 - AA

Figure 110A - page 130

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 233 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 110

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: sodium/glutamate symport carrier protein

Val His Gly Phe Gly Val Leu Leu Gly Arg Tyr Val Ile Ser Lys Val
1 5 10 15

Lys Phe Leu Arg Asp Tyr Asp Ile Pro Glu Pro Val Val Gly Gly Val
20 25 30

Leu Val Ala Phe Phe Ile Met Leu Ala Arg Gln Phe Tyr His Phe Gly
35 40 45

Leu Gln Phe Asp Ser Ser Leu Lys Asp Pro Leu Met Leu Thr Phe Phe
50 55 60

Ile Thr Ile Gly Leu Ser Ala Asp Phe Lys Ser Leu Gln Lys Gly Gly
65 70 75 80

Lys Met Leu Ala Val Phe Leu Leu Ala Val Ala Gly Phe Val Val Cys
85 90 95

Gln Asn Ala Val Gly Ile Ser Ile Ala Ser Leu Leu Gly Val Asn Pro
100 105 110

Leu Met Gly Leu Leu Gly Gly Ser Ile Ala Leu Val Gly Gly His Gly
115 120 125

Thr Ser Ala Ala Trp Ala Asn Phe Phe Thr Gln Pro Pro Tyr His Phe
130 135 140

Ser Ser Ser Leu Glu Val Gly Met Ala Cys Ala Thr Phe Gly Leu Val
145 150 155 160

Ser Gly Gly Ile Ile Gly Gly Pro Val Ala Lys Tyr Leu Ile Ser Lys
165 170 175

Tyr Lys Leu Glu Pro Lys Asp Thr Lys Glu Lys Asp Thr Leu Glu Gly
180 185 190

Val Val Ser Lys Gly Phe Glu Thr Pro Lys Glu Gln Arg Leu Ile Thr
195 200 205

Ala Ser Ser Phe Val Glu Thr Leu Ala Leu Ile Ala Ile Ala Leu Leu
210 215 220

Val Gly Thr Phe Phe Ile Ala Phe Asp Ala
225 230

(2) INFORMATION FOR SEQ ID NO:1933_f3_3 - AA

Figure 11A - page 131

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP III

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Asn | Pro | Ser | Leu | Gly | Ser | Asn | Pro | Leu | Unk | Gln | Lys | Ala | Met |
| 1 | | | | 5 | | | | 10 | | | | | | 15 | |
| Lys | Asn | Lys | Unk | Ile | Ser | Lys | Ser | Leu | Pro | Tyr | Tyr | Arg | Lys | Met | Pro |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Asn | Gly | Ala | Glu | Val | Tyr | Gly | Val | Unk | Ile | Leu | Leu | Pro | Leu | Phe | Lys |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Glu | Asn | Thr | Unk | Unk | Trp | Trp | Gly | Val | Leu | Met | Ile | Phe | Phe | Ile | Unk |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Unk | Unk | Val | Met | Lys | Ser | Leu | Lys | Thr | Gly | Ala | Ile | Tyr | Phe | | |
| 65 | | | | | 70 | | | | | 75 | | | | | |

(2) INFORMATION FOR SEQ ID NO:194415_c1_9 - AA

Figure 112 A-page 132

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 470 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 112

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Arg | Lys | Phe | Leu | Asp | Gly | Ala | Lys | Ser | Glu | Val | Leu | Lys | Tyr | Asp | 1 | 5 | 10 | 15 |
| Val | Ile | Ser | Phe | Asp | Ile | Phe | Asp | Thr | Leu | Leu | Leu | Arg | Pro | Phe | Ile | 20 | 25 | 30 | |
| Lys | Pro | Thr | Asp | Leu | Phe | Leu | Tyr | Ile | Glu | Thr | Lys | Tyr | Asn | Ile | Lys | 35 | 40 | 45 | |
| Gly | Phe | His | Gln | Ala | Arg | Ile | Leu | Ala | Glu | Met | Gln | Ser | Arg | Lys | Leu | 50 | 55 | 60 | |
| Ser | Lys | Arg | Gln | Asp | Ile | Thr | Leu | Asp | Glu | Ile | Tyr | His | Gln | Ile | Pro | 65 | 70 | 75 | 80 |
| Lys | Glu | Phe | His | Ser | Tyr | Lys | Gly | Val | Glu | Ile | Ala | Thr | Glu | Lys | Glu | 85 | 90 | 95 | |
| Val | Leu | Val | Pro | Asn | Leu | Glu | Met | Leu | Glu | Leu | Tyr | Arg | Phe | Ala | Lys | 100 | 105 | 110 | |
| Glu | Asn | Asn | Lys | Arg | Val | Ile | Ile | Val | Ser | Asp | Met | Tyr | Leu | Pro | Leu | 115 | 120 | 125 | |
| Glu | Val | Leu | Glu | Asp | Ile | Leu | Ile | Ser | Lys | Gly | Phe | Asp | Gly | Tyr | Thr | 130 | 135 | 140 | |
| Asn | Phe | Tyr | Leu | Ser | Asn | His | Ile | Met | Leu | Thr | Lys | His | Ser | Lys | Asp | 145 | 150 | 155 | 160 |
| Leu | Phe | Lys | His | Val | Leu | Lys | Gln | Glu | Asn | Ile | Thr | Asn | Thr | Gln | Ile | 165 | 170 | 175 | |
| Leu | His | Ile | Gly | Asp | Asn | Ser | Trp | Ala | Asp | Asp | Ala | Met | Pro | Lys | Ser | 180 | 185 | 190 | |
| Leu | Gly | Ile | Ala | Thr | Leu | Phe | Arg | Lys | Ser | Val | Leu | Lys | Gln | Leu | Glu | 195 | 200 | 205 | |
| Glu | Val | Phe | Pro | Lys | Tyr | Lys | Thr | Phe | Asn | Pro | Thr | Ser | Val | Ala | Gln | 210 | 215 | 220 | |
| Ser | Phe | Ile | Leu | Gly | Ser | Leu | Cys | Val | Phe | Tyr | Lys | Asn | Tyr | Ile | Gln | 225 | 230 | 235 | 240 |

Figure 113A - page 134

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPD 113

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: GLUTATHIONE-REGULATED POTASSIUM-EFFLUX SYSTEM PRO

Val Leu Lys Phe Phe Glu Asp Ser Lys Gln Leu Ser Thr Pro Met Gly
1 5 10 15

Lys Ser Ala Val Gly Ile Leu Ile Phe Gln Asp Ile Ala Ala Ile Pro
20 25 30

Met Leu Leu Ile Leu Thr Ile Leu Gly Ser Lys Asp Ser His Val Asn
35 40 45

Leu Leu Ile Leu Lys Thr Leu Ile Ser Ala Gly Ile Ile Leu Ile Leu
50 55 60

Leu Leu Leu Pro Gly Lys Lys Gly Ala Asn Leu Ile Leu Glu Gln Ala
65 70 75 80

Lys Asp Thr Arg Leu Pro Glu Ile Phe Ile Gly Thr Asp Phe Ser Asp
85 90 95

Cys Leu Gln Arg Gly Gly Val Glu Pro Phe Phe Trp Val Phe Tyr Val
100 105 110

Phe Gly Gly Val His Cys Gly His Gly Asp Phe
115 120

(2) INFORMATION FOR SEQ ID NO:19536375_c2_25 -AA

Figure 114 A - page 135

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 98 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 114

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|
| Met | Pro | Val | Ile | Ile | Gly | Tyr | Ile | Cys | Thr | Gly | Thr | Val | Leu | Ala | Ala | | | |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | | | | |
| Phe | Phe | Lys | Ile | Asn | Asp | Phe | Asn | Leu | Leu | Ser | Asp | Ile | Gly | Glu | Phe | | | |
| | | | 20 | | | | | 25 | | | | | 30 | | | | | |
| Gly | Ile | Val | Phe | Leu | Met | Phe | Lys | Lys | Gly | Ile | Glu | Phe | Asn | Phe | Asp | | | |
| | | 35 | | | | | 40 | | | | | 45 | | | | | | |
| Lys | Leu | Lys | Ser | Ile | Lys | Gln | Glu | Val | Leu | Val | Phe | Gly | Leu | Leu | Gln | | | |
| | | 50 | | | | 55 | | | | | 60 | | | | | | | |
| Val | Val | Leu | Cys | Ala | Leu | Ile | Ala | Phe | Leu | Leu | Gly | Tyr | Phe | Val | Leu | | | |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 | | | |
| Gly | Leu | Ser | Pro | Phe | Phe | Pro | Leu | Phe | Leu | Ala | Trp | Gly | Phe | His | Ser | | | |
| | | | | 85 | | | | | 90 | | | | | 95 | | | | |
| Leu | Gln | Pro | | | | | | | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:19536458_f3_15:-AA

Figure 115 A - page 136

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 115

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: VIRULENCE FACTOR MVIN

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ile | Leu | Ala | Leu | Leu | Ile | Ser | Lys | Glu | Lys | Thr | His | Leu | Glu | Ala | 1 | 5 | 10 | 15 |
| Leu | Tyr | Tyr | Leu | Ser | Tyr | Gly | Val | Leu | Gly | Gly | Val | Ala | Gln | Ile | | 20 | 25 | 30 | |
| Leu | Leu | His | Phe | Tyr | Pro | Leu | Val | Lys | Leu | Gly | Leu | Trp | Asp | Leu | Leu | 35 | 40 | 45 | |
| Phe | Lys | Gly | Leu | Leu | Gly | Phe | Lys | Thr | Lys | Asn | Thr | Asn | Lys | Lys | Glu | 50 | 55 | 60 | |
| Tyr | Arg | Leu | Asn | Arg | Ala | Lys | Lys | Asp | Leu | Lys | Ala | Phe | Phe | Lys | Gln | 65 | 70 | 75 | 80 |
| Phe | Phe | Pro | Ser | Val | Leu | Gly | Asn | Ser | Ser | Ala | Gln | Ile | Ala | Ser | Phe | 85 | 90 | 95 | |
| Leu | Asp | Thr | Thr | Ile | Ala | Ser | Phe | Leu | Ala | Ser | Gly | Ser | Val | Ser | Tyr | 100 | 105 | 110 | |
| Leu | Tyr | Tyr | Ala | Asn | Arg | Val | Phe | Gln | Leu | Pro | Leu | Ala | Leu | Phe | Ala | 115 | 120 | 125 | |
| Ile | Ala | Ile | Ser | Thr | Ala | Leu | Phe | Pro | Ser | Ile | Ala | Ile | Ala | Leu | Lys | 130 | 135 | 140 | |
| Asn | Asn | Gln | Gln | Asp | Leu | Ile | Leu | Gln | Arg | Leu | Gln | Lys | Ala | Trp | Phe | 145 | 150 | 155 | 160 |
| Phe | Leu | Val | Gly | Val | Leu | Leu | Leu | Cys | Ser | Ile | Gly | Gly | Ile | Met | Leu | 165 | 170 | 175 | |
| Ser | Lys | Glu | Ile | Thr | Glu | Leu | Leu | Phe | Glu | Arg | Gly | Gln | Phe | Ser | Pro | 180 | 185 | 190 | |
| Lys | Asp | Thr | Leu | Ile | Thr | Ser | Gln | Val | Phe | Ser | Leu | Tyr | Leu | Leu | Gly | 195 | 200 | 205 | |
| Leu | Leu | Pro | Phe | Gly | Leu | Thr | Lys | Leu | Phe | Ser | Leu | Trp | Leu | Tyr | Ala | 210 | 215 | 220 | |
| Lys | Leu | Glu | Gln | Lys | Lys | Ala | Ala | Lys | Ile | Ser | Leu | Ile | Ser | Leu | Phe | 225 | 230 | 235 | 240 |

Leu Gly Leu Ala Ala Ser Leu Ser Leu Met Pro Leu Leu Gly Val Leu
245 250 255

Gly Leu Arg

(2) INFORMATION FOR SEQ ID NO:19537968_f1_1 -AA

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 80 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 116

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Met Leu Asn Lys Pro Lys Pro Leu Phe Leu Leu Leu Val Unk Pro Phe
1 5 10 15

Phe Tyr Leu Cys Asp Leu Val Ala His Leu Ser Thr Arg Ile Asp Leu
20 25 30

Met Unk Ser Cys Unk Val Unk Unk Unk Unk Unk Unk Pro Unk Pro Unk
35 40 45

Unk Lys His Asp Phe Asn Gly Phe Phe Ser Asp Phe Leu Gly Unk Leu
50 55 60

Phe Phe Leu His Gly Phe Unk Phe Ser Asn Ser Ser Gly Asp Lys Ser
65 70 75 80

Leu

(2) INFORMATION FOR SEQ ID NO:19541302_c1_3 - AA

Figure 117 A - page 139

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 117

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Leu | Lys | Tyr | Pro | Thr | Met | Phe | Met | Cys | Ala | Asp | Ala | Val | Ile | Ile |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Ser | Lys | Ala | Asp | Met | Ile | Glu | Val | Phe | Asn | Phe | Arg | Val | Ser | Gln | Val |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Lys | Glu | Asp | Met | Gln | Lys | Leu | Lys | Pro | Glu | Ala | Pro | Ile | Phe | Leu | Met |
| | | | 35 | | | | 40 | | | | | 45 | | | |
| Ser | Ser | Lys | Asp | Pro | Lys | Ser | Leu | Glu | Asp | Phe | Lys | Asn | Phe | Leu | Leu |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Glu | Lys | Lys | Arg | Glu | Asn | Tyr | Gln | Ser | Thr | His | Ser | Phe | | | |
| 65 | | | | | 70 | | | | | 75 | | | | | |

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Ser Leu Ile Val
180

Figure 119A - page 141

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 212 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 119

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xii) SEQUENCE DESCRIPTION: FLAGELLAR M-RING PROTEIN

[illegible]

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 147 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 120

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Val Ile Lys Lys Gly Tyr Ile Arg Gly Asp Leu Met Arg Ile Val Arg
1 5 10 15

Asn Leu Phe Leu Val Ser Phe Val Ala Tyr Ser Ser Ala Phe Ala Ala
20 25 30

Asp Leu Glu Thr Gly Thr Lys Asn Asp Lys Lys Ser Gly Lys Lys Phe
35 40 45

Tyr Lys Leu His Lys Asn His Gly Ser Glu Thr Glu Thr Lys Asn Asp
50 55 60

Lys Lys Leu Tyr Asp Phe Thr Lys Asn Ser Gly Leu Glu Gly Val Asp
65 70 75 80

Leu Glu Lys Ser Pro Asn Leu Lys Ser His Lys Lys Ser Asp Lys Lys
85 90 95

Phe Tyr Lys Gln Leu Ala Lys Asn Asn Ile Ala Glu Gly Val Ser Met
100 105 110

Pro Ile Val Asn Phe Asn Lys Ala Leu Ser Phe Gly Pro Tyr Phe Glu
115 120 125

Arg Thr Lys Ser Lys Lys Thr Gln Tyr Met Asp Gly Gly Leu Met Met
130 135 140

His Ile Arg Phe
145

(2) INFORMATION FOR SEQ ID NO:19626250_c1_21³-AA

Figure 121A - page 143

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP121

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: spoIIIE gene product

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Met | Ile | Asp | Pro | Lys | Met | Val | Glu | Phe | Ser | Ile | Tyr | Ala | Asp | Ile | 1 | 5 | 10 | 15 |
| Pro | His | Leu | Leu | Thr | Pro | Ile | Ile | Thr | Asp | Pro | Lys | Lys | Ala | Ile | Gly | 20 | 25 | 30 | |
| Ala | Leu | Gln | Ser | Val | Ala | Lys | Glu | Met | Glu | Arg | Arg | Tyr | Ser | Leu | Met | 35 | 40 | 45 | |
| Ser | Glu | Tyr | Lys | Val | Lys | Thr | Ile | Asp | Ser | Tyr | Asn | Glu | Gln | Ala | Gln | 50 | 55 | 60 | |
| Ser | Asn | Asp | Val | Glu | Ala | Phe | Pro | Tyr | Leu | Ile | Val | Val | Ile | Asp | Glu | 65 | 70 | 75 | 80 |
| Leu | Ala | Asp | Leu | Met | Met | Thr | Gly | Gly | Lys | Glu | Ala | Glu | Phe | Pro | Ile | 85 | 90 | 95 | |
| Ala | Arg | Ile | Ala | Gln | Met | Gly | Arg | Ala | Ser | Gly | Leu | His | Leu | Ile | Val | 100 | 105 | 110 | |
| Ala | Thr | Gln | Arg | Pro | Ser | Val | Asp | Val | Val | Thr | Gly | Leu | Ile | Lys | Thr | 115 | 120 | 125 | |
| Asn | Leu | Pro | Ser | Arg | Val | Ser | Phe | Arg | Val | Gly | Thr | Lys | Ile | Asp | Ser | 130 | 135 | 140 | |
| Lys | Val | Ile | Leu | Asp | Thr | Asp | Gly | Ala | Gln | Ser | Leu | Leu | Gly | Arg | Gly | 145 | 150 | 155 | 160 |
| Asp | Met | Leu | Phe | Thr | Pro | Pro | Gly | Thr | Asn | Gly | Leu | Val | Arg | Leu | His | 165 | 170 | 175 | |
| Ala | Pro | Phe | Ala | Thr | Glu | Asp | Glu | Ile | Lys | Lys | Ile | Val | Asp | Phe | Ile | 180 | 185 | 190 | |
| Lys | Ala | Gln | Lys | Glu | Val | Glu | Tyr | Asp | Lys | Asp | Phe | Leu | Leu | Glu | Glu | 195 | 200 | 205 | |
| Ser | Arg | Met | Pro | Leu | Asp | Thr | Pro | Asn | Tyr | Gln | Gly | Asp | Asp | Ile | Leu | 210 | 215 | 220 | |
| Glu | Arg | Ala | Lys | Ala | Val | Ile | Leu | Glu | Lys | Lys | Ile | Thr | Ser | Thr | Ser | 225 | 230 | 235 | 240 |

Phe Leu Gln Arg Gln Leu Lys Ile Gly Tyr Asn Gln Ala Ala Thr Ile
245 250 255
Thr Asp Glu Leu Glu Ala Gln Gly Phe Leu Ser Pro Arg Asn Ala Lys
260 265 270
Gly Asn Arg Glu Ile Leu Gln Asn Phe
275 280

Figure 121A-page 144

(2) INFORMATION FOR SEQ ID NO:197166_f2_7-AA

Figure 122A - page 145

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 122

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| Met | Asn | Phe | Phe | Lys | Ile | Leu | Leu | Met | Glu | Leu | Arg | Ala | Ile | Val | Ser | 1 | 5 | 10 | 15 |
| His | Lys | Gly | Val | Leu | Leu | Ile | Leu | Ile | Gly | Ala | Pro | Leu | Ile | Tyr | Gly | 20 | 25 | 30 | |
| Leu | Leu | Tyr | Pro | Leu | Pro | Tyr | Leu | Lys | Asp | Ile | Val | Thr | Gln | Gln | Lys | 35 | 40 | 45 | |
| Ile | Ala | Leu | Val | Asp | Glu | Asp | Asn | Ser | Phe | Leu | Ser | Arg | Gln | Leu | Ala | 50 | 55 | 60 | |
| Phe | Met | Val | Gln | Ser | Ser | Asn | Glu | Leu | Glu | Ile | Ala | Phe | Phe | Ser | Pro | 65 | 70 | 75 | 80 |
| Ser | Met | Leu | Glu | Ala | Lys | Lys | Leu | Leu | Lys | Glu | Glu | Lys | Ile | Tyr | Gly | 85 | 90 | 95 | |
| Ile | Leu | His | Ile | Pro | Ser | His | Phe | Glu | Ala | Asn | Ile | Tyr | Lys | Gln | Ser | 100 | 105 | 110 | |
| Ala | Cys | Asn | Asp | Arg | Phe | Leu | Cys | Glu | Arg | Gln | Leu | Leu | Phe | Asp | Leu | 115 | 120 | 125 | |
| Trp | Cys | Val | Ser | Glu | Cys | Gly | Gly | Gly | Glu | His | Gln | Arg | Leu | Lys | Arg | 130 | 135 | 140 | |

(2) INFORMATION FOR SEQ ID NO:19720300_c3_17-AA

Figure 123A - page 146

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 123

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Leu | Leu | Ala | Leu | Asn | Ala | Ala | Val | Gly | Leu | Trp | Gln | Val | Thr | Ser |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Tyr | Ala | Phe | Thr | Ala | Cys | Trp | Ser | Trp | | | | | | | |
| | | | 20 | | | | | 25 | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:2001403_f3_2- AA

Figure 124A- page 147

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 124

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: hypothetical protein X16 (ORFX16) (and hom. to ch

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Phe | Cys | Tyr | Arg | Arg | Val | Cys | Phe | Thr | Thr | Lys | Leu | Ala | Leu | 1 | 5 | 10 | 15 |
| Ser | Ala | Ser | Ser | Phe | Leu | Ala | Gly | Ile | Ala | Leu | Phe | Val | Ala | His | Leu | 20 | 25 | 30 | |
| Gly | Phe | Met | Asp | Pro | Gln | Ile | Gly | Pro | Leu | Val | Pro | Val | Leu | Lys | Ser | 35 | 40 | 45 | |
| Tyr | Trp | Leu | Asn | Ile | His | Val | Ser | Val | Ile | Thr | Ala | Ser | Tyr | Gly | Phe | 50 | 55 | 60 | |
| Leu | Gly | Leu | Cys | Phe | Val | Leu | Gly | Ile | Leu | Ser | Leu | Val | Leu | Phe | Ile | 65 | 70 | 75 | 80 |
| Leu | Arg | Lys | Gln | Gly | Arg | Phe | Asn | Leu | Asp | Lys | Thr | Ile | Leu | Ser | Ile | 85 | 90 | 95 | |
| Ser | Ala | Ile | Asn | Glu | Met | Ser | Met | Ile | Leu | Gly | Leu | Phe | Met | Leu | Thr | 100 | 105 | 110 | |
| Ala | Gly | Asn | Phe | Leu | Gly | Gly | Val | Trp | Ala | Asn | Glu | Ser | Trp | Gly | Arg | 115 | 120 | 125 | |
| Tyr | Trp | Gly | Trp | Asp | Pro | Lys | Glu | Thr | Trp | Ala | Leu | Ile | Ser | Ile | Cys | 130 | 135 | 140 | |
| Val | Tyr | Ala | Leu | Ile | Leu | His | Leu | Arg | Phe | Leu | Gly | Ser | Gln | Asn | Trp | 145 | 150 | 155 | 160 |
| Pro | Phe | Ile | Leu | Ala | Ser | Ser | Ser | Val | Leu | Gly | Phe | Tyr | Ser | Val | Leu | 165 | 170 | 175 | |
| Met | Thr | Leu | Phe | Trp | Arg | Glu | Leu | Leu | Pro | Phe | Trp | Leu | Ala | Gln | Leu | 180 | 185 | 190 | |
| Cys | Arg | | | | | | | | | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:20023400_f2_3-AA

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Val Gly Gly Leu Ala Met Leu Gly Phe Phe Tyr Asn Ile Glu Lys Ile
1 5 10 15

Ser Leu Ala Thr Ala Thr Ala Phe Ser Gln Cys Ala Pro Unk Tyr Thr
20 25 30

Val Leu Leu Ser Pro Leu Leu Leu Lys Glu Lys Leu Lys Arg Ser Ala
35 40 45

Leu Ile Ser Ala Cys Ile Gly Leu Val Gly Val Val Leu Ile Ser Asp
50 55 60

Pro Ser Val Glu Asn Val Gly Pro Ser
65 70

(2) INFORMATION FOR SEQ ID NO:20032561_f1_1-AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

Figure 126A-page 149

(ii) MOLECULE TYPE: protein

HPP 126

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SODIUM/PROLINE SYMPORTER

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Cys | Trp | Thr | Asp | Leu | Ile | Gln | Gly | Leu | Leu | Met | Met | Ser | Ala | Leu |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Ile | Val | Val | Pro | Ile | Val | Met | Ile | Ile | His | Leu | Gly | Gly | Ile | Gly | Glu |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Gly | Ile | Lys | Ile | Ile | Arg | Glu | Ile | Lys | Pro | Glu | Asn | Leu | Ser | Phe | Unk |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Gln | Gly | Ser | Ser | Val | Val | Ala | Ile | Ile | Ser | Ser | Leu | Ala | Trp | Gly | Leu |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Gly | Tyr | Phe | Gly | Gln | Pro | His | Ile | Leu | Val | Arg | Phe | Met | Ser | Ile | Arg |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 |
| Ser | Ile | Arg | Asp | Val | Pro | Lys | Ala | Thr | Thr | Ile | Gly | Ile | Ser | Trp | Met |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| Val | Ile | Ser | Leu | Ile | Gly | Ala | Cys | Val | Met | Gly | Leu | Leu | Gly | Val | Ala |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Tyr | Val | His | Lys | Unk | Asp | Leu | Ser | Leu | Glu | Asp | Pro | Glu | Lys | Ile | Phe |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| Ile | Val | Met | Ser | Gln | Leu | Leu | Phe | Asn | Pro | Trp | Ile | Thr | Gly | Ile | Leu |
| | 130 | | | | | 135 | | | | | 140 | | | | |
| Leu | Ser | Ala | Ile | Leu | Ala | Ala | Val | Met | Ser | Thr | Ala | Ser | Ser | Gln | Leu |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 |
| Leu | Val | Ser | Ser | Ser | Thr | Ile | Ala | Glu | Asp | Phe | Tyr | Ala | Thr | Ile | Phe |
| | | | | 165 | | | | | 170 | | | | | 175 | |
| Asn | Lys | Asn | Ala | Pro | Gln | Lys | Leu | Val | Met | Thr | Ile | Ser | Arg | Leu | Ser |
| | | | 180 | | | | | 185 | | | | | 190 | | |
| Val | Leu | Gly | Val | Ala | Cys | Ile | Ala | Phe | Phe | Ile | Ser | Thr | Asp | Lys | Asn |
| | | 195 | | | | | 200 | | | | | 205 | | | |
| Ala | Ser | Ile | Leu | Ser | Ile | Val | Ser | Tyr | Ala | Trp | Ala | Gly | Phe | Gly | Ala |
| | 210 | | | | | 215 | | | | | 220 | | | | |
| Ser | Phe | Gly | Ser | Val | Ile | Leu | Phe | Ser | Leu | Phe | Trp | Ser | Arg | Met | Thr |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 |

| | | | | | | | | | | | | | | | |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|-----|-----|------------|------------|------------|------------|-----|
| Arg | Ile | Gly | Ala | Ile 245 | Ala | Gly | Met | Leu | Ser | Gly | Ala | Ser | Thr | Val 255 | Ile |
| Leu | Tyr | Asp | Lys 260 | Phe | Gly | Lys | Ser | Phe 265 | Leu | Asp | Ile | Tyr | Glu 270 | Ile | Val |
| Pro | Gly | Phe 275 | Ile | Val | Ala | Ser | Val 280 | Ala | Ile | Val | Ala | Phe 285 | Ser | Leu | Phe |
| Ser | Ser 290 | Val | Arg | Ser | Gly | Thr 295 | Lys | Glu | Ala | Phe | Glu 300 | Thr | Met | Leu | Lys |
| Glu 305 | Ile | Glu | Ser | Leu | Lys 310 | His | | | | | | | | | |

Figure 126A - page 1SD

Figure 127A - page 151

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 114 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 127

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

[illegible]

(2) INFORMATION FOR SEQ ID NO:203192_c3_14-AA

Figure 128A-page 152

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 199 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 128

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: flagellar biosynthesis protein flhF

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Val | Gly | Pro | Thr | Gly | Val | Gly | Lys | Thr | Thr | Thr | Leu | Ala | Lys | 1 | 5 | 10 | 15 |
| Leu | Ala | Ala | Arg | Tyr | Ser | Arg | Met | Leu | Ala | Lys | Lys | Tyr | Lys | Val | Gly | 20 | 25 | 30 | |
| Ile | Ile | Thr | Leu | Asp | Asn | Tyr | Arg | Ile | Gly | Ala | Leu | Glu | Gln | Leu | Ser | 35 | 40 | 45 | |
| Trp | Tyr | Ala | Asn | Lys | Met | Lys | Met | Ser | Ile | Glu | Ala | Val | Ile | Asp | Ala | 50 | 55 | 60 | |
| Lys | Asp | Phe | Ala | Lys | Glu | Ile | Glu | Ala | Leu | Glu | Tyr | Cys | Asp | Phe | Ile | 65 | 70 | 75 | 80 |
| Leu | Val | Asp | Thr | Thr | Gly | His | Ser | Gln | Tyr | Asp | Lys | Glu | Lys | Ile | Ala | 85 | 90 | 95 | |
| Gly | Leu | Lys | Glu | Phe | Ile | Asp | Gly | Gly | Tyr | Asn | Ile | Asp | Val | Ser | Leu | 100 | 105 | 110 | |
| Val | Leu | Ser | Val | Thr | Thr | Lys | Tyr | Glu | Asp | Met | Lys | Asp | Ile | Tyr | Asp | 115 | 120 | 125 | |
| Ser | Phe | Gly | Val | Leu | Gly | Ile | Asp | Thr | Leu | Ile | Phe | Thr | Lys | Leu | Asp | 130 | 135 | 140 | |
| Glu | Ser | Arg | Gly | Leu | Gly | Asn | Leu | Phe | Ser | Leu | Val | His | Glu | Ser | Gln | 145 | 150 | 155 | 160 |
| Lys | Pro | Ile | Ser | Tyr | Leu | Ser | Val | Gly | Gln | Glu | Val | Pro | Met | Asp | Leu | 165 | 170 | 175 | |
| Lys | Val | Ala | Thr | Asn | Glu | Tyr | Leu | Val | Asp | Cys | Met | Leu | Asp | Gly | Phe | 180 | 185 | 190 | |
| Ser | Asn | Pro | Asn | Lys | Glu | Gln | Ala | | | | | | | | | 195 | 200 | | |

(2) INFORMATION FOR SEQ ID NO:2035936_c2_13 - AA

Figure 129A - page 153

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 129

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: vacuolating cytotoxin Hpylori

| | | | | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Gly | Gly | Ala | Ser | Phe | Ile | Ser | Gly | Gly | Asn | Gly | Thr | Leu | Tyr | Gly | 1 | | 5 | | 10 | | 15 |
| Leu | Asn | Val | Gly | Tyr | Asp | Arg | Leu | Val | Lys | Ser | Val | Ile | Leu | Gly | Gly | | 20 | | 25 | | 30 | |
| Tyr | Val | Ala | Tyr | Gly | Tyr | Ser | Gly | Phe | Asn | Gly | Asn | Ile | Met | His | Ser | | 35 | | 40 | | 45 | |
| Leu | Ala | Asn | Asn | Val | Asp | Val | Gly | Met | Tyr | Ala | Arg | Ala | Phe | Leu | Lys | | 50 | | 55 | | 60 | |
| Arg | Asn | Glu | Phe | Thr | Leu | Ser | Ala | Asn | Glu | Thr | Tyr | Gly | Gly | Asn | Ala | 65 | | 70 | | 75 | | 80 |
| Ser | His | Ile | Asn | Ser | Ser | Asn | Ser | Leu | Leu | Ser | Val | Leu | Asn | Gln | Arg | | 85 | | 90 | | 95 | |
| Tyr | Asn | Tyr | Asn | Thr | Trp | Thr | Thr | Ser | Val | Asn | Gly | Asn | Tyr | Gly | Tyr | | 100 | | 105 | | 110 | |
| Asp | Phe | Met | Phe | Lys | Gln | Lys | Ser | Val | Val | Leu | Lys | Pro | Gln | Val | Gly | | 115 | | 120 | | 125 | |
| Leu | Ser | Tyr | His | Phe | Ile | Gly | Leu | Ser | Gly | Met | Lys | Gly | Lys | Met | Gln | | 130 | | 135 | | 140 | |
| Asn | Pro | Ala | Tyr | Gln | Gln | Phe | Val | Met | His | Ser | Asn | Pro | Ser | Asn | Glu | 145 | | 150 | | 155 | | 160 |
| Ser | Val | Leu | Thr | Leu | Asn | Met | Gly | Leu | Glu | Ser | Arg | Lys | Tyr | Phe | Gly | | 165 | | 170 | | 175 | |
| Lys | Asn | Ser | Tyr | Tyr | Phe | Val | Thr | Ala | Arg | Leu | Gly | Arg | Asp | Leu | Leu | | 180 | | 185 | | 190 | |
| Ile | Lys | Ala | Lys | Gly | Asp | Asn | Val | Val | Arg | Phe | Val | Gly | Glu | Asn | Thr | | 195 | | 200 | | 205 | |
| Leu | Leu | Tyr | Arg | Lys | Gly | Glu | Ile | Phe | Asn | Thr | Phe | Ala | Ser | Val | Ile | | 210 | | 215 | | 220 | |
| Thr | Gly | Gly | Glu | Met | His | Leu | Trp | Arg | Leu | Met | Tyr | Val | Asn | Ala | Gly | 225 | | 230 | | 235 | | 240 |

Val Gly Leu Lys Met Gly Leu Gln Tyr Gln Asp Leu Asn Ile Thr Gly Figure 129A-154
245 250 255

Asn Val Gly Met Arg Val Ala Phe
260

(2) INFORMATION FOR SEQ ID NO:2040717_c2_3-AA

Figure 130A - page 155

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 338 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP130

(iii) HYPOTHETICAL: YES

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asp | Gly | Tyr | Gly | Phe | Lys | Met | Gln | Asp | Leu | Gly | Gln | Lys | Thr | Gln | 1 | 5 | 10 | 15 |
| Val | Ile | Gln | His | Ile | Phe | Ala | Gly | Asp | Asp | Val | Ser | Ala | Leu | Glu | Val | 20 | 25 | 30 | |
| Lys | Glu | Asn | Glu | Cys | Val | Lys | Ile | Met | Thr | Gly | Ala | Met | Val | Pro | Lys | 35 | 40 | 45 | |
| Gly | Ile | Glu | Thr | Ile | Val | Pro | Ile | Glu | Cys | Met | Leu | Glu | Ser | His | Lys | 50 | 55 | 60 | |
| Asp | Phe | Ala | Leu | Ala | Pro | Lys | Asp | Phe | Lys | Ile | His | Ala | Asn | Ile | Arg | 65 | 70 | 75 | 80 |
| Gln | Lys | Gly | Glu | Asn | Ala | Ser | Leu | Asn | Ser | Val | Leu | Val | Pro | Lys | Asn | 85 | 90 | 95 | |
| Thr | Arg | Leu | Asn | Tyr | Gly | His | Ile | Ala | Leu | Ile | Ala | Ser | Gln | Gly | Phe | 100 | 105 | 110 | |
| Lys | Glu | Ile | Lys | Ala | Phe | Arg | Lys | Leu | Lys | Ile | Ala | Leu | Phe | Ser | Ser | 115 | 120 | 125 | |
| Gly | Asp | Glu | Leu | Val | Pro | Leu | Gly | Gln | Asn | Ala | Leu | Glu | Cys | Gln | Val | 130 | 135 | 140 | |
| Tyr | Asp | Val | Asn | Ser | Val | Gly | Val | Phe | Asn | Met | Leu | Lys | Asn | Tyr | Asn | 145 | 150 | 155 | 160 |
| Thr | His | Phe | Leu | Gly | Val | Leu | Lys | Asp | Asp | Lys | Asn | Leu | Gln | Leu | Lys | 165 | 170 | 175 | |
| Ile | Leu | Glu | Leu | Gln | Gly | Tyr | Asp | Val | Ile | Leu | Ser | Ser | Ala | Gly | Val | 180 | 185 | 190 | |
| Ser | Val | Gly | Asp | Lys | Asp | Phe | Phe | Lys | Asp | Ala | Leu | Lys | Glu | Arg | Asn | 195 | 200 | 205 | |
| Ala | Leu | Phe | Tyr | Tyr | Glu | Lys | Val | Asn | Leu | Lys | Pro | Gly | Lys | Pro | Val | 210 | 215 | 220 | |
| Thr | Leu | Ala | Gln | Leu | Asn | Gln | Ser | Ile | Ile | Ile | Gly | Leu | Pro | Gly | Asn | 225 | 230 | 235 | 240 |

[illegible]

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 145 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

HPP 131

[illegible]

(2) INFORMATION FOR SEQ ID NO:2042312_f2_10: -AA

Figure 132 A - page 158

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 132

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|
| Met | Pro | Ile | Asn | Pro | Leu | Tyr | Leu | Phe | Pro | Asn | Leu | Phe | Thr | Ala | Ser | | | |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | | | | |
| Ser | Ile | Phe | Leu | Gly | Met | Met | Ser | Ile | Phe | Tyr | Ala | Ser | Ser | Tyr | Gln | | | |
| | | | 20 | | | | | 25 | | | | | 30 | | | | | |
| Phe | Val | Met | Ala | Cys | Trp | Leu | Val | Val | Ala | Ser | Leu | Ile | Leu | Asp | Gly | | | |
| | | | 35 | | | | 40 | | | | | 45 | | | | | | |
| Leu | Asp | Gly | Arg | Val | Ala | Arg | Leu | Thr | Lys | His | His | | | | | | | |
| | 50 | | | | | 55 | | | | | 60 | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:207817_f3_2-AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

Figure 133A - page 159

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 133

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Leu | Arg | Val | Leu | Leu | Phe | Phe | Cys | Phe | Leu | Phe | Leu | Gln | Ala | 1 | 5 | 10 | 15 |
| Glu | Asp | Lys | Ser | Gln | Glu | Leu | Ser | Ser | Ile | Gln | Lys | Gln | Met | Ala | Leu | 20 | 25 | 30 | |
| Val | Asp | Lys | Lys | Leu | Ala | Lys | Asp | Asp | Asn | Val | Trp | Leu | Lys | Lys | Phe | 35 | 40 | 45 | |
| Glu | Asn | Tyr | Lys | Ile | Tyr | Asn | Gln | Ile | Tyr | Thr | Glu | Lys | Glu | Ser | Val | 50 | 55 | 60 | |
| Arg | Gln | Glu | Leu | Arg | Arg | Leu | Lys | Asn | Lys | Lys | Ser | Lys | Asp | Leu | Leu | 65 | 70 | 75 | 80 |
| Lys | Ile | Ser | Thr | Leu | Glu | His | Thr | Leu | Lys | Ala | Leu | Glu | Ser | Gln | Gln | 85 | 90 | 95 | |
| Lys | Met | Phe | Glu | Ser | Tyr | Gly | Val | Asn | Pro | Phe | Lys | Asp | Leu | Ile | Glu | 100 | 105 | 110 | |
| Arg | Pro | Asn | Ile | Pro | Asn | Ile | Pro | Asn | Ile | Ala | Asn | Pro | Ile | Ala | Ile | 115 | 120 | 125 | |
| Ile | Asp | Gly | Ile | Ser | Phe | Ile | Lys | Ser | Met | Arg | Leu | Lys | His | Glu | Asn | 130 | 135 | 140 | |
| Leu | Lys | Asn | Asn | Gln | Thr | Ser | Leu | Gly | Glu | Val | Leu | Lys | Leu | Leu | Asp | 145 | 150 | 155 | 160 |
| Gln | Lys | His | Gln | Leu | Leu | Asn | Gln | Trp | His | Ala | Leu | Asp | Lys | Ser | Ala | 165 | 170 | 175 | |
| Lys | Leu | Ser | Asp | Glu | Ile | Tyr | Gln | Thr | Gln | Ala | Lys | Arg | Leu | Glu | Leu | 180 | 185 | 190 | |
| Gln | Gly | Ala | Gln | Asn | Ile | Leu | Lys | Thr | Thr | Ile | Gly | Ile | Phe | Gln | Lys | 195 | 200 | 205 | |
| Asp | Ser | Asp | Glu | Ala | Ile | Ser | Ile | Val | Lys | Ser | Gln | Val | Lys | Asn | Gln | 210 | 215 | 220 | |
| Leu | Phe | Lys | Leu | Val | Tyr | Val | Phe | Leu | Ala | Ala | Leu | Leu | Ser | Val | Val | 225 | 230 | 235 | 240 |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe | Ala | Trp | Ile | Leu | Lys | Ile | Ile | Ser | Ser | Lys | Tyr | Ile | Glu | Asn | Asn |
| | | | | 245 | | | | | 250 | | | | | 255 | |
| Glu | Arg | Val | Tyr | Thr | Val | Asn | Lys | Ala | Ile | Asn | Phe | Val | Asn | Val | Ser |
| | | | 260 | | | | | 265 | | | | | 270 | | |
| Val | Ile | Val | Ile | Phe | Phe | Phe | Leu | Ile | | | | | | | |
| | | 275 | | | | | 280 | | | | | | | | |

Figure 133A - page 160

(2) INFORMATION FOR SEQ ID NO:2082012_c1_2_AA

Figure 134A - page 161

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 134

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Ser | Ala | Leu | Leu | Ser | Lys | Met | Gly | Thr | Tyr | Ala | Leu | Leu | Arg | 1 | 5 | 10 | 15 |
| Phe | Leu | Leu | Pro | Leu | Phe | Pro | Glu | Leu | Ser | Glu | Ile | Tyr | Leu | Thr | Pro | 20 | 25 | 30 | |
| Ile | Ala | Ile | Val | Ala | Leu | Cys | Met | Ile | Ile | Tyr | Gly | Gly | Phe | Leu | Ala | 35 | 40 | 45 | |
| Tyr | Ala | Gln | Lys | Asp | Leu | Lys | Thr | Leu | Ile | Ala | Tyr | Ser | Ser | Phe | Ser | 50 | 55 | 60 | |
| His | Met | Gly | Val | Val | Val | Leu | Gly | Val | Phe | Ser | Phe | Asn | Val | Glu | Gly | 65 | 70 | 75 | 80 |
| Val | Ser | Gly | Ala | Val | Phe | Met | Met | Phe | Ala | His | Gly | Val | Ile | Val | Met | 85 | 90 | 95 | |
| Gly | Leu | Phe | Leu | Leu | Ala | Gly | Ile | Leu | Glu | Glu | Arg | Ala | Ser | Ser | Leu | 100 | 105 | 110 | |
| Glu | Ile | Ala | Arg | Phe | Gly | Ser | Ile | Ala | Lys | Ser | Ala | Pro | Val | Phe | Ala | 115 | 120 | 125 | |
| Ala | Phe | Phe | Met | Ile | Val | Leu | Met | Ala | Asn | Val | Gly | Met | Pro | Leu | Ser | 130 | 135 | 140 | |
| Ile | Gly | Phe | Val | Gly | Glu | Phe | Leu | Asn | Leu | Leu | Gly | Phe | Phe | Ala | Thr | 145 | 150 | 155 | 160 |
| Tyr | Pro | Leu | Leu | Ala | Ile | Ile | Ala | Gly | Thr | Ser | Leu | Ile | Leu | Ser | Ala | 165 | 170 | 175 | |
| Val | Tyr | Ile | Leu | Thr | Ser | Tyr | Lys | Asp | Val | Phe | Phe | Gly | Asn | Leu | Lys | 180 | 185 | 190 | |
| Thr | Gly | Asn | Asn | Gln | Ile | Ser | Val | Phe | Glu | Asp | Leu | Asn | Ala | Arg | Glu | 195 | 200 | 205 | |
| Val | Gly | Val | Leu | Ser | Val | Ile | Leu | Ala | Phe | Asp | Leu | Asn | Phe | Arg | Asp | 210 | 215 | 220 | |
| Leu | Tyr | Lys | Ser | Ala | Phe | Lys | Thr | Asp | 225 | 230 | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:20836042_f2_4-AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP135

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Glu | Leu | Ile | Ser | Asn | Asn | Pro | Asn | Ala | Ser | Gln | Gln | Ser | Ile | Val |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| | | | | | | | | | | | | | | | |
| Ile | Pro | Leu | Glu | Thr | Phe | Ala | Leu | Ala | Arg | Ala | Leu | Lys | Gly | Ile | Phe |
| | | | 20 | | | | | 25 | | | | | 30 | | |

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 117 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

```
(ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: YES
```

(xi) SEQUENCE DESCRIPTION:

[illegible]

(2) INFORMATION FOR SEQ ID NO:20976500_c2_7-AA

Figure 137A - page 164

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP137

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: UREASE OPERON UREC PROTEIN

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Ile | Phe | Gly | Thr | Asp | Gly | Val | Arg | Gly | Lys | Ala | Gly | Val | Lys | 1 | 5 | 10 | 15 |
| Leu | Thr | Pro | Met | Phe | Val | Met | Arg | Leu | Gly | Ile | Ala | Ala | Gly | Leu | Tyr | 20 | 25 | 30 | |
| Phe | Lys | Lys | His | Ser | Gln | Thr | Asn | Lys | Ile | Leu | Ile | Gly | Lys | Asp | Thr | 35 | 40 | 45 | |
| Arg | Lys | Ser | Gly | Tyr | Met | Val | Glu | Asn | Ala | Leu | Val | Ser | Ala | Leu | Thr | 50 | 55 | 60 | |
| Ser | Ile | Gly | Tyr | Asn | Val | Ile | Gln | Ile | Gly | Pro | Met | Pro | Thr | Pro | Ala | 65 | 70 | 75 | 80 |
| Ile | Ala | Phe | Leu | Thr | Glu | Asp | Met | Arg | Cys | Asp | Ala | Gly | Ile | Met | Ile | 85 | 90 | 95 | |
| Ser | Ala | Ser | His | Asn | Pro | Phe | Glu | Asp | Asn | Gly | Ile | Lys | Phe | Phe | Asn | 100 | 105 | 110 | |
| Ser | Tyr | Gly | Tyr | Lys | Leu | Lys | Glu | Glu | Glu | Glu | Arg | Ala | Ile | Glu | Glu | 115 | 120 | 125 | |
| Ile | Phe | His | Asp | Glu | Glu | Leu | Leu | His | Ser | Ser | Tyr | Lys | Val | Gly | Glu | 130 | 135 | 140 | |
| Ser | Val | Gly | Ser | Ala | Lys | Arg | Ile | Asp | Asp | Val | Ile | Gly | Pro | Leu | Tyr | 145 | 150 | 155 | 160 |
| Arg | Ala | Phe | Glu | Ala | Leu | Tyr | Thr | Gln | Thr | Phe | | | | | | 165 | 170 | | |

(2) INFORMATION FOR SEQ ID NO:2111040_f3_4-AA

Figure 138A - page 165

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 138

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Val Arg Ala Val Phe Val Phe Gly Leu Lys Ala Ala Phe Cys Ile Gly
1 5 10 15
Ile Phe Phe Tyr Gly Ala Tyr Tyr Phe Leu Asp Glu Phe Leu Ile Lys
20 25 30
Leu

(2) INFORMATION FOR SEQ ID NO:214812_c1_4 -AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 139

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: L-lactate permease

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|----|----|----|
| Val | Phe | Leu | Thr | Gly | Ser | Asp | Thr | Ser | Ser | Asn | Leu | Leu | Phe | Gly | Ser | 1 | 5 | 10 | 15 |
| Leu | Gln | Met | Val | Ile | Ala | Thr | Gln | Leu | Gly | Leu | Pro | Glu | Val | Leu | Phe | 20 | 25 | 30 | |
| Leu | Ala | Ala | Asn | Thr | Ser | Gly | Gly | Val | Val | Gly | Lys | Met | Ile | Ser | Pro | 35 | 40 | 45 | |
| Gln | Ser | Ile | Ala | Ile | Ala | Cys | Ala | Ala | Val | Gly | Leu | Val | Gly | Lys | Glu | 50 | 55 | 60 | |
| Ser | Glu | Met | Phe | Arg | Phe | Thr | Val | Lys | Tyr | Ser | Ile | Ala | Leu | Ala | Ile | 65 | 70 | 75 | 80 |
| Ile | Met | Gly | Ile | Val | Leu | His | Ser | Tyr | Arg | Leu | Cys | Phe | Leu | Leu | Tyr | 85 | 90 | 95 | |
| Tyr | Ser | Ser | Tyr | Ser | Tyr | Leu | Met | Glu | Gly | Val | 100 | 105 | | | | | | | |

Figure 140A-page 167

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 65 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 140

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: penicillin-binding protein 2

Val Gly Met Tyr Glu Val Cys Asn His Lys Asp Gly Thr Ala Tyr His
1 5 10 15

Ser Thr Arg Gly Ser Lys Val Thr Leu Ala Cys Lys Thr Gly Thr Ala
20 25 30

Gln Val Val Glu Ile Ala Gln Asn Ile Val Asn Arg Met Lys Glu Lys
35 40 45

Asp Met Glu Tyr Phe His Unk Pro Unk Arg Gly Leu Arg His Ile Phe
50 55 60

Unk Leu
65

168

HPP 141

Val Pro Ile Thr Ser Ile
130

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 69 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 142

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Val Arg Ser Gly Lys Arg Leu Gly Tyr Thr Asn Gln Val Ile Thr Asp
1 5 10 15

Ile Val Asn Ile Gly Ile Gly Gly Ser Asp Leu Gly Ala Leu Met Val
20 25 30

Cys Thr Ala Leu Lys Arg Tyr Gly His Pro Arg Leu Lys Met His Phe
35 40 45

Val Ser Asn Val Glu Trp His Ala Asp Phe Arg Arg Phe Gly Lys Asn
50 55 60

Gln Pro Gly Gln Arg Ala
65 70

```
Val Asn
    130
```


(2) INFORMATION FOR SEQ ID NO:21503772_f2_4 - AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 144

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Unk | Gly | Ile | Ser | Leu | Leu | His | Leu | Ser | Leu | Glu | Gln | Lys | Ile | Ser |
| 1 | | | | 5 | | | | 10 | | | | | | 15 | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Phe | Leu | Gly | Unk | Asn | Leu | Met | Leu | Unk | Pro | Val | Unk | Glu | Val | Leu |
| | | | 20 | | | | | 25 | | | | | 30 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe | Ser | Ile | Leu | Arg | Arg | Lys | Ile | Lys | Arg | Gln | Lys | Ala | Thr | His | Ala |
| | | | 35 | | | | 40 | | | | | 45 | | | |

Gly

(2) INFORMATION FOR SEQ ID NO:21511555_c2_17: -AA

Figure 145A -page 172

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 145

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Glu | Lys | Leu | Ile | Glu | Arg | Val | Leu | Phe | Ala | Thr | Arg | Trp | Leu |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Leu | Ala | Pro | Leu | Cys | Ile | Ala | Met | Ser | Leu | Val | Leu | Val | Val | Leu | Gly |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Tyr | Val | Phe | Met | Lys | Glu | Leu | Trp | His | Met | Leu | Ser | His | Leu | Asn | Thr |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Ile | Ser | Glu | Thr | Asp | Leu | Val | Leu | Ser | Ala | Leu | Gly | Leu | Val | Asp | Leu |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Leu | Val | His | Gly | Arg | Ala | Cys | Phe | Asp | Gly | Ala | Ala | Arg | Gln | Leu | |
| 65 | | | | | 70 | | | | | 75 | | | | | |

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 101 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

[illegible]

(2) INFORMATION FOR SEQ ID NO:21573938_f2_3-AA

Figure 147A - page 174

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 147

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: vacuolating cytotoxin of Hpylori

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Asp | Met | Lys | Asp | Ala | Val | Gly | Thr | Tyr | Lys | Leu | Unk | Arg | Ala |
| 1 | | | | 5 | | | | | 10 | | | | | 15 |

(2) INFORMATION FOR SEQ ID NO:21618785_c3_28 - A A

Figure 148A - page 175

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 367 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 148

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: VIRB4 PROTEIN PRECURSOR

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Phe | Met | Ser | Met | Thr | Leu | Asn | Ala | Met | Gly | Gln | Phe | Ala | Tyr | Asn | 1 | 5 | 10 | 15 |
| Phe | Pro | Ala | Asn | Ile | Ser | Lys | Asp | Lys | Gln | Lys | Leu | Thr | Met | Val | Tyr | 20 | 25 | 30 | |
| Met | Asp | Lys | Asp | Tyr | Gly | Ala | Tyr | Gly | Asn | Ile | Val | Ala | Met | Gly | Gly | 35 | 40 | 45 | |
| Glu | Tyr | Val | Lys | Ile | Glu | Leu | Gly | Thr | Asp | Thr | Gly | Leu | Asn | Pro | Phe | 50 | 55 | 60 | |
| Ala | Trp | Ala | Ala | Cys | Val | Gln | Lys | Thr | Asn | Ala | Thr | Met | Glu | Gln | Lys | 65 | 70 | 75 | 80 |
| Gln | Thr | Ala | Ile | Ser | Val | Val | Lys | Glu | Leu | Val | Lys | Asn | Leu | Ala | Thr | 85 | 90 | 95 | |
| Lys | Ser | Asp | Glu | Lys | Asp | Glu | Asn | Gly | Asn | Ser | Ile | Ser | Phe | Ser | Leu | 100 | 105 | 110 | |
| Ala | Asp | Ser | Asn | Thr | Leu | Ala | Ala | Ala | Val | Thr | Asn | Leu | Ile | Thr | Gly | 115 | 120 | 125 | |
| Asp | Met | Asn | Leu | Asp | Tyr | Pro | Ile | Thr | Gln | Leu | Ile | Asn | Ala | Phe | Gly | 130 | 135 | 140 | |
| Lys | Asp | His | Asn | Asp | Pro | Asn | Gly | Leu | Val | Ala | Arg | Leu | Ala | Pro | Phe | 145 | 150 | 155 | 160 |
| Cys | Lys | Ser | Thr | Asn | Gly | Glu | Phe | Gln | Trp | Leu | Phe | Asp | Asn | Lys | Ala | 165 | 170 | 175 | |
| Thr | Asp | Arg | Leu | Asp | Phe | Ser | Lys | Thr | Ile | Ile | Gly | Val | Asp | Gly | Ser | 180 | 185 | 190 | |
| Ser | Phe | Leu | Asp | Asn | Asn | Asp | Val | Ser | Pro | Phe | Ile | Cys | Phe | Tyr | Leu | 195 | 200 | 205 | |
| Phe | Ala | Arg | Ile | Gln | Glu | Ala | Met | Asp | Gly | Arg | Arg | Phe | Val | Leu | Asp | 210 | 215 | 220 | |
| Ile | Asp | Glu | Ala | Trp | Lys | Tyr | Leu | Gly | Asp | Pro | Lys | Val | Ala | Tyr | Phe | 225 | 230 | 235 | 240 |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Val | Arg | Asp | Met | Leu | Lys | Thr | Ala | Arg | Lys | Arg | Asn | Ala | Ile | Val | Arg | |
| | | | | 245 | | | | | 250 | | | | | 255 | | |
| Leu | Ala | Thr | Gln | Ser | Ile | Thr | Asp | Leu | Leu | Ala | Cys | Pro | Ile | Ala | Asp | |
| | | | 260 | | | | | 265 | | | | | 270 | | | |
| Thr | Ile | Arg | Glu | Gln | Cys | Pro | Thr | Lys | Ile | Phe | Leu | Arg | Asn | Asp | Gly | |
| | | 275 | | | | | 280 | | | | | 285 | | | | |
| Gly | Asn | Leu | Ser | Asp | Tyr | Gln | Arg | Leu | Ala | Asn | Val | Thr | Glu | Lys | Glu | |
| | 290 | | | | | 295 | | | | | 300 | | | | | |
| Phe | Glu | Ile | Ile | Thr | Lys | Gly | Leu | Asp | Arg | Lys | Ile | Leu | Tyr | Lys | Gln | |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 | |
| Asp | Gly | Ser | Pro | Ser | Val | Ile | Ala | Ser | Phe | Asn | Leu | Arg | Gly | Ile | Pro | |
| | | | | 325 | | | | | 330 | | | | | 335 | | |
| Lys | Glu | Tyr | Leu | Lys | Ile | Leu | Ser | Thr | Asp | Thr | Val | Phe | Val | Lys | Glu | |
| | | | 340 | | | | | 345 | | | | | 350 | | | |
| Ile | Asp | Lys | Ile | Ile | Gln | Asn | His | Ser | Ile | Ile | Asp | Lys | Tyr | Gln | Pro | |
| | | 355 | | | | | 360 | | | | | 365 | | | | |

(2) INFORMATION FOR SEQ ID NO:21647676_f1_7-AA

Figure 149A-page 177

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1026 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 149

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: mature-parasite-infected erythrocyte surface anti

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Val | Cys | Leu | Asp | His | Gln | Val | Gly | Ala | Gly | Lys | Thr | Leu | Cys | Ala | Ile | |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | | |
| Ala | Ser | Cys | Met | Glu | Gln | Lys | Arg | Met | Gly | Leu | Val | Asn | Lys | Thr | Leu | |
| | | | 20 | | | | | 25 | | | | | 30 | | | |
| Ile | Ala | Val | Pro | Asn | His | Leu | Thr | Lys | Gln | Trp | Gly | Asp | Glu | Phe | Tyr | |
| | | 35 | | | | | 40 | | | | | 45 | | | | |
| Lys | Ala | Tyr | Pro | Asn | Ala | Asn | Val | Leu | Val | Val | Asp | Ser | Lys | Asp | Thr | |
| | | 50 | | | | 55 | | | | | 60 | | | | | |
| Thr | Glu | Lys | Glu | Arg | Glu | Leu | Leu | Phe | Asn | Gln | Ile | Ala | Asn | Asn | Asn | |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 | |
| Tyr | Asp | Ala | Val | Val | Ile | Ala | His | Thr | His | Leu | Glu | Leu | Leu | Ser | Asn | |
| | | | | 85 | | | | | 90 | | | | | 95 | | |
| Pro | Arg | Gly | Ile | Ile | Glu | Glu | Leu | Lys | Glu | Glu | Glu | Leu | Val | Asn | Ala | |
| | | | 100 | | | | | 105 | | | | | | 110 | | |
| Glu | Lys | Asn | Phe | Glu | Arg | Gln | Glu | Leu | Ala | Tyr | Lys | Asn | Asn | Pro | Arg | |
| | | 115 | | | | | 120 | | | | | 125 | | | | |
| Glu | Thr | Lys | Lys | Pro | Asn | Glu | Arg | Ala | Phe | Lys | Asn | Lys | Leu | Asp | Lys | |
| | | 130 | | | | 135 | | | | | 140 | | | | | |
| Ile | Arg | Ala | Lys | Tyr | Asp | Ala | Ile | Leu | Glu | Lys | Gln | Gly | Ser | His | Ile | |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 | |
| Asp | Ile | Ser | Gln | Met | Gly | Ile | Asp | Asn | Leu | Ile | Val | Asp | Glu | Ala | His | |
| | | | | 165 | | | | | 170 | | | | | 175 | | |
| Leu | Phe | Lys | Asn | Leu | Ala | Phe | Glu | Thr | Ser | Met | Glu | Lys | Ile | Ala | Gly | |
| | | | 180 | | | | | 185 | | | | | 190 | | | |
| Leu | Gly | Asn | Gln | Gln | Gly | Ser | Asn | Arg | Ala | Arg | Asp | Leu | Phe | Ile | Lys | |
| | | 195 | | | | | 200 | | | | | 205 | | | | |
| Thr | Arg | Tyr | Leu | His | Gln | Asn | Asp | Lys | Lys | Ile | Met | Phe | Leu | Thr | Gly | |
| | | 210 | | | | 215 | | | | | 220 | | | | | |
| Thr | Pro | Ile | Ala | Asn | Ser | Leu | Ser | Glu | Met | Tyr | His | Leu | Gln | Arg | Tyr | |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 | |

| | | | | | | | | | | | | | | | | |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|--|
| Leu | Thr | Pro | Asp | Val 245 | Leu | Lys | Glu | Arg | Gly 250 | Leu | Glu | Phe | Phe | Asp 255 | Asp | |
| Trp | Ala | Lys | Thr 260 | Tyr | Gly | Glu | Val | Val 265 | Asn | Asp | Phe | Glu | Leu 270 | Asp | Thr | |
| Ser | Ala | Gln 275 | Ser | Tyr | Lys | Met | Val 280 | Asn | Arg | Phe | Ser | Lys 285 | Phe | Ser | Asp | |
| Val | Gln 290 | Gly | Leu | Ser | Thr | Met 295 | Tyr | Arg | Ala | Phe | Ala 300 | Asp | Ile | Val | Ser | |
| Asn 305 | Asp | Asp | Ile | Leu | Lys 310 | His | Asn | Pro | His | Phe 315 | Val | Pro | Lys | Val | Tyr 320 | |
| Gly | Asp | Lys | Pro | Ile 325 | Asn | Val | Val | Val | Lys 330 | Arg | Ser | Glu | Glu | Val 335 | Ala | |
| Gln | Phe | Ile | Gly 340 | Val | Ala | Leu | Glu | Asn 345 | Gly | Lys | Tyr | Asn | Glu 350 | Gly | Ser | |
| Ile | Ile | Asp 355 | Arg | Met | Gln | Lys | Cys 360 | Glu | Gly | Lys | Lys | Ser 365 | Gln | Lys | Gly | |
| Gln | Asp 370 | Asn | Ile | Leu | Ser | Cys 375 | Thr | Thr | Asp | Ala | Arg 380 | Lys | Val | Ala | Leu | |
| Asp 385 | Tyr | Arg | Leu | Ile | Asp 390 | Pro | Asn | Ala | Lys | Val 395 | Glu | Lys | Glu | Phe | Ser 400 | |
| Lys | Ser | Tyr | Ala | Met 405 | Ala | Lys | Asn | Ile | Tyr 410 | Glu | Asn | Tyr | Leu | Glu 415 | Thr | |
| His | Ala | Thr | Lys 420 | Gly | Thr | Gln | Leu | Gly 425 | Phe | Ile | Gly | Leu | Ser 430 | Thr | Pro | |
| Lys | Thr | His 435 | Ser | Gln | Lys | Val | Ser 440 | Leu | Glu | Ala | Leu | Asp 445 | Asn | Ala | His | |
| Glu | Thr 450 | Glu | Asn | Lys | Asn | Pro 455 | Leu | Asp | Lys | Ala | Gln 460 | Glu | Leu | Leu | Glu | |
| Ser 465 | Leu | Ser | Ser | Tyr | Asp 470 | Glu | Lys | Gly | Asn | Leu 475 | Ile | Ala | Pro | Ser | Lys 480 | |
| Lys | Glu | Leu | Glu | Asn 485 | Glu | Leu | Lys | Glu | Lys 490 | Glu | Ala | Lys | Ser | Val 495 | Asn | |
| Leu | Asp | Glu | Glu 500 | Ile | Ala | Lys | Gly | Cys 505 | Ser | Phe | Asp | Val | Tyr 510 | Ser | Asp | |
| Val | Leu | Arg 515 | His | Leu | Val | Gln | Met 520 | Gly | Ile | Pro | Gln | Asn 525 | Glu | Ile | Ala | |
| Phe | Ile 530 | His | Asp | Ala | Lys | Thr 535 | Glu | Glu | Gln | Lys | Gln 540 | Asp | Leu | Phe | Lys | |
| Lys 545 | Leu | Asn | Arg | Gly | Gly 550 | Val | Arg | Val | Leu | Leu 555 | Gly | Ser | Pro | Ala | Lys 560 | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Gly | Val | Gly | Thr | Asn | Val | Gln | Glu | Arg | Leu | Val | Ala | Met | His | Glu | |
| | | | | 565 | | | | | 570 | | | | | 575 | | |
| Leu | Asp | Cys | Pro | Trp | Arg | Pro | Asp | Glu | Leu | Leu | Gln | Met | Glu | Gly | Arg | |
| | | | 580 | | | | | 585 | | | | | 590 | | | |
| Gly | Ile | Arg | Gln | Gly | Asn | Ile | Leu | His | Gln | Asn | Asp | Pro | Glu | Asn | Phe | |
| | | 595 | | | | | 600 | | | | | 605 | | | | |
| Arg | Met | Lys | Ile | Tyr | Arg | Tyr | Ala | Thr | Glu | Lys | Thr | Tyr | Asp | Ser | Arg | |
| | 610 | | | | | 615 | | | | | 620 | | | | | |
| Met | Trp | Gln | Ile | Ile | Glu | Thr | Lys | Ser | Lys | Gly | Ile | Glu | Gln | Phe | Arg | |
| 625 | | | | | 630 | | | | | 635 | | | | | 640 | |
| Asn | Ala | His | Lys | Leu | Gly | Leu | Asn | Glu | Leu | Glu | Asp | Phe | Asn | Met | Gly | |
| | | | | 645 | | | | | 650 | | | | | 655 | | |
| Ser | Ser | Asn | Ala | Ser | Glu | Met | Lys | Ala | Glu | Ala | Thr | Gly | Asn | Pro | Leu | |
| | | | 660 | | | | | 665 | | | | | 670 | | | |
| Ile | Ile | Glu | Glu | Val | Lys | Leu | Arg | Ala | Glu | Ile | Lys | Ser | Glu | Glu | Ser | |
| | | 675 | | | | | 680 | | | | | 685 | | | | |
| Lys | Tyr | Lys | Ala | Phe | Asn | Lys | Glu | His | Tyr | Phe | Asn | Glu | Glu | Ser | Leu | |
| | 690 | | | | | 695 | | | | | 700 | | | | | |
| Lys | Asn | Asn | Ala | Ser | Lys | Leu | Asp | Tyr | Leu | Lys | Gln | Glu | Leu | Lys | Asp | |
| 705 | | | | | 710 | | | | | 715 | | | | | 720 | |
| Leu | Glu | Thr | Leu | Gln | Arg | Ser | Val | Ile | Ile | Pro | Thr | His | Thr | Glu | Ile | |
| | | | | 725 | | | | | 730 | | | | | 735 | | |
| Lys | Leu | Tyr | Asp | Leu | Lys | Asn | Glu | Glu | Ser | Lys | Asp | Tyr | Glu | Leu | Ile | |
| | | | 740 | | | | | 745 | | | | | 750 | | | |
| Lys | Val | Lys | Glu | Val | Glu | Pro | Leu | Lys | Glu | Asn | Ala | Ser | Met | Ser | Glu | |
| | | 755 | | | | | 760 | | | | | 765 | | | | |
| Glu | Leu | Thr | His | Lys | Lys | Leu | Lys | Glu | Gln | Asn | Lys | Gln | Ile | Ala | Glu | |
| | | | | | | 775 | | | | | 780 | | | | | |
| Gln | Asn | Lys | Glu | Lys | Leu | Asp | Ala | Ile | Lys | Lys | Gln | Phe | Ala | Ser | Asn | |
| 785 | | | | | 790 | | | | | 795 | | | | | 800 | |
| Leu | Asn | Thr | Leu | Phe | Val | Asn | Glu | Glu | Glu | Asp | Tyr | Lys | Leu | Leu | Glu | |
| | | | | 805 | | | | | 810 | | | | | 815 | | |
| Tyr | Lys | Gly | Phe | Val | Val | Asn | Ala | Tyr | Lys | Thr | Lys | Tyr | Gln | Val | Glu | |
| | | | 820 | | | | | 825 | | | | | 830 | | | |
| Phe | Ser | Leu | Ser | Pro | Lys | Asp | Asn | Pro | Asn | Ile | Ala | Tyr | Ser | Pro | Ser | |
| | | 835 | | | | | 840 | | | | | 845 | | | | |
| Asn | Met | Val | Tyr | Lys | Asn | Asp | Thr | Ile | Asn | Met | Phe | Ser | Ser | Tyr | Asn | |
| | 850 | | | | | 855 | | | | | 860 | | | | | |
| Phe | Cys | Ala | Glu | Ile | Lys | Phe | Asp | Gly | Phe | Leu | Lys | Arg | Leu | Asp | Asn | |
| 865 | | | | | 870 | | | | | 875 | | | | | 880 | |

[illegible]

(2) INFORMATION FOR SEQ ID NO:21687842_f3_3 -AA

Figure 150A - page 181

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 107 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 150

(iii) HYPOTHETICAL: YES

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Leu | Val | Ser | Leu | Ile | Val | Ala | Leu | Val | Phe | Cys | Cys | Phe | Leu |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Gly | Ala | Val | Glu | Leu | Pro | Gly | Val | Tyr | Gln | Thr | Gln | Glu | Phe | Leu | Tyr |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Met | Lys | Ser | Ser | Phe | Val | Glu | Phe | Phe | Glu | His | Asn | Gly | Lys | Phe | Tyr |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Ala | Tyr | Gly | Ile | Ser | Asp | Val | Unk | Unk | Ser | Lys | Ala | Lys | Lys | Asp | Lys |
| | | 50 | | | | 55 | | | | | 60 | | | | |
| Leu | Asn | Pro | Asn | Pro | Lys | Leu | Arg | Asn | Arg | Ser | Asp | Lys | Gly | Val | Val |
| 65 | | | | | 70 | | | | 75 | | | | | 80 | |
| Phe | Leu | Ser | Asp | Leu | Ile | Lys | Val | Gly | Glu | Gln | Ser | Tyr | Lys | Gly | Gly |
| | | | | 85 | | | | 90 | | | | | | 95 | |
| Lys | Ala | Unk | Asn | Phe | Unk | Asp | Gly | Lys | Thr | Ser | Met | | | | |
| | | | 100 | | | | | 105 | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:21699087_f1_3-AA

Figure 151A-page 182

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 151

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Glu | Glu | Glu | Lys | Thr | Glu | Leu | Pro | Ser | Ala | Lys | Lys | Ile | Gln |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Lys | Ala | Arg | Glu | Glu | Gly | Asn | Val | Pro | Lys | Ser | Met | Glu | Val | Val | Gly |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Val | Phe | Arg | Val | Ile | Gly | Trp | Ala | Asn | Glu | Tyr | Phe | Cys | Phe | Phe | Tyr |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Met | Val | Gly | Gly | Met | Ala | Leu | Ala | Arg | Cys | Ile | Ala | Met | Cys | | |
| 50 | | | | | | 55 | | | | | 60 | | | | |

(2) INFORMATION FOR SEQ ID NO:21720017_c3_38-AA

Figure 152 A - page 183

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 236 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 152

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Thr | Leu | Val | Lys | Asn | Thr | Ile | Tyr | Ser | Phe | Leu | Leu | Leu | Ser | 1 | 5 | 10 | 15 |
| Val | Leu | Met | Ala | Glu | Asp | Ile | Thr | Ser | Gly | Leu | Lys | Gln | Leu | Asp | Asn | 20 | 25 | 30 | |
| Thr | Tyr | Gln | Glu | Thr | Asn | Gln | Gln | Val | Leu | Lys | Asn | Leu | Asp | Glu | Ile | 35 | 40 | 45 | |
| Phe | Ser | Thr | Thr | Ser | Pro | Ser | Ala | Asn | Asn | Lys | Ile | Gly | Gln | Glu | Asp | 50 | 55 | 60 | |
| Ala | Leu | Asn | Ile | Lys | Lys | Ala | Ala | Ile | Ala | Leu | Arg | Gly | Asp | Leu | Ala | 65 | 70 | 75 | 80 |
| Leu | Leu | Lys | Ala | Asn | Phe | Glu | Ala | Asn | Glu | Leu | Phe | Phe | Ile | Ser | Glu | 85 | 90 | 95 | |
| Asp | Val | Ile | Phe | Lys | Thr | Tyr | Met | Ser | Ser | Pro | Glu | Leu | Leu | Leu | Thr | 100 | 105 | 110 | |
| Tyr | Met | Lys | Ile | Asn | Pro | Leu | Asp | Gln | Lys | Thr | Ala | Glu | Gln | Gln | Cys | 115 | 120 | 125 | |
| Gly | Ile | Ser | Asp | Lys | Val | Leu | Val | Leu | Tyr | Cys | Glu | Gly | Lys | Leu | Lys | 130 | 135 | 140 | |
| Ile | Glu | Gln | Glu | Lys | Gln | Asn | Ile | Arg | Glu | Arg | Leu | Glu | Thr | Ser | Leu | 145 | 150 | 155 | 160 |
| Lys | Ala | Tyr | Gln | Ser | Asn | Ile | Gly | Gly | Thr | Ala | Ser | Leu | Ile | Thr | Ala | 165 | 170 | 175 | |
| Ser | Gln | Thr | Leu | Val | Glu | Ser | Leu | Lys | Asn | Lys | Asn | Phe | Ile | Lys | Gly | 180 | 185 | 190 | |
| Ile | Lys | Lys | Leu | Met | Leu | Ala | His | Asn | Lys | Val | Phe | Leu | Asn | Tyr | Leu | 195 | 200 | 205 | |
| Glu | Glu | Leu | Asp | Ala | Leu | Glu | Arg | Ser | Leu | Glu | Gln | Ser | Lys | Arg | Gln | 210 | 215 | 220 | |
| Tyr | Leu | Gln | Glu | Arg | Gln | Ser | Ser | Lys | Ile | Ile | Val | Lys | 225 | 230 | 235 | | | | |

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 82 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HP 153

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Val Ser Glu Lys Asp Arg Ala Phe Leu Leu Ala Ser Leu Ser Cys Val
1 5 10 15

Asp Tyr Val Val Val Phe Gly Glu Asp Thr Pro Ile Lys Leu Ile Gln
20 25 30

Ala Leu Lys Pro Asp Ile Leu Val Lys Gly Ala Asp Tyr Leu Asn Lys
35 40 45

Glu Val Ile Gly Ser Glu Leu Ala Lys Glu Thr Arg Leu Ile Glu Phe
50 55 60

Glu Glu Gly Tyr Ser Thr Ser Ala Ile Ile Glu Lys Ile Lys Arg Thr
65 70 75 80

His Asn Asp

185

Ile Gln His Trp Val
65

(2) INFORMATION FOR SEQ ID NO:21976637_c3_5-AA

Figure 155A - page 186

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 63 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 155

(iii) HYPOTHETICAL: YES

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Tyr | Asp | Lys | Ser | Leu | Cys | Lys | Thr | Met | Ala | Leu | Ala | Leu | Lys | Ala |
| 1 | | | | 5 | | | | 10 | | | | | 15 | | |
| Leu | Gly | Val | Lys | Arg | Ala | Met | Val | Val | Asn | Gly | Gly | Gly | Thr | Gly | Glu |
| | | | 20 | | | | 25 | | | | | | 30 | | |
| Ile | Val | Leu | His | Asp | Ile | Thr | His | Ala | Cys | Glu | Leu | Lys | Asn | Asn | Glu |
| | | 35 | | | | 40 | | | | | | 45 | | | |
| Ile | Leu | Glu | Tyr | Asp | Leu | Ser | Ala | Lys | Asp | Phe | Asp | Leu | Pro | Pro | Ser |
| 50 | | | | | | 55 | | | | 60 | | | | | |

| | | | | | | | | | | | | | | | |
|------------|------------|------------|------------|-----------|-----------|------------|------------|------------|-----------|-----------|------------|------------|------------|-----------|-----------|
| Met 1 | Pro | Ile | Val | Leu 5 | Gln | Leu | His | Ala | Leu 10 | Tyr | Asn | Glu | Glu | Asn 15 | Asn |
| Tyr | Thr | Gln | Tyr 20 | Leu | Leu | Ser | Val | Met 25 | Leu | Pro | Cys | Met | Trp 30 | Leu | Ile |
| Phe | Ile | Ala 35 | Ile | Gly | Met | Leu | Asn 40 | Phe | Ile | Gln | Lys | Thr 45 | Ser | Asn | Met |
| Arg | Glu 50 | Leu | Leu | Ile | Ser | Ile 55 | Val | Ala | Asn | Val | Cys 60 | Val | Phe | Ser | Phe |
| Trp 65 | Gly | Met | Gly | Met | Ala 70 | Phe | Tyr | Phe | Asn | Leu 75 | Ile | Gly | Met | Glu | Gly 80 |
| Asn | Tyr | Ala | His | Leu 85 | Ser | Leu | Val | Phe | Leu 90 | Ala | Val | Val | Leu | Met 95 | Thr |
| Leu | Ile | Unk | Ser 100 | Gly | Phe | Val | Val | Leu 105 | Val | Leu | Ala | Phe | Gln 110 | Lys | Unk |
| Unk | Leu | Lys 115 | Pro | Leu | Val | Arg | Leu 120 | Gly | Ser | Ile | Pro | Leu 125 | Gln | Ala | Leu |
| Arg | Unk 130 | Leu | Gly | Asp | Leu | Pro 135 | Ala | Lys | Gln | His | Gly 140 | Asn | Phe | Trp | Glu |
| Phe 145 | Trp | Glu | Pro | Leu | Leu | Ala | His | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:22164962_f1_1-AA

Figure 157A - page 188

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 148 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

HPP 157

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| Met | Glu | Val | Met | Asp | Glu | Ala | Leu | Leu | Arg | Ser | Lys | Arg | Phe | Asp | Arg | 1 | 5 | 10 | 15 |
| Arg | Ile | Phe | Ile | Ser | Leu | Pro | Asp | Leu | Leu | Glu | Arg | Gln | Ser | Ile | Leu | 20 | 25 | 30 | |
| Glu | Lys | Leu | Leu | Glu | Asn | Lys | Lys | His | Ala | Leu | Asp | Tyr | Leu | Lys | Ile | 35 | 40 | 45 | |
| Ala | Lys | Ile | Cys | Val | Gly | Phe | Ser | Gly | Ala | Met | Leu | Ala | Thr | Leu | Ile | 50 | 55 | 60 | |
| Asn | Glu | Ser | Ala | Leu | Asn | Ala | Leu | Lys | His | Gln | Arg | Lys | Glu | Ile | Thr | 65 | 70 | 75 | 80 |
| His | Gly | Asp | Ile | Leu | Glu | Val | Lys | Asp | Lys | Ile | Ala | Tyr | Gly | Lys | Lys | 85 | 90 | 95 | |
| Lys | Pro | Gln | Thr | Leu | Asp | Glu | Asn | Gln | Lys | Glu | Leu | Val | Ala | Leu | Tyr | 100 | 105 | 110 | |
| Gln | Ser | Ala | Lys | Ala | Leu | Ser | Ala | Tyr | Trp | Leu | Glu | Ile | Glu | Phe | Asp | 115 | 120 | 125 | |
| Lys | Ala | Ser | Leu | Leu | Gly | Glu | Phe | Ile | Ala | Phe | Asn | Glu | Asn | Lys | Ile | 130 | 135 | 140 | |
| His | Ala | Arg | Ala | Arg | 145 | | | | | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:22265691_c3_14 - AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 227 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

HPP 158

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: D-XYLOSE TRANSPORT ATP-BINDING PROTEIN

[illegible]

(2) INFORMATION FOR SEQ ID NO:22303918_c1_9-AA

Figure 159A - page 190

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 272 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 159

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asn | Lys | Leu | Phe | Leu | Ala | Phe | Ile | Val | Gly | Gly | Met | Leu | Leu | Ser | 1 | 5 | 10 | 15 |
| Ala | Asp | Ala | Leu | Asn | Asp | Lys | Ile | Glu | Asn | Leu | Met | Gly | Glu | Arg | Ser | 20 | 25 | 30 | |
| Tyr | His | Met | Asn | Lys | Leu | Phe | Leu | Glu | Arg | Leu | Phe | Lys | Asn | Arg | Lys | 35 | 40 | 45 | |
| Asp | Phe | Tyr | Glu | Met | Gly | Arg | Leu | Asp | Ser | Leu | Lys | Leu | Leu | Asn | Thr | 50 | 55 | 60 | |
| Leu | Lys | Glu | Asn | Gly | Leu | Leu | Ser | Phe | Asn | Phe | Asp | Lys | Pro | Ser | Val | 65 | 70 | 75 | 80 |
| Leu | Lys | Ile | Thr | Phe | Lys | Ala | Ser | Ser | Asn | Pro | Leu | Ala | Phe | Ala | Lys | 85 | 90 | 95 | |
| Ser | Ile | Asn | Asn | Ser | Leu | Asn | Met | Met | Gly | Tyr | Ser | Tyr | Val | Leu | Pro | 100 | 105 | 110 | |
| Ile | Arg | Met | Gln | Ser | Ser | Ser | Gly | Glu | Asn | Val | Phe | Ser | Tyr | Glu | Leu | 115 | 120 | 125 | |
| Lys | Thr | Glu | Tyr | Val | Leu | Asp | Pro | Asn | Ile | Leu | Ile | Glu | Thr | Met | Lys | 130 | 135 | 140 | |
| Arg | His | Gly | Phe | Asp | Phe | Met | Asp | Ile | Arg | Arg | Val | Ser | Leu | Lys | Glu | 145 | 150 | 155 | 160 |
| Trp | Glu | Tyr | Asp | Phe | Ala | Leu | Gln | Lys | Ile | Lys | Leu | Pro | Asn | Ala | Arg | 165 | 170 | 175 | |
| Ala | Leu | Val | Leu | Ser | Ser | Asp | Pro | Val | Glu | Phe | Lys | Glu | Ala | Ser | Gly | 180 | 185 | 190 | |
| Lys | Tyr | Trp | Leu | Ser | Val | Asn | Gln | Asn | Ala | Tyr | Leu | Lys | Ile | Ser | Ser | 195 | 200 | 205 | |
| Asn | Asn | Pro | Leu | Trp | Gln | Pro | Lys | Ile | Ile | Phe | Tyr | Asp | Glu | Asn | Leu | 210 | 215 | 220 | |
| Lys | Ile | Ile | Gln | Ile | Ile | Ala | Lys | Glu | Asn | Arg | Gln | Gln | Glu | Ile | Ala | 225 | 230 | 235 | 240 |

Leu Asn Leu Leu Asp Gly Val Arg Phe Ile His Ile Thr Asp Ala Lys
245 250 255

Figure 159A - page 191

Asn Pro Ile Ile Leu Lys Asn Gly Ile Ser Val Val Phe Asp Ala Met
260 265 270

Pro

(2) INFORMATION FOR SEQ ID NO:22370182_c1_12 - AA

Figure 160A - page 192

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 160

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: H.influenzae lic-1 operon licA-licD genes

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ser | Arg | Pro | Phe | Lys | Thr | Ile | Lys | Lys | Pro | Pro | Gln | Pro | Pro |
| 1 | | | | 5 | | | | 10 | | | | | 15 | |

(2) INFORMATION FOR SEQ ID NO:22379952_f2_8 - AA

Figure 1b1A - page 193

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP161

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: biopolymer transport exbB protein

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| Met | Unk | Thr | His | Asp | Arg | Arg | Lys | Leu | Arg | Ile | Unk | Leu | Thr | Gln | Thr | 1 | 5 | 10 | 15 |
| Thr | Thr | Leu | Val | Ala | Thr | Ile | Gly | Ser | Asn | Ala | Pro | Tyr | Ile | Gly | Leu | 20 | 25 | 30 | |
| Leu | Gly | Thr | Val | Met | Gly | Ile | Met | Leu | Thr | Phe | Met | Asp | Leu | Gly | Ser | 35 | 40 | 45 | |
| Ala | Ser | Gly | Ile | Asp | Thr | Lys | Ala | Ile | Met | Thr | Asn | Leu | Ala | Leu | Ala | 50 | 55 | 60 | |
| Leu | Lys | Ala | Thr | Gly | Met | Gly | Leu | Leu | Val | Ala | Ile | Pro | Ala | Ile | Val | 65 | 70 | 75 | 80 |
| Ile | Tyr | Asn | Leu | Leu | Val | Arg | Lys | Ser | Glu | Ile | Leu | Val | Thr | Lys | Trp | 85 | 90 | 95 | |
| Asp | Ile | Phe | His | His | Pro | Val | Asp | Thr | Gln | Ser | His | Glu | Val | Tyr | Ser | 100 | 105 | 110 | |
| Lys | Ala | | | | | | | | | | | | | | | | | | |

Figure 162A - page 194

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 66 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 162

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: probable cadmium-transporting ATPase

Met Ile Ala Val Leu Pro Pro Leu Phe Ser Met Gly Ser Phe Asp Glu
1 5 10 15

Trp Ile Tyr Arg Gly Leu Val Ala Leu Met Val Ser Cys Pro Cys Ala
20 25 30

Leu Val Ile Ser Val Pro Leu Gly Tyr Phe Gly Gly Val Gly Ala Ala
35 40 45

Ser Arg Lys Gly Ile Leu Met Lys Gly Val His Val Leu Glu Gly Ala
50 55 60

Tyr Pro Asn
65

(2) INFORMATION FOR SEQ ID NO:22447252_c3_8-AA

Figure 163A - page 195

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 163

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Gln | His | Phe | Asn | Phe | Leu | Tyr | Lys | Asp | Ser | Leu | Phe | Ser | Ile | Ala | 1 | 5 | 10 | 15 |
| Leu | Phe | Thr | Phe | Ile | Ile | Ala | Leu | Val | Ile | Leu | Leu | Glu | Gln | Ala | Arg | 20 | 25 | 30 | |
| Ala | Tyr | Phe | Thr | Arg | Lys | Arg | Asn | Lys | Lys | Phe | Leu | Gln | Lys | Phe | Ala | 35 | 40 | 45 | |
| Gln | Asn | Gln | Asn | Ala | Tyr | Ala | Ser | Ser | Glu | Asn | Leu | Asp | Glu | Leu | Leu | 50 | 55 | 60 | |
| Lys | His | Ala | Lys | Ile | Ser | Ser | Leu | Met | Phe | Leu | Ala | Arg | Ala | Tyr | Ser | 65 | 70 | 75 | 80 |
| Lys | Ala | Asp | Val | Glu | Met | Ser | Ile | Glu | Ile | Leu | Lys | Gly | Leu | Leu | Asn | 85 | 90 | 95 | |
| Arg | Pro | Leu | Lys | Asp | Glu | Glu | Lys | Ile | Ala | Val | Leu | Asp | Leu | Leu | Ala | 100 | 105 | 110 | |
| Lys | Asn | Tyr | Phe | Ser | Val | Gly | Tyr | Leu | Gln | Lys | Thr | Lys | Asp | Thr | Val | 115 | 120 | 125 | |
| Lys | Glu | Ile | Leu | Arg | Phe | Ser | Pro | Arg | Asn | Val | Glu | Ala | Leu | Leu | Lys | 130 | 135 | 140 | |
| Leu | Leu | His | Ala | Tyr | Glu | Leu | Glu | Lys | Asp | Tyr | Ser | Lys | Ala | Leu | Glu | 145 | 150 | 155 | 160 |
| Thr | Leu | Glu | Cys | Leu | Glu | Glu | Leu | Glu | Val | Pro | Lys | Ile | Glu | Thr | Ile | 165 | 170 | 175 | |
| Lys | Asn | Tyr | Leu | Tyr | Leu | Met | His | Leu | Ile | Glu | Asn | Lys | Glu | Asp | Ala | 180 | 185 | 190 | |
| Ala | Lys | Ile | Leu | His | Val | Ser | Lys | Ala | Ser | Leu | Asp | Leu | Lys | Lys | Ile | 195 | 200 | 205 | |
| Ala | Leu | Asn | His | Leu | Lys | Ser | His | Asp | Glu | Asn | Leu | Phe | Trp | Gln | Glu | 210 | 215 | 220 | |
| Ile | Asp | Thr | Thr | Glu | Arg | Leu | Glu | Asn | Val | Ile | Asp | Leu | Leu | Trp | Asp | 225 | 230 | 235 | 240 |

[illegible]

(2) INFORMATION FOR SEQ ID NO:22453166_c2_2 - AA

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein HPP 164

(iii) HYPOTHETICAL: YES

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | His | Leu | Thr | Arg | Gly | Ile | Lys | His |
| 1 | | | | 5 | | | | | 10 |

(2) INFORMATION FOR SEQ ID NO:22460468_c1_8 - AA

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 165.

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: penicillin-binding protein 2

| | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Val | Ile | Leu | Gly | Ser | His | Gly | Lys | Glu | Glu | Tyr |
| 1 | | | | 5 | | | | | 10 | | |

(2) INFORMATION FOR SEQ ID NO:22542803_c1_14:-AA

Figure 166A-page 199

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 166

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|----|----|----|
| Met | Lys | Lys | Val | Ile | Val | Ala | Leu | Gly | Val | Leu | Ala | Phe | Ala | Asn | Val | 1 | 5 | 10 | 15 |
| Leu | Met | Ala | Thr | Asp | Val | Lys | Ala | Leu | Val | Lys | Gly | Cys | Ala | Ala | Cys | 20 | 25 | 30 | |
| His | Gly | Val | Lys | Phe | Glu | Lys | Lys | Ala | Leu | Gly | Lys | Ser | Lys | Ile | Val | 35 | 40 | 45 | |
| Asn | Met | Met | Ser | Glu | Lys | Glu | Ile | Glu | Glu | Asp | Leu | Met | Ala | Phe | Lys | 50 | 55 | 60 | |
| Ser | Gly | Ala | Asn | Lys | Asn | Pro | Val | Met | Thr | Arg | Lys | Leu | Lys | Asn | | 65 | 70 | 75 | |

(2) INFORMATION FOR SEQ ID NO:22667967_f1_2 - AA

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 94 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 167

(iii) HYPOTHETICAL: YES

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: influenzae type B lipooligosaccharide

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|----|----|----|
| Met | Gly | Ile | Ala | Thr | Ser | Leu | Ile | Ser | Glu | Val | Ser | Lys | Phe | Tyr | Tyr | 1 | 5 | 10 | 15 |
| Ala | Leu | Lys | Tyr | His | Ala | Lys | Phe | Met | Ser | Leu | Gly | Glu | Leu | Gly | Cys | 20 | 25 | 30 | |
| Tyr | Ala | Ser | His | Tyr | Ser | Leu | Trp | Gln | Lys | Cys | Ile | Glu | Leu | Asn | Glu | 35 | 40 | 45 | |
| Ala | Ile | Cys | Ile | Leu | Glu | Asp | Asp | Ile | Thr | Leu | Lys | Glu | Asp | Phe | Lys | 50 | 55 | 60 | |
| Glu | Gly | Leu | Asp | Phe | Leu | Glu | Lys | His | Ile | Gln | Glu | Leu | Gly | Tyr | Ala | 65 | 70 | 75 | 80 |
| Arg | Leu | Met | His | Leu | Leu | Tyr | Asp | Ala | Ser | Val | Lys | Ser | Glu | Pro | 85 | 90 | 95 | | |

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 103 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 168

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Val Glu Phe Tyr Ser Lys Asn Phe Unk Gly Phe Ser Asp Cys Ala Phe
1 5 10 15

Arg Phe Tyr His Glu Val Phe Gln Ile Val Trp Leu Leu Leu Ile Val
20 25 30

Leu Unk Phe Phe Ser Ala Lys Glu Ser Unk Pro Ser Glu Pro Pro Asn
35 40 45

Leu Ala Lys Leu Tyr Leu Asn Gly Ala Ile Phe Ser Thr Glu Asp Phe
50 55 60

Asp Lys Glu Val Asp Lys Ile Leu Lys Thr Pro Ser Ile Lys Gly Val
65 70 75 80

Leu Leu Leu Ile Asp Ser Pro Gly Trp Gly Cys Val Ser Glu Arg Gly
85 90 95

Ile Glu Arg Lys Lys Ser Leu Ile
100

Figure 164A - page 202

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 169

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Met His Leu Lys Ser Gly Ala Val Phe Ile Ser Asp Ala His Phe Leu
1 5 10 15

Pro Lys Ser Pro His Leu Ile His Thr Leu Lys Glu Leu Leu Ser Ala
20 25 30

Lys Pro Pro Gln Val Phe Phe Met Gly Asp Ile Phe His Val Leu Val
35 40 45

Gly Tyr Leu Pro Leu Asp Lys Glu Gln Gln Lys Ile Ile Asp Leu Ile
50 55 60

His Ala Leu Ser Glu Ile Ser Gln Val Phe Tyr Phe Glu Gly Asn His
65 70 75 80

Asp Phe Ser Met Arg Phe Val Phe Asn Ser Lys Val Met Val Phe Glu
85 90 95

Arg Gln Asn Gln Pro Ala Leu Phe Gln Tyr Asp Asn Lys Arg Phe Leu
100 105 110

Leu Ala His Gly Asp Leu Phe Ile Thr Lys Ala Tyr Glu Phe Tyr Ile
115 120 125

Thr Gln Leu Thr Ser Thr Trp Ala Arg Phe Phe Leu Thr Phe Leu Asn
130 135 140

Leu Leu Ser Phe Lys Thr Leu Tyr Pro Phe
145 150

(2) INFORMATION FOR SEQ ID NO:22692187_c2_10 -AA

Figure 170A - page 203

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP170

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: FLAGELLAR P-RING PROTEIN PRECURSOR

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gln | Asp | Leu | Asp | Asn | Asn | Met | Ser | Leu | Asp | Thr | Ala | His | Asn | Thr |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Leu | Ser | Ser | Asn | Gly | Lys | Asn | Ile | Thr | Ile | Ala | Gly | Val | Val | Lys | Ala |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Leu | Gln | Lys | Ile | Gly | Val | Ser | Ala | Lys | Gly | Met | Val | Ser | Ile | Leu | Gln |
| | | 35 | | | | | 40 | | | | | 45 | | | |

(2) INFORMATION FOR SEQ ID NO:22704567_c2_27- AA

Figure 171A - page 204

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 171

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Gln | Pro | Met | Lys | Ser | Lys | Lys | Leu | Tyr | Leu | Ala | Leu | Ile | Ile | Gly | 1 | 5 | 10 | 15 |
| Val | Leu | Leu | Ala | Phe | Leu | Thr | Leu | Ser | Ser | Trp | Leu | Gly | Asn | Ser | Gly | 20 | 25 | 30 | |
| Leu | Val | Gly | Arg | Phe | Gly | Val | Trp | Phe | Ala | Ala | Ile | Asn | Lys | Lys | Tyr | 35 | 40 | 45 | |
| Phe | Gly | Tyr | Leu | Ser | Leu | Ile | Asn | Leu | Pro | Tyr | Leu | Ala | Trp | Val | Leu | 50 | 55 | 60 | |
| Phe | Leu | Leu | Tyr | Arg | Ala | Lys | Asn | Pro | Phe | Thr | Glu | Ile | Val | Leu | Glu | 65 | 70 | 75 | 80 |
| Lys | Thr | Leu | Gly | His | Leu | Leu | Gly | Ile | Leu | Ser | Leu | Leu | Phe | Leu | Gln | 85 | 90 | 95 | |
| Ser | Ser | Leu | Leu | Asn | Gln | Gly | Glu | Ile | Gly | Asn | Ser | Ala | Arg | Leu | Phe | 100 | 105 | 110 | |
| Leu | His | Pro | Phe | Ile | Gly | Asp | Phe | Gly | Leu | Tyr | Val | Leu | Ile | Met | Leu | 115 | 120 | 125 | |
| Met | Val | Val | Ile | Ser | Tyr | Leu | Ile | Leu | Phe | Lys | Leu | Pro | Pro | Lys | Ser | 130 | 135 | 140 | |
| Val | Phe | Tyr | Pro | Tyr | Met | Asn | Lys | Thr | Gln | Ser | Leu | Leu | Lys | Glu | Ile | 145 | 150 | 155 | 160 |
| Tyr | Lys | Gln | Cys | Leu | Gln | Ala | Phe | Ser | Pro | Asn | Phe | Ser | Leu | Lys | Lys | 165 | 170 | 175 | |
| Glu | Gly | Phe | Glu | Asn | Thr | Pro | Ser | Asp | Ser | Gln | Lys | Lys | Glu | Thr | Asn | 180 | 185 | 190 | |
| Asn | Asp | Lys | Glu | Lys | Glu | Asn | Leu | Lys | Glu | Asn | Pro | Ile | Asp | Glu | Asn | 195 | 200 | 205 | |
| His | Asn | Thr | Pro | Asn | Glu | Glu | Ser | Phe | Leu | Ala | Ile | Pro | Thr | Pro | Tyr | 210 | 215 | 220 | |
| Asn | Thr | Thr | Leu | Asn | Asn | Ser | Glu | Pro | Gln | Glu | Gly | Leu | Val | Gln | Ile | 225 | 230 | 235 | 240 |

Ser Pro His Pro Pro Thr His Tyr Thr Ile Tyr Pro Lys Arg Asn Arg
 245 250 255

Phe Asp Asp Leu Thr Asn Pro Thr Leu Lys Glu Pro Lys Gln Glu Thr
 260 265 270

Lys Glu Arg Glu Pro Thr Leu Lys Lys Glu Thr Pro Thr Thr Leu Lys
 275 280 285

Pro Ile Met Pro Ile Ser Ala Ser Thr Gln Lys Ile Met Thr Lys Gln
 290 295 300

Lys Thr Thr Lys Pro Leu Thr Thr Pro
 305 310

(2) INFORMATION FOR SEQ ID NO:23437502_c1_25-AA

Figure 172A - page 206

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 172

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Met | Leu | Ser | Arg | Asp | Ile | Val | Gln | Tyr | Ser | Lys | Ile | Arg | Thr | Glu |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Leu | Tyr | Ala | Tyr | Leu | Thr | Tyr | Leu | Phe | Ser | His | Asn | Ile | Arg | Asn | His |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Leu | Pro | Glu | Ile | Thr | Leu | Asp | Tyr | Leu | Asn | Arg | Gln | Ile | Ser | Lys | Met |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Gln | Ala | Glu | Ile | Lys | Met | Ala | Lys | Ser | Phe | Phe | Val | Leu | Asp | Ala | Lys |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Gly | Met | Leu | Met | Leu | Lys | Pro | Ser | Gln | Phe | Lys | Glu | Gln | Gly | His | Lys |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 |
| Glu | Gly | Leu | Leu | Glu | His | Asp | Leu | Thr | Glu | Gly | Ile | Glu | Leu | Glu | Ser |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| His | Val | Ser | Phe | Ser | Asp | Lys | Tyr | Tyr | Phe | Tyr | Gln | Ala | Val | Asn | Glu |
| | | | 100 | | | | | 105 | | | | | | 110 | |
| Lys | Arg | Cys | Ile | Leu | Thr | Asp | Pro | Tyr | Pro | Ser | Lys | Lys | Gly | Asn | His |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| Leu | Val | Val | Ser | Ala | Ser | Tyr | Pro | Val | Tyr | Asp | Gln | Asn | Asn | Asp | Leu |
| | 130 | | | | | 135 | | | | | 140 | | | | |
| Ala | Phe | Val | Val | Cys | Leu | Gln | Ile | Pro | Leu | Arg | Val | Ala | Ile | Glu | Ile |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 |
| Ser | Ser | Pro | Ser | Lys | Tyr | Phe | Lys | Thr | Phe | Ser | Glu | Gly | Ser | Met | Val |
| | | | | 165 | | | | | 170 | | | | | 175 | |
| Met | Tyr | Phe | Met | Ile | Ser | Ile | Met | Leu | Thr | Leu | Val | Ser | Leu | Leu | Leu |
| | | | 180 | | | | | 185 | | | | | 190 | | |
| Phe | Val | Lys | Cys | Ile | Ser | Ser | Phe | Trp | Thr | Ala | Ile | Val | His | Phe | Ser |
| | | 195 | | | | | 200 | | | | | 205 | | | |
| Ser | Phe | Asp | Ile | Lys | Glu | Val | Phe | His | Pro | Ile | Val | Leu | Leu | Thr | Leu |
| | 210 | | | | | 215 | | | | | 220 | | | | |
| Ala | Leu | Ala | Thr | Phe | Asp | Leu | Val | Lys | Ala | Ile | Phe | Glu | Glu | Glu | Val |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Leu | Gly | Lys | Asn | Ser | Gly | Asp | Asn | His | His | Ala | Ile | His | Arg | Thr | Met | |
| | | | | 245 | | | | | 250 | | | | | 255 | | |
| Ile | Arg | Phe | Leu | Gly | Ser | Ile | Ile | Ile | Ala | Leu | Ala | Ile | Glu | Ala | Leu | |
| | | | 260 | | | | | 265 | | | | | 270 | | | |
| Met | Leu | Val | Phe | Lys | Phe | Ser | Val | Ser | Glu | Pro | Asp | Lys | Ile | Thr | Tyr | |
| | | 275 | | | | | 280 | | | | | 285 | | | | |
| Ala | Val | Tyr | Leu | Ala | Ile | Gly | Val | Ala | Val | Leu | Leu | Ile | Ser | Leu | Ala | |
| | 290 | | | | | 295 | | | | | 300 | | | | | |
| Ile | Tyr | Val | Lys | Phe | Ala | Tyr | Ser | Val | Leu | Pro | Lys | Arg | Glu | Arg | | |
| 305 | | | | | 310 | | | | | 315 | | | | | | |

- AA

(A) LENGTH: 162 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

H PP 173

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION:

[illegible]

Figure 174A - page 209

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HDP 174

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Met Val Ile His Glu Lys Ile Lys Ser Arg Phe Ser Arg Asn Trp Ser
1 5 10 15

Leu Arg Asn Arg Gly Arg His Phe Ala Ser Ser Ser Val Tyr Phe Phe
20 25 30

Ser Leu Leu Val Ile Thr Ala Val Asn Arg Ser Ser Ala Val Ala Trp
35 40 45

Leu Leu Met Pro Glu His Leu Ile Gly Trp Phe Leu Ile Ser Phe Ser
50 55 60

Gly Glu Phe Val Ala Asp Met Ala Phe Gly Lys Lys Ser Lys Ile Phe
65 70 75 80

Lys Thr Arg Phe Gly Ile Ser Ile Val Ser Gly Val Ser Leu Leu Leu
85 90 95

Gly Ala Tyr Gln Arg Phe Tyr Phe Leu Tyr Gly Leu Ala Leu Leu Ile
100 105 110

Gly Gly Leu Ser Phe Leu
115

(2) INFORMATION FOR SEQ ID NO:23438887_f1_1-AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 175

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Val | Asn | Asp | Lys | Arg | Unk | Val | Leu | Ala | Met | Val | Unk | Met | Leu | Ile |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Unk | Ser | Leu | Ala | Asn | Ile | Phe | Phe | Asn | Tyr | Leu | Phe | Ile | Phe | Gly | Trp |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Lys | Trp | Gly | Phe | Lys | Ala | Gly | Asp | Ser | His | Arg | Asp | Arg | Ala | Cys | Asp |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Arg | Gly | Phe | Ser | Leu | Asn | Ala | Ala | Phe | Leu | Ala | Gln | Lys | Arg | Gly | Val |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Val | Phe | Tyr | Gln | Thr | Asp | Phe | Leu | Tyr | Leu | Gln | Ser | Phe | Leu | Gln | Leu |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 |
| Lys | Ala | Val | Cys | Leu | Lys | Ala | Arg | Arg | Asn | Leu | Ala | Leu | Leu | Leu | |
| | | | | 85 | | | | | 90 | | | | | | 95 |

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid

(ii) MOLECULE TYPE: protein

HPP 176

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Ala Gly Glu Arg Asn Arg Arg Met Leu Glu Ile Lys
85 90

(2) INFORMATION FOR SEQ ID NO:234391_f2_8-AA

Figure 177A - page 212

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 177

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| Met | Val | Phe | Trp | Gly | Ala | Val | Phe | Phe | Leu | Trp | Asp | Arg | Thr | Ala | Trp | 1 | 5 | 10 | 15 |
| Lys | Arg | Leu | Met | Val | Phe | Leu | Asn | Ser | Leu | Unk | Unk | Met | Leu | Ala | Ala | 20 | 25 | 30 | |
| Leu | Ser | Leu | Gly | Ser | Phe | Leu | Gly | Ala | Trp | Ile | Lys | Asn | Glu | Ala | His | 35 | 40 | 45 | |
| Thr | Thr | Gln | Ile | Val | Leu | Ile | Ser | Ser | Leu | Pro | Leu | Ile | Phe | Met | Met | 50 | 55 | 60 | |
| Gly | Phe | Val | Trp | Pro | Phe | Glu | Ser | Leu | Pro | Ser | Tyr | Leu | Gln | Val | Phe | 65 | 70 | 75 | 80 |
| Val | Gln | Ile | Val | Pro | Ala | Tyr | His | Gly | Ile | Ser | Leu | Leu | Gly | Arg | Leu | 85 | 90 | 95 | |
| Asn | Gln | Met | His | Ala | Glu | Phe | Ile | Asp | Val | Ser | Ile | His | Phe | Tyr | Ala | 100 | 105 | 110 | |
| Leu | Ile | Ala | Ile | Phe | Ile | Val | Ser | Phe | Ile | Gly | Cys | Val | Phe | Lys | Leu | 115 | 120 | 125 | |
| Ser | Ser | Leu | Lys | Lys | Ala | Cys | Glu | Asn | Ala | 130 | 135 | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:23439633_f2_2-AA

Figure 178A - page 213

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 296 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 178

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Arg | Lys | Asn | Ile | Leu | Ala | Tyr | Tyr | Gly | Ala | Asn | Phe | Leu | Leu |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Ile | Ile | Ala | Gln | Ser | Leu | Pro | His | Ala | Ile | Leu | Thr | Pro | Leu | Leu | Leu |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Ser | Lys | Gly | Leu | Ser | Leu | Ser | Glu | Ile | Leu | Leu | Val | Gln | Thr | Phe | Phe |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Ser | Phe | Cys | Val | Leu | Val | Ala | Glu | Tyr | Pro | Ser | Gly | Val | Leu | Ala | Asp |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Leu | Met | Ser | Arg | Lys | Asn | Leu | Phe | Leu | Val | Ser | Asn | Val | Phe | Leu | Ile |
| 65 | | | | 70 | | | | | 75 | | | | | 80 | |
| Ala | Ser | Phe | Ser | Leu | Val | Leu | Phe | Phe | Asp | Ser | Phe | Ile | Leu | Met | Leu |
| | | | 85 | | | | | | 90 | | | | | 95 | |
| Leu | Ala | Trp | Gly | Leu | Tyr | Gly | Leu | Tyr | Ser | Ala | Cys | Ser | Ser | Gly | Thr |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Ile | Glu | Ala | Ser | Leu | Ile | Thr | Asp | Ile | Lys | Glu | Asn | Lys | Lys | Asp | Leu |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| Ser | Lys | Phe | Leu | Ala | Lys | Asn | Asn | Gln | Ile | Thr | Tyr | Leu | Gly | Met | Ile |
| | 130 | | | | | 135 | | | | | 140 | | | | |
| Ile | Gly | Ser | Ser | Leu | Gly | Ser | Phe | Leu | Tyr | Leu | Lys | Val | His | Ala | Met |
| 145 | | | | | 150 | | | | 155 | | | | | | 160 |
| Leu | Tyr | Val | Val | Gly | Ile | Phe | Leu | Ile | Met | Leu | Cys | Ala | Leu | Thr | Ile |
| | | | | 165 | | | | | 170 | | | | | 175 | |
| Ile | Ile | Tyr | Phe | Lys | Glu | Lys | Glu | Gly | Asp | Phe | Lys | Ser | Gln | Lys | Asn |
| | | | 180 | | | | | 185 | | | | | 190 | | |
| Leu | Lys | Leu | Leu | Lys | Glu | Gln | Val | Lys | Gly | Ser | Leu | Lys | Glu | Leu | Lys |
| | | 195 | | | | | 200 | | | | | 205 | | | |
| Asp | Asn | Pro | Lys | Leu | Lys | Ile | Leu | Leu | Val | Gly | His | Leu | Ile | Thr | Pro |
| | 210 | | | | | 215 | | | | | 220 | | | | |
| Val | Phe | Phe | Met | Ser | His | Phe | Gln | Met | Trp | Gln | Ala | Tyr | Phe | Leu | Lys |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 |

Gln Gly Val Lys Glu Gln Tyr Leu Phe Val Phe Tyr Ile Ala Phe Gln
245 250 255
Val Ile Ser Ile Pro His Ser Phe Phe Lys Ser Gln Lys Leu Gln Pro
260 265 270
Lys Asn Arg Pro Glu Phe Ala Phe Gly Val Ala Ala Leu Ala Pro Cys
275 280 285
Cys Leu Ala Ile Ser Leu Ile Val Ser
290 295

Figure 178A - page 214

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 179

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | His | Glu | Gln | Gly | Ser | Ile | Ser | Phe | Ile | Gly | Glu | Gln | Gly | Ala | Lys | |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | | |
| Arg | Leu | Leu | Tyr | Ile | Leu | Tyr | Lys | Leu | Ala | Phe | Asn | Ala | Lys | Ser | Asn | |
| | | | 20 | | | | | 25 | | | | | 30 | | | |
| Lys | Ile | Ala | Leu | Asp | Arg | His | Tyr | Ala | Lys | Met | Phe | Leu | Gln | Val | Val | |
| | | 35 | | | | | 40 | | | | | 45 | | | | |
| Ala | Arg | Thr | Leu | Ile | Lys | Asn | Val | Asn | Ile | Leu | Glu | Glu | Gln | Gly | Phe | |
| | 50 | | | | | 55 | | | | | 60 | | | | | |
| Ile | Glu | Val | Ile | Lys | Gly | Lys | Gln | Arg | Tyr | Leu | Tyr | Val | Tyr | Leu | Lys | |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 | |
| Asp | Tyr | Arg | Glu | Leu | Glu | Cys | Leu | Val | Lys | Ser | Lys | Met | Ala | Lys | Tyr | |
| | | | | 85 | | | | | 90 | | | | | 95 | | |
| Val | Met | Tyr | Leu | Arg | Gln | Phe | Phe | Asp | Tyr | Leu | Asp | Arg | Lys | Arg | Arg | |
| | | | 100 | | | | | 105 | | | | | 110 | | | |
| Tyr | Gly | Phe | Asp | Phe | Thr | Leu | Lys | Asn | Leu | Ala | Phe | Ala | Lys | Thr | Lys | |
| | | 115 | | | | | 120 | | | | | 125 | | | | |
| Glu | Ser | Leu | Pro | Arg | His | Leu | Asn | Asp | Lys | Asp | Leu | Lys | Ser | Phe | Leu | |
| | 130 | | | | | 135 | | | | | 140 | | | | | |
| Lys | Thr | Leu | Leu | Asp | Tyr | Lys | Pro | Ala | Thr | Ser | Phe | Glu | Lys | Arg | Asn | |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 | |
| Lys | Cys | Ile | Leu | Leu | Ile | Val | Ile | Leu | Gly | Gly | Leu | Arg | Lys | Cys | Glu | |
| | | | | 165 | | | | | 170 | | | | | 175 | | |
| Val | Leu | Asn | Ile | Glu | Leu | Lys | His | Ile | Gln | Val | Glu | Glu | Gln | Asn | Tyr | |
| | | | 180 | | | | | 185 | | | | | 190 | | | |
| Ser | Ile | Leu | Ile | Gln | Gly | Lys | Gly | Arg | Lys | Glu | Arg | Lys | Ala | Tyr | Ile | |
| | | 195 | | | | | 200 | | | | | 205 | | | | |
| Lys | Lys | Ser | Leu | Leu | Glu | Pro | Ser | Leu | Asn | Ala | Trp | Ile | Ser | Asp | Asp | |
| | 210 | | | | | 215 | | | | | 220 | | | | | |
| Tyr | Arg | Leu | Lys | Tyr | Phe | Asn | Gly | Ala | Tyr | Leu | Phe | Lys | Lys | Asp | Lys | |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 | |

Gln Lys Ser Gln Asn Ser Leu Thr Leu Tyr Asn Leu Ser Pro
245 250

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 184 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 180

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: weak homology to [Rhodo. capsulatus] membrane-ass

Val Val Phe Lys Ile Leu Ser Leu Trp Leu Gly Val Phe Cys Phe Leu
1 5 10 15

Arg Ala Thr His Leu Tyr Leu Gly Glu Glu Pro Lys Tyr Lys Asp Asn
20 25 30

Phe Thr His Phe Glu Tyr Ala Asn Pro Asn Ala Arg Lys Gly Gly Val
35 40 45

Leu Arg Asn Asp Ala Ile Gly Thr Phe Asp Ser Leu Asn Pro Phe Ala
50 55 60

Leu Lys Gly Thr Lys Ala Glu Gly Leu Asp Leu Ile Tyr Asp Thr Leu
65 70 75 80

Met Val Gln Ser Leu Asp Glu Pro Phe Ala Glu Tyr Pro Leu Ile Ala
85 90 95

Lys Asp Ala Glu Val Ala Lys Asp Asn Ser Tyr Val Ile Phe Thr Leu
100 105 110

Asp Lys Arg Ala Arg Phe Ser Asn Asn Ala Pro Ile Leu Ala Ser Asp
115 120 125

Val Lys Phe Ser Phe Asp Thr Ile Met Lys Leu Gly Ser Pro Leu Tyr
130 135 140

Arg Gln Tyr Tyr Gln Asp Val Lys Lys Ala Val Ile Leu Asp Lys His
145 150 155 160

His Val Lys Phe Ile Tyr Lys Thr Thr Glu Asn Lys Glu Leu Pro Leu
165 170 175

Ile Leu Gly Gln Leu Gln Ile Phe Ser
180 185

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 181

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Val Ala Met Ile Asp Cys Ala Ile Ile Gly Gly Gly Pro Ala Gly Leu
1 5 10 15

Ser Ala Gly Leu Tyr Ala Thr Arg Gly Gly Val Lys Asn Ala Val Leu
20 25 30

Phe Glu Lys Gly Met
35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 116 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Met Val Leu Ile Ala Leu Leu Gly Unk Phe Ser Ser Val Ser Leu Ser
1 5 10 15

Ala Lys Ser Leu Leu Arg Asp Asp Gly Ile Leu Val Ser Asp Leu Lys
20 25 30

Gly Met Lys Ser Glu Leu Ser Asp Ala Pro Ala Trp Val Phe Unk Asp
35 40 45

Pro Lys Val Pro Tyr Glu Glu Met Gly Val Ala Tyr Ile Pro Val Asn
50 55 60

Asn Lys Tyr Leu Gly Ile Glu Gln Ala Thr Leu Asn Ala Lys Leu Ser
65 70 75 80

Leu Ile Val Val Phe His Glu Ile Met Leu Lys Tyr Lys Lys Arg Phe
85 90 95

Met Glu Gln Phe His Glu Ser Glu Gln Thr Ala Thr Asn Ile Ser Tyr
100 105 110

Ala Ser Ile Thr Thr
115

(2) INFORMATION FOR SEQ ID NO:23468781_f1_1-AA

Figure 183A - page 220

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

HPP 183

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: penicillin-binding protein 2

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Val | Lys | Met | Gly | Val | Gly | Leu | Ser | Phe | Leu | Glu | Asn | Leu | His | Ile |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Thr | Glu | Asn | Thr | Thr | Ile | Pro | Thr | Pro | Pro | Phe | Ile | Glu | Val | Gly | Lys |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Arg | Lys | Phe | Arg | Asp | Trp | Lys | Lys | Thr | Gly | His | Gly | Asn | Ser | Asn | Leu |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Tyr | Lys | Ala | Ile | Arg | Glu | Ser | Val | Asp | Val | Tyr | Phe | Tyr | Lys | Phe | Gly |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Leu | Glu | Ile | Ser | Ile | Glu | Asn | Ser | Leu | Asn | Leu | | | | | |
| 65 | | | | | 70 | | | | | 75 | | | | | |

(2) INFORMATION FOR SEQ ID NO:23473437_f3_3-AA

Figure 184A - page 221

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 181 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 184

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Gly | Lys | Ser | Leu | Arg | Tyr | Ser | Leu | Asn | Leu | Asp | Leu | Asn | Gln | Lys | 1 | 5 | 10 | 15 |
| Ala | Asp | Leu | Phe | Phe | Thr | Glu | Leu | Glu | Pro | Thr | Gly | Leu | Thr | Leu | Ser | 20 | 25 | 30 | |
| Pro | Ile | Met | Lys | Arg | Phe | Thr | Ile | Lys | Gly | Asp | Phe | Asp | Ser | Gly | Leu | 35 | 40 | 45 | |
| Lys | Ser | Tyr | Asp | Met | Ser | Tyr | Met | Tyr | Ala | Ser | Leu | Gln | Ala | Ile | Ser | 50 | 55 | 60 | |
| Ala | Ile | Arg | Arg | Leu | Pro | Leu | Gly | Leu | Tyr | Asp | Gly | Val | His | Val | Tyr | 65 | 70 | 75 | 80 |
| Ser | Lys | Thr | Pro | Met | Lys | Asp | Ile | Glu | Lys | Leu | Arg | Asn | Ala | Leu | Lys | 85 | 90 | 95 | |
| Thr | Ile | Asn | His | His | Gly | Ile | Gly | Ile | Glu | Gly | Trp | Trp | Gln | Gln | Asn | 100 | 105 | 110 | |
| Gly | Asn | Phe | Phe | Ser | Ala | Met | Glu | Leu | Glu | Lys | Arg | Ala | Leu | Phe | Ile | 115 | 120 | 125 | |
| Val | Leu | Met | Leu | Ile | Ile | Leu | Met | Ala | Ser | Leu | Asn | Ile | Ile | Ser | Ser | 130 | 135 | 140 | |
| Leu | Leu | Met | Val | Val | Met | Asn | Arg | Arg | Lys | Glu | Ile | Ala | Leu | Leu | Phe | 145 | 150 | 155 | 160 |
| Ser | Met | Gly | Ser | Ser | Gln | Lys | Glu | Ile | Gln | Lys | Thr | Phe | Phe | Tyr | Leu | 165 | 170 | 175 | |
| Gly | Asn | Ile | Ile | Ser | Leu | 180 | | | | | | | | | | | | | |

```
(i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 246 amino acids
      (B) TYPE: amino acid
      (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
      (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:
```

HPP 185

| | | | | | | | | | | | | | | | |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Met 1 | Lys | Lys | Thr | Phe 5 | Leu | Ile | Ala | Leu | Ala 10 | Leu | Thr | Ala | Ser | Leu 15 | Ile |
| Gly | Ala | Glu | Asn 20 | Thr | Lys | Trp | Asp | Tyr 25 | Lys | Asn | Lys | Glu | Asn 30 | Gly | Pro |
| His | Arg | Trp 35 | Asp | Lys | Leu | His | Lys 40 | Asp | Phe | Glu | Val | Cys 45 | Lys | Ser | Gly |
| Lys | Ser 50 | Gln | Ser | Pro | Ile | Asn 55 | Ile | Glu | His | Tyr | Tyr 60 | His | Thr | Gln | Asp |
| Lys 65 | Ala | Asp | Leu | Gln | Phe 70 | Lys | Tyr | Ala | Ala | Ser 75 | Lys | Pro | Lys | Ala | Val 80 |
| Phe | Phe | Thr | His | His 85 | Thr | Leu | Lys | Ala | Ser 90 | Phe | Glu | Pro | Thr | Asn 95 | His |
| Ile | Asn | Tyr | Arg 100 | Gly | His | Asp | Tyr | Val 105 | Leu | Asp | Asn | Val | His 110 | Phe | His |
| Ala | Pro | Met 115 | Glu | Phe | Leu | Ile | Asn 120 | Asn | Lys | Thr | Arg | Pro 125 | Leu | Ser | Ala |
| His | Phe 130 | Val | His | Lys | Asp | Ala 135 | Lys | Gly | Arg | Leu | Leu 140 | Val | Leu | Ala | Ile |
| Gly 145 | Phe | Glu | Glu | Gly | Lys 150 | Glu | Asn | Pro | Asn | Leu 155 | Asp | Pro | Ile | Leu | Glu 160 |
| Gly | Ile | Gln | Lys | Lys 165 | Gln | Asn | Leu | Lys | Glu 170 | Val | Ala | Leu | Asp | Ala 175 | Phe |
| Leu | Pro | Lys | Ser 180 | Ile | Asn | Tyr | Tyr | His 185 | Phe | Asn | Gly | Ser | Leu 190 | Thr | Ala |
| Pro | Pro | Cys 195 | Thr | Glu | Gly | Val | Ala 200 | Trp | Phe | Val | Ile | Glu 205 | Glu | Pro | Leu |
| Glu | Val 210 | Ser | Ala | Lys | Gln | Leu 215 | Ala | Glu | Ile | Lys | Lys 220 | Arg | Met | Lys | Asn |
| Ser 225 | Pro | Asn | Gln | Arg | Pro 230 | Val | Gln | Pro | Asp | Tyr 235 | Asn | Thr | Val | Ile | Ile 240 |

Lys Ser Ser Ala Glu Thr Arg
245

(2) INFORMATION FOR SEQ ID NO:23486342_f2_4-AA

Figure 186A - page 224

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 421 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 186

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: UDP-N-ACETYLMURAMOYLALANINE--D-GLUTAMATELIGASE

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Ile | Ser | Leu | Leu | Gly | His | Gly | Lys | Thr | Thr | Leu | Ala | Leu | Gly |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Arg | Phe | Phe | Lys | Lys | Asn | His | Asn | Glu | Val | Lys | Phe | Phe | Asp | Asp | Lys |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Phe | Pro | Ala | Phe | Phe | Lys | Asp | Ser | Glu | Gly | Phe | Leu | Cys | Tyr | Pro | Ser |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Lys | Asp | Phe | Asn | Pro | Asn | Asp | Ser | Gln | Leu | Glu | Ile | Val | Ser | Pro | Gly |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Ile | Ser | Phe | Thr | His | Pro | Leu | Val | Met | Lys | Ala | Lys | His | Leu | Met | Ser |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 |
| Glu | Tyr | Asp | Tyr | Ile | Asp | Ser | Leu | Phe | Asp | His | Ser | Phe | Thr | Pro | Thr |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| Met | Ile | Ser | Ile | Ser | Gly | Thr | Asn | Gly | Lys | Thr | Thr | Thr | Thr | Glu | Met |
| | | | 100 | | | | | 105 | | | | | | 110 | |
| Leu | Thr | Thr | Leu | Leu | Glu | Asp | Phe | Lys | Ala | Val | Ser | Gly | Gly | Asn | Ile |
| | | | 115 | | | | 120 | | | | | 125 | | | |
| Gly | Thr | Pro | Leu | Ile | Glu | Leu | Phe | Glu | Lys | Arg | Ser | Pro | Leu | Trp | Val |
| | 130 | | | | | 135 | | | | | 140 | | | | |
| Leu | Glu | Thr | Ser | Ser | Phe | Ser | Leu | His | Tyr | Thr | Asn | Lys | Ala | Tyr | Pro |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 |
| Leu | Ile | Tyr | Leu | Leu | Ile | Asn | Val | Glu | Ala | Asp | His | Leu | Thr | Trp | His |
| | | | | 165 | | | | | 170 | | | | | 175 | |
| Cys | Asn | Phe | Glu | Asn | Tyr | Leu | Asn | Ala | Lys | Leu | Lys | Val | Leu | Thr | Leu |
| | | | 180 | | | | | 185 | | | | | 190 | | |
| Met | Pro | Lys | Thr | Ser | Leu | Ala | Ile | Leu | Pro | Leu | Lys | Phe | Lys | Glu | His |
| | | 195 | | | | | 200 | | | | | 205 | | | |
| Pro | Ile | Val | Gln | Asn | Ser | Gln | Ala | Gln | Lys | Ile | Phe | Phe | Asp | Lys | Ser |
| | 210 | | | | | 215 | | | | | 220 | | | | |
| Glu | Glu | Val | Leu | Glu | Cys | Leu | Lys | Ile | Pro | Ser | Asn | Ala | Leu | Phe | Phe |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 |

[illegible]

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 53 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: iron(II) transport system

Met Lys Glu Ile Ile Val Ala Leu Val Gly Gln Pro Asn Val Gly Lys
1 5 10 15

Ser Ser Leu Ile Asn Ala Leu Ser Asn Thr His Leu Lys Val Gly Asn
20 25 30

Phe Thr Glu Val Thr Val Asp Lys Met Glu Val Ser Leu Ile Gln Lys
35 40 45

Asp His Gln Ile Asn Ser
50

(2) INFORMATION FOR SEQ ID NO:23493756_c1_6-AA

Figure 189A - page 228

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 189

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ile | Glu | Trp | Met | Gln | Asn | His | Arg | Lys | Tyr | Leu | Val | Val | Thr | Ile | 1 | 5 | 10 | 15 |
| Trp | Ile | Ser | Thr | Ile | Ala | Phe | Ile | Ala | Ala | Gly | Met | Ile | Gly | Trp | Gly | 20 | 25 | 30 | |
| Gln | Tyr | Ser | Phe | Ser | Leu | Asp | Ser | Asp | Ser | Ala | Ala | Lys | Val | Gly | Gln | 35 | 40 | 45 | |
| Ile | Lys | Ile | Ser | Gln | Glu | Glu | Leu | Ala | Gln | Glu | Tyr | Arg | Arg | Leu | Lys | 50 | 55 | 60 | |
| Asp | Ala | Tyr | Ala | Glu | Ser | Ile | Pro | Asp | Phe | Lys | Glu | Leu | Thr | Glu | Asp | 65 | 70 | 75 | 80 |
| Gln | Ile | Lys | Ala | Met | His | Leu | Glu | Lys | Ser | Ala | Leu | Asp | Ser | Leu | Ile | 85 | 90 | 95 | |
| Asn | Gln | Ala | Leu | Leu | Arg | Asn | Phe | Ala | Leu | Asp | Leu | Gly | Leu | Gly | Ala | 100 | 105 | 110 | |
| Thr | Lys | Gln | Glu | Val | Ala | Lys | Glu | Ile | Arg | Lys | Thr | Asn | Val | Phe | Gln | 115 | 120 | 125 | |
| Lys | Asp | Gly | Val | Phe | Asp | Glu | Glu | Leu | Tyr | Lys | Asn | Ile | Leu | Lys | Gln | 130 | 135 | 140 | |
| Ser | His | Tyr | Arg | Pro | Lys | His | Phe | Glu | Glu | Ser | Val | Glu | Arg | Leu | Leu | 145 | 150 | 155 | 160 |
| Ile | Leu | Gln | Lys | Ile | Ser | Ala | Leu | Phe | Pro | Lys | Thr | Thr | Thr | Pro | Leu | 165 | 170 | 175 | |
| Glu | Gln | Ser | Ser | Leu | Ser | Leu | Trp | Ala | Lys | Leu | Gln | Asp | Lys | Leu | Asp | 180 | 185 | 190 | |
| Ile | Leu | Ile | Leu | Asn | Pro | Asn | Asp | Val | Lys | Ile | Ser | Leu | Asn | Glu | Glu | 195 | 200 | 205 | |
| Glu | Met | Lys | Lys | Tyr | Tyr | Glu | Asn | His | Arg | Lys | Asp | Phe | Lys | Lys | Pro | 210 | 215 | 220 | |
| Thr | Ser | Phe | Lys | Thr | Arg | Ser | Leu | Tyr | Phe | Asp | Ala | Ser | Leu | Glu | Lys | 225 | 230 | 235 | 240 |

Thr Asp Leu Lys Glu Leu Glu Glu Tyr Tyr His Lys Asn Lys Val Ser
245 250 255

Figure 189 A-page 229

Tyr Leu Asp Lys Gly Gly Asn Tyr Arg Ile Leu Lys Ala Phe Lys Ser
260 265 270

Lys Ser Ser Met Ile
275

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 83 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP-190

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Met Val Lys His Tyr Leu Phe Met Ala Val Ser Gln Val Phe Phe Ser
1 5 10 15

Phe Phe Leu Val Leu Phe Phe Ile Ser Ser Ile Val Leu Leu Ile Ser
20 25 30

Ile Ala Ser Val Thr Leu Val Ile Lys Val Ser Phe Leu Asp Leu Val
35 40 45

Gln Leu Phe Leu Tyr Ser Leu Pro Gly Thr Ile Phe Phe Ile Leu Pro
50 55 60

Unk Thr Phe Phe Ala Ala Cys Unk Trp Gly Phe Gln Gly Leu Ala Met
65 70 75 80

Thr Met Asn Cys

(2) INFORMATION FOR SEQ ID NO:23515833_f1_3-AA

Figure 191A - page 231

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 191

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|----|
| Val | His | Arg | Phe | Ser | Arg | Asn | Pro | Cys | Ala | Ser | Cys | Asn | Arg | Ala | Arg | 1 | 5 | 10 | 15 |
| Ser | Cys | Ser | Arg | Leu | Ser | Arg | Ser | Leu | Val | Ser | Ala | Val | Thr | Trp | Trp | 20 | 25 | 30 | |
| Leu | Ser | Leu | Ser | Phe | Ser | Val | Val | Ser | Ala | Leu | Phe | Ser | Leu | Val | Ser | 35 | 40 | 45 | |
| Ser | Val | Ile | Leu | Trp | Val | Ser | Ser | Val | Phe | Ser | Leu | Phe | Ser | Leu | Ser | 50 | 55 | 60 | |
| Phe | Ser | Val | Val | Asn | Ser | Leu | Phe | Ser | Ser | Val | Ser | Arg | Ser | Leu | Ala | 65 | 70 | 75 | 80 |
| Ala | Asn | Lys | Arg | Val | Phe | Ser | Leu | Ala | Lys | Met | Ser | Phe | Ser | Val | Phe | 85 | 90 | 95 | |
| Ser | Ser | Ala | Phe | Ser | Leu | Val | Ser | Leu | Leu | Leu | Phe | Cys | His | Asn | 100 | 105 | 110 | | |

232

HPP 192

Leu Phe Asn Asp Ile Thr Arg Leu Leu
130 135

(2) INFORMATION FOR SEQ ID NO:23531562_c2_11 - AA

Figure 193A - page 233

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 123 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 193

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: H⁺-transporting ATP synthase

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| Val | Met | Ala | Leu | Leu | Lys | Ile | Ser | Val | Val | Val | Pro | Glu | Gly | Glu | Val | 1 | 5 | 10 | 15 |
| Tyr | Thr | Gly | Glu | Val | Lys | Ser | Val | Val | Leu | Pro | Gly | Val | Glu | Gly | Glu | 20 | 25 | 30 | |
| Phe | Gly | Val | Leu | Tyr | Gly | His | Ser | Asn | Met | Ile | Thr | Leu | Leu | Gln | Ala | 35 | 40 | 45 | |
| Gly | Val | Val | Glu | Ile | Glu | Thr | Glu | Asn | Gln | Lys | Glu | His | Ile | Ala | Ile | 50 | 55 | 60 | |
| Asn | Trp | Gly | Tyr | Ala | Glu | Val | Thr | Asn | Glu | Arg | Val | Asp | Ile | Leu | Ala | 65 | 70 | 75 | 80 |
| Asp | Gly | Ala | Val | Phe | Ile | Lys | Lys | Gly | Ser | Asp | Asp | Arg | Asp | Asp | Ala | 85 | 90 | 95 | |
| Ile | Ser | Arg | Ala | Lys | Lys | Leu | Leu | Glu | Asp | Ala | Ser | Ser | Asp | Arg | Leu | 100 | 105 | 110 | |
| Ala | Val | Ser | Ser | Val | Leu | Ala | Lys | Ile | Glu | Ser | Leu | 115 | 120 | | | | | | |

(2) INFORMATION FOR SEQ ID NO:23535937_f1_2-AA

Figure 194A - page 234

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 194

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: UDP-N-ACETYLMURAMYL-TRYPEPTIDE SYNTHETASE

Met Tyr Ser Leu Leu Leu Asp Leu Asn Lys Lys Thr Ala Leu Leu Gly
1 5 10 15

Thr Arg Gly Phe Phe Ile Asp Asp Lys His Ile Lys Glu Lys Gly Leu
20 25 30

Thr Thr Pro Thr Leu Leu Glu Leu Tyr Ser Asp Leu Glu Glu Ala Ile
35 40 45

Arg Leu Lys Cys Glu Tyr Phe Ile Met Glu Val Ser Ser His Ala Ile
50 55 60

Val Gln Asn Ala Ser Leu Gly Leu Ile Ser Leu Leu Lys Phe Ser Pro
65 70 75 80

Ile Ser Gln Ala Ile Ile
85

(2) INFORMATION FOR SEQ ID NO:23539006_f3_2-AA

Figure 195A - page 235

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 195

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Unk | Unk | Ala | Ile | Arg | Phe | Pro | Unk | Unk | Leu | Phe | Ser | Tyr | Pro |
| 1 | | | | 5 | | | | 10 | | | | | | 15 | |
| Lys | Pro | Lys | Ile | Lys | Ala | Thr | Asn | Thr | Ser | Unk | Thr | Val | Leu | Phe | Ala |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Tyr | Pro | Leu | Lys | Pro | His | Glu | Met | Ala | Leu | Leu | Ala | Leu | Ala | Thr | Ser |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Leu | Leu | Ala | Pro | Ile | Phe | Asn | Ala | Ile | His | Ser | Thr | Asn | Ala | Leu | Asn |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Ala | Ile | Lys | Pro | Asp | Gly | Thr | Gly | Ser | Lys | Ile | Asn | Pro | Ile | Ile | Met |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 |
| Pro | Met | Lys | Ile | Lys | Asn | Lys | Ala | Met | Arg | | | | | | |
| | | | | 85 | | | | | 90 | | | | | | |

(2) INFORMATION FOR SEQ ID NO:23564012_c2_3-AA

Figure 196A - page 236

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 196

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Thr | Asn | Phe | Tyr | Lys | Ile | Lys | Leu | Leu | Phe | Ala | Trp | Cys | Leu |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Ile | Ile | Gly | Met | Phe | Asn | Ala | Pro | Leu | Asn | Ala | Asp | Gln | Asn | Thr | Asp |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Ile | Lys | Asp | Ile | Ser | Pro | Glu | Asp | Met | Ala | Leu | Asn | Ser | Val | Gly | Leu |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Val | Ser | Arg | Asp | Gln | Leu | Lys | Ile | Glu | Ile | Pro | Lys | Glu | Thr | Leu | Glu |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Gln | Lys | Val | Thr | Ile | Leu | Asn | Asp | Tyr | Asn | Asp | Lys | Asn | Val | Asn | Ile |
| 65 | | | | 70 | | | | | 75 | | | | | | 80 |
| Lys | Phe | Asp | Asp | Ile | Ser | Leu | Gly | Ser | Phe | Gln | Pro | Asn | Asp | Asn | Leu |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| Gly | Ile | Asn | Ala | Met | Trp | Gly | Ile | Gln | Asn | Leu | Leu | | | | |
| | | | 100 | | | | | 105 | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:23567137_f1_1-AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 197

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*(xi) SEQUENCE DESCRIPTION: vacuolating cytotoxin - *Helicobacter pylori*

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| Val | Tyr | Ser | Arg | Phe | Phe | Ala | Asn | Gln | His | Glu | Phe | Asp | Phe | Glu | Ala | 1 | 5 | 10 | 15 |
| Gln | Gly | Ala | Leu | Gly | Ser | Asp | Gln | Ser | Ser | Leu | Asn | Phe | Lys | Ser | Thr | 20 | 25 | 30 | |
| Leu | Leu | Gln | Asp | Leu | Asn | Gln | Ser | Tyr | Asn | Tyr | Leu | Ala | Tyr | Ser | Ala | 35 | 40 | 45 | |
| Thr | Ala | Arg | Ala | Ser | Tyr | Gly | Tyr | Asp | Phe | Ala | Phe | Phe | Arg | Asn | Ala | 50 | 55 | 60 | |
| Leu | Val | Leu | Lys | Pro | Ser | Val | Gly | Val | Ser | Tyr | Asn | His | Leu | Gly | Ser | 65 | 70 | 75 | 80 |
| Thr | Asn | Phe | Lys | Ser | Asn | Ser | Gln | Ser | Gln | Val | Ala | Leu | Lys | Asn | Gly | 85 | 90 | 95 | |
| Ala | Ser | Ser | Gln | His | Leu | Phe | Asn | Ala | Asn | Ala | Thr | Trp | Lys | Arg | Val | 100 | 105 | 110 | |
| Ile | Ile | Met | Gly | Thr | Leu | His | Thr | Phe | Ile | Cys | Met | Trp | Glu | Phe | Tyr | 115 | 120 | 125 | |
| Lys | Ser | Ser | Leu | Thr | Leu | Asp | Arg | Met | Met | Trp | Arg | Leu | 130 | 135 | 140 | | | | |

(2) INFORMATION FOR SEQ ID NO:23573294_c1_11-AA

Figure 198A - page 238

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 230 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 198

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ile | Asp | Asn | Leu | Asp | Gly | Ala | Lys | Asp | Ala | Gln | Leu | Ile | Lys | Lys | 1 | 5 | 10 | 15 |
| Ala | Tyr | Ala | Phe | Leu | Cys | Leu | Gly | Gly | Asp | Gly | Thr | Ile | Leu | Gly | Ala | 20 | 25 | 30 | |
| Leu | Arg | Met | Thr | His | Ala | His | Asn | Lys | Pro | Cys | Phe | Gly | Val | Arg | Ile | 35 | 40 | 45 | |
| Gly | Asn | Leu | Gly | Phe | Leu | Ser | Ala | Val | Glu | Leu | Asn | Gly | Leu | Lys | Asp | 50 | 55 | 60 | |
| Phe | Leu | Gln | Asp | Leu | Lys | Gln | Asn | Arg | Ile | Lys | Leu | Glu | Glu | His | Leu | 65 | 70 | 75 | 80 |
| Ala | Leu | Glu | Gly | Arg | Ile | Gly | Asn | Thr | Ser | Phe | Tyr | Ala | Ile | Asn | Glu | 85 | 90 | 95 | |
| Ile | Val | Ile | Ala | Lys | Lys | Lys | Ala | Leu | Gly | Val | Leu | Asp | Ile | Lys | Ala | 100 | 105 | 110 | |
| Cys | Ala | Gly | His | Thr | Pro | Phe | Asn | Thr | Tyr | Lys | Gly | Asp | Gly | Leu | Ile | 115 | 120 | 125 | |
| Ile | Ala | Thr | Pro | Leu | Gly | Ser | Thr | Ala | Tyr | Asn | Leu | Ser | Ala | His | Gly | 130 | 135 | 140 | |
| Pro | Ile | Val | His | Ala | Leu | Ser | Gln | Ser | Tyr | Ile | Leu | Thr | Pro | Leu | Cys | 145 | 150 | 155 | 160 |
| Asp | Phe | Ser | Leu | Thr | Gln | Arg | Pro | Leu | Val | Leu | Gly | Ala | Glu | Phe | Cys | 165 | 170 | 175 | |
| Leu | Ser | Phe | Cys | Ala | His | Glu | Asp | Ala | Leu | Val | Val | Ile | Asp | Gly | Gln | 180 | 185 | 190 | |
| Ala | Thr | Tyr | Asp | Leu | Lys | Ala | Asn | Gln | Pro | Leu | Tyr | Ile | Gln | Lys | Ser | 195 | 200 | 205 | |
| Pro | Thr | Thr | Thr | Lys | Leu | Leu | Gln | Lys | Asn | Ser | Arg | Asp | Tyr | Phe | Lys | 210 | 215 | 220 | |
| Val | Leu | Lys | Glu | Lys | Leu | Leu | | | | | | | | | | 225 | 230 | | |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 190 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: channel component of the sodium-type flagellar mo

Met Unk Glu Asn Gly Arg Gly Val Pro Lys Asp Tyr Lys Lys Ala Val
1 5 10 15

Glu Tyr Phe Gln Lys Ala Val Asp Asn Asp Ile Pro Arg Gly Tyr Asn
20 25 30

Asn Leu Gly Val Met Tyr Lys Glu Gly Lys Gly Val Pro Lys Asp Glu
35 40 45

Lys Lys Ala Val Glu Tyr Phe Arg Ile Ala Thr Glu Lys Gly Tyr Thr
50 55 60

Asn Ala Tyr Ile Asn Leu Gly Ile Met Tyr Met Glu Gly Arg Gly Val
65 70 75 80

Pro Ser Asn Tyr Ala Lys Ala Thr Glu Cys Phe Arg Lys Ala Met His
85 90 95

Lys Gly Asn Val Unk Ala Tyr Ile Leu Leu Gly Asp Ile Tyr Tyr Ser
100 105 110

Gly Met Ile Asn Trp Val Leu Ser Arg Thr Lys Ile Arg Leu Val His
115 120 125

Tyr Lys Met Ala Ala Asp Val Ser Ser Ser Arg Ala Tyr Unk Gly Leu
130 135 140

Ser Glu Ser Tyr Unk Tyr Gly Unk Gly Val Glu Lys Unk Lys Lys Arg
145 150 155 160

Unk Lys Asn Thr Cys Lys Lys His Ala Ile Leu Thr Leu Ile Lys Ile
165 170 175

Val Arg Lys Arg Thr Leu Gln Ala Asp Asn Ser Gln Ala Trp Ala
180 185 190

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 182 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Met Ile Val Gly Leu Ile Gly Val Val Glu Lys Ile Ser Ala Leu Glu
1 5 10 15

Ala His Ile Glu Val Gln Gly Val Val Tyr Gly Val Gln Val Ser Met
20 25 30

Arg Thr Ala Ala Leu Leu Gln Thr Gly Gln Lys Ala Arg Leu Lys Ile
35 40 45

Leu Gln Val Ile Lys Glu Asp Ala His Leu Leu Tyr Gly Phe Leu Glu
50 55 60

Glu Ser Glu Lys Ile Leu Phe Glu Arg Leu Leu Lys Ile Asn Gly Val
65 70 75 80

Gly Gly Arg Ile Ala Leu Ala Ile Leu Ser Ser Phe Ser Pro Asn Glu
85 90 95

Phe Glu Asn Ile Ile Ala Thr Lys Glu Val Lys Arg Leu Gln Gln Val
100 105 110

Pro Gly Ile Gly Lys Lys Leu Ala Asp Lys Ile Met Val Asp Leu Ile
115 120 125

Gly Phe Phe Ile Gln Asp Glu Asn Arg Pro Ala Arg Asn Glu Val Phe
130 135 140

Leu Ala Leu Glu Ser Leu Gly Phe Lys Ser Ala Glu Ile Asn Pro Val
145 150 155 160

Leu Lys Thr Leu Lys Pro His Leu Ser Ile Glu Ala Ala Ile Lys Glu
165 170 175

Ala Leu Gln Gln Leu Arg Ser
180

(2) INFORMATION FOR SEQ ID NO:23610905_c1_15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

Figure 201A - page 241

(ii) MOLECULE TYPE: protein

HPP 201

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| Val | Gly | Val | Leu | Leu | Ala | Leu | Phe | Phe | Phe | Tyr | Ala | Lys | Asn | Asn | Leu | 1 | 5 | 10 | 15 |
| Leu | Glu | Asn | Thr | Gln | Ile | Arg | Met | Gln | Tyr | Thr | Ala | Asp | Ala | Ile | Ala | 20 | 25 | 30 | |
| Lys | Ser | Leu | Leu | Glu | Leu | Asn | Asn | Ala | Ser | Ser | Leu | Glu | Pro | Leu | Lys | 35 | 40 | 45 | |
| Ile | Leu | Glu | Glu | Arg | Phe | Lys | Asn | Thr | Pro | Phe | Val | Leu | Leu | Asp | Ala | 50 | 55 | 60 | |
| Asp | Asn | Arg | Val | Lys | Phe | Ser | Asn | Ile | Gly | Val | Phe | Val | Ala | Ser | Phe | 65 | 70 | 75 | 80 |
| Lys | Asn | Asp | Ala | Leu | Ile | Lys | Thr | Pro | Tyr | Phe | Ala | Leu | Lys | Lys | Gln | 85 | 90 | 95 | |
| Gly | Phe | Tyr | Leu | Thr | Asp | Ser | Ala | Pro | Thr | Asn | Arg | Leu | Gly | Val | Ser | 100 | 105 | 110 | |
| Lys | Ile | Ile | Ile | Ala | Glu | Glu | Glu | Ile | Gln | Lys | Ile | Phe | Ile | Pro | Leu | 115 | 120 | 125 | |
| Tyr | Lys | Met | Ile | Gly | Tyr | Val | Phe | Leu | Gly | Ala | Ser | Leu | Phe | Val | Ala | 130 | 135 | 140 | |
| Leu | Ile | Ala | Met | Trp | Leu | Tyr | Lys | Ile | Pro | 145 | 150 | | | | | | | | |

10AA

Figure 202A - page 242

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 287 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 202

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Val 1 | Val | Ile | Met | Ile 5 | Leu | Val | Cys | Phe | Leu 10 | Ala | Cys | Ser | Gln | Glu 15 | Ser |
| Phe | Ile | Lys | Met 20 | Gln | Lys | Lys | Ala | Gln 25 | Glu | Gln | Glu | Asn | Asp 30 | Gly | Ser |
| Lys | Arg | Pro 35 | Ser | Tyr | Val | Asp | Ser 40 | Asp | Tyr | Glu | Val | Phe 45 | Ser | Glu | Thr |
| Ile | Phe 50 | Leu | Gln | Asn | Met | Val 55 | Tyr | Gln | Pro | Ile | Glu 60 | Glu | Arg | Asn | Ala |
| Phe 65 | Phe | Gln | Leu | Thr | Lys 70 | Asp | Glu | Asp | Asn | Ser 75 | Phe | Asn | Pro | Glu | Asn 80 |
| Ser | Val | Ile | Leu | Leu 85 | Asn | Glu | Pro | Ser | Asp 90 | Asn | Ser | Glu | Lys | Asn 95 | Leu |
| Leu | Ser | Tyr | Pro 100 | Asn | Asp | Pro | Asn | Asn 105 | Asn | Glu | Asp | Asn | Ala 110 | Asn | Asn |
| Ser | Gln | Lys 115 | Asn | Pro | Phe | Leu | Tyr 120 | Lys | Pro | Lys | Arg | Lys 125 | Thr | Lys | Asn |
| Pro | Lys 130 | Leu | Ile | Glu | Tyr | Ser 135 | Gln | Gln | Asp | Phe | Tyr 140 | Pro | Leu | Lys | Asn |
| Gly 145 | Asp | Ile | Ile | Met | Ser 150 | Lys | Glu | Gly | Asp | Gln 155 | Trp | Leu | Ile | Glu | Ile 160 |
| Gln | Ser | Lys | Ala | Leu 165 | Lys | Arg | Phe | Leu | Lys 170 | Asp | Gln | Asn | Asp | Lys 175 | Asp |
| Arg | Gln | Ile | Gln 180 | Thr | Phe | Thr | Phe | Asn 185 | Asp | Thr | Lys | Thr | Gln 190 | Ile | Ala |
| Gln | Ile | Lys 195 | Gly | Lys | Ile | Ser | Ser 200 | Tyr | Val | Tyr | Thr | Thr 205 | Asn | Asn | Gly |
| Ser | Leu 210 | Ser | Leu | Arg | Pro | Phe 215 | Tyr | Glu | Ser | Phe | Leu 220 | Leu | Glu | Lys | Lys |
| Ser 225 | Asp | Asn | Val | Tyr | Thr 230 | Ile | Glu | Asn | Lys | Ala 235 | Leu | Asp | Thr | Met | Glu 240 |

Ile Ser Lys Cys Gln Met Val Leu Lys Lys His Ser Thr Asp Lys Leu
245 250 255
Asp Ser Gln His Lys Ala Ile Ser Ile Asp Leu Asp Phe Lys Lys Glu
260 265 270
Arg Phe Lys Ser Asp Thr Glu Leu Phe Leu Glu Cys Leu Lys Glu Ser
275 280 285

Figure 202 A - page 243

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 419 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 203

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Met 1 | Ala | Ala | Pro | Leu 5 | Leu | Ala | Leu | Pro | Phe 10 | Leu | Ser | Asn | Pro | Leu 15 | Val |
| Leu | Gly | Ala | Leu 20 | Ala | Val | Ile | Gly | Val 25 | Gly | Ala | Tyr | Leu | Tyr 30 | Pro | Asn |
| Lys | Gln | Asp 35 | Ser | Leu | Val | Val | Gln 40 | Ala | Asp | Gly | Leu | Tyr 45 | Ser | Glu | Ile |
| Leu | Gly 50 | Phe | Phe | Ile | Ser | Phe 55 | Ser | Ser | Lys | Ile | Leu 60 | Lys | Gly | Ile | Gly |
| Glu 65 | Pro | Leu | Ala | Asn | Val 70 | Ile | Gln | Pro | Phe | Gly 75 | Met | Val | Leu | Gly | Met 80 |
| Leu | Leu | Ile | Leu | Leu 85 | Tyr | Ser | Phe | Lys | Arg 90 | Tyr | Gln | Asn | Asn | Asp 95 | Leu |
| Phe | Glu | Ile | Lys 100 | Thr | Phe | Leu | Met | Leu 105 | Phe | Val | Phe | Val | Gly 110 | Tyr | Leu |
| Ser | Leu | Tyr 115 | His | Tyr | Ala | Phe | Lys 120 | Ser | Asp | Gly | Ser | Ser 125 | Ser | Gly | Asn |
| Gly | Arg 130 | Ser | Ser | Phe | Ala | Phe 135 | Gln | Asn | His | Val | Thr 140 | Glu | Ile | Phe | Asp |
| Thr 145 | Pro | Ala | Asn | Leu | Leu 150 | Asn | Ala | Gly | Ile | Ser 155 | Asn | Val | Val | Lys | Glu 160 |
| Tyr | Gln | Thr | Asn | Ser 165 | Ala | Arg | Glu | His | Lys 170 | Asn | Ile | Asp | Thr | His 175 | His |
| Ser | Ile | Thr | Asn 180 | Ala | Asn | Ile | Ser | Phe 185 | His | Val | Arg | Gln | Ile 190 | Leu | Thr |
| Ser | Leu | Asn 195 | Lys | Leu | Tyr | Glu | Asp 200 | Phe | Lys | Ile | Asn | Asn 205 | Gly | Leu | Ser |
| Leu | Lys 210 | Thr | Leu | Ile | Ala | Ala 215 | Val | Leu | Leu | Leu | Val 220 | Ile | Leu | Gly | Leu |
| Glu 225 | Leu | Phe | Leu | Leu | Phe 230 | Lys | Val | Phe | Cys | Tyr 235 | Val | Phe | Met | Thr | Tyr 240 |

[illegible]

(2) INFORMATION FOR SEQ ID NO:23635968_f3_2-AA

Figure 204A - page 246

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 181 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 204

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: cation efflux system proteins

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ile | Val | Gly | Ala | Ile | Leu | Val | Leu | Phe | Phe | Gly | Thr | Tyr | Ser | Phe | 1 | 5 | 10 | 15 |
| Ile | Asn | Thr | Pro | Val | Asp | Ala | Phe | Unk | Asp | Ile | Ser | Pro | Thr | Gln | Val | 20 | 25 | 30 | |
| Lys | Ile | Ile | Leu | Lys | Leu | Pro | Gly | Ser | Ser | Pro | Glu | Glu | Met | Glu | Asn | 35 | 40 | 45 | |
| Asn | Ile | Ala | Arg | Pro | Leu | Glu | Leu | Glu | Leu | Gly | Leu | Lys | Gly | Gln | 50 | 55 | 60 | | |
| Lys | Ser | Leu | Arg | Ser | Ile | Ser | Lys | Tyr | Ser | Ile | Ser | Asp | Ile | Thr | Ile | 65 | 70 | 75 | 80 |
| Asp | Phe | Asp | Asp | Ser | Val | Asp | Ile | Tyr | Leu | Ala | Arg | Asn | Ile | Val | Asn | 85 | 90 | 95 | |
| Glu | Arg | Leu | Ser | Ser | Val | Met | Lys | Asp | Leu | Pro | Val | Gly | Val | Glu | Gly | 100 | 105 | 110 | |
| Gly | Met | Ala | Pro | Ile | Val | Thr | Pro | Leu | Ser | Asp | Ile | Phe | Met | Phe | Thr | 115 | 120 | 125 | |
| Ile | Asp | Gly | Asn | Ile | Thr | Glu | Ile | Glu | Lys | Arg | Gln | Leu | Leu | Asp | Phe | 130 | 135 | 140 | |
| Val | Ile | Arg | Pro | Gln | Leu | Arg | Met | Ile | Ser | Gly | Val | Ala | Asp | Val | Asn | 145 | 150 | 155 | 160 |
| Ser | Ile | Gly | Gly | Phe | Ser | Arg | Ala | Phe | Val | Ile | Val | Pro | Asp | Phe | Asn | 165 | 170 | 175 | |
| Asp | Met | Ala | Arg | Leu | Gly | 180 | | | | | | | | | | | | | |

Figure 205A - page 247

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 205

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Val Leu Lys Phe Gln Lys Leu Pro Leu Leu Phe Val Ser Ile Leu Tyr
1 5 10 15

Asn Gln Ser Pro Leu Leu Ala Phe Asp Tyr Lys Phe Ser Gly Val Ala
20 25 30

Glu Ser Val Ser Lys Val Gly Phe Asn His Ser Lys Leu Asn Ser Lys
35 40 45

Glu Gly Ile Phe Pro Thr Ala Thr Phe Val Thr Ala Thr Ile Lys Leu
50 55 60

Gln Val Asn Tyr Lys Ser Ala Pro
65 70

(2) INFORMATION FOR SEQ ID NO:23671689_f3_6: -AA -

Figure 2D6 - page 248

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 206

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Val | Glu | Gln | Ala | Ile | Asn | Lys | Lys | Asn | Glu | Leu | Val | Leu | Lys | Arg |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Cys | Unk | Arg | Val | Thr | Unk | Ile | Ile | Arg | Ile | Ile | Thr | Leu | Ile | Arg | Ser |
| | | | 20 | | | | | 25 | | | | | 30 | | |

| | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe | Gln | Ala | Pro | Leu | His | Ser | Met | Leu | Met | Gln | Unk |
| | | 35 | | | | | 40 | | | | |

(2) INFORMATION FOR SEQ ID NO:23728388_f2_6-AA

Figure 207A - page 249

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 207

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: serotonin transport protein

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Asn | His | Phe | Ser | Lys | Leu | Gly | Phe | Val | Leu | Ala | Ala | Leu | Gly | 1 | 5 | 10 | 15 |
| Ser | Ala | Ile | Gly | Leu | Gly | His | Ile | Trp | Arg | Phe | Pro | Tyr | Met | Thr | Gly | 20 | 25 | 30 | |
| Val | Ser | Gly | Gly | Gly | Ala | Phe | Val | Leu | Leu | Phe | Leu | Phe | Leu | Ser | Leu | 35 | 40 | 45 | |
| Ser | Val | Gly | Ala | Ala | Met | Phe | Ile | Ala | Glu | Met | Leu | Leu | Gly | Gln | Ser | 50 | 55 | 60 | |
| Thr | Gln | Lys | Asn | Val | Thr | Glu | Ala | Phe | Lys | Glu | Leu | Asp | Ile | Asn | Pro | 65 | 70 | 75 | 80 |
| Lys | Lys | Arg | Trp | Lys | Tyr | Ala | Gly | Ile | Met | Leu | Ile | Ser | Gly | Pro | Leu | 85 | 90 | 95 | |
| Ile | Leu | Thr | Phe | Tyr | Gly | Thr | Ile | Leu | Gly | Trp | Val | Leu | Tyr | Tyr | Leu | 100 | 105 | 110 | |
| Val | Ser | Ile | Ser | Phe | Asn | Leu | Pro | Ser | Ser | Ile | Gln | Glu | Ser | Glu | Gln | 115 | 120 | 125 | |
| Ile | Phe | Thr | Gln | Thr | Leu | Gln | Ser | Ile | Gly | Leu | Gln | Ser | Ile | Gly | Leu | 130 | 135 | 140 | |
| Phe | Ser | Val | Leu | Phe | Ile | Thr | Gly | Trp | Ile | Val | Ser | Arg | Gly | Ile | Lys | 145 | 150 | 155 | 160 |
| Glu | Gly | Ile | Glu | Lys | Leu | Asn | Leu | Val | Leu | Met | Pro | Leu | Leu | Phe | Ala | 165 | 170 | 175 | |
| Thr | Phe | Phe | Gly | Leu | Leu | Phe | Tyr | Ala | Met | Ser | Met | Asp | Ser | Phe | Ser | 180 | 185 | 190 | |
| Lys | Ala | Phe | His | Phe | Met | Leu | Ile | Ser | Ser | Gln | Lys | Ile | | | | 195 | 200 | 205 | |

(2) INFORMATION FOR SEQ ID NO:23831562_f2_19-AA

Figure 208A-page 250

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 208

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Lys | Val | Cys | Val | Ser | Ala | Trp | Gly | Leu | Pro | Lys | Ile | Leu | Glu | 1 | 5 | 10 | 15 |
| Glu | Arg | Leu | Lys | Glu | Lys | Tyr | Gly | Asp | Asp | Trp | Glu | Lys | His | Val | Lys | 20 | 25 | 30 | |
| Ala | Lys | Ala | Ile | Asn | Glu | Glu | Glu | Leu | Glu | Glu | Gln | Val | Lys | Ala | Lys | 35 | 40 | 45 | |
| Ala | Lys | Glu | Gln | Gln | Lys | Thr | Gln | Arg | Glu | Lys | Thr | Leu | Asn | Gly | Phe | 50 | 55 | 60 | |
| Leu | Lys | Lys | Val | Gly | Leu | Lys | Lys | Arg | Asp | Met | Leu | Gln | Ser | Thr | Met | 65 | 70 | 75 | 80 |
| Leu | Phe | Asp | Glu | Val | Lys | Glu | Ala | Asp | Val | Leu | Phe | Gln | Ala | Glu | Arg | 85 | 90 | 95 | |
| Lys | Ile | Gly | Asp | Trp | Ile | Phe | Ser | Ser | Ala | Val | Phe | Phe | Phe | Ala | Leu | 100 | 105 | 110 | |
| Ala | Leu | Ile | Glu | Ala | Ile | Ile | Ile | Val | Cys | Leu | Leu | Pro | Leu | Lys | Glu | 115 | 120 | 125 | |
| Lys | Val | Pro | Tyr | Leu | Val | Thr | Phe | Ser | Asn | Ala | Thr | Gln | Asn | Phe | Ala | 130 | 135 | 140 | |
| Ile | Val | Gln | Arg | Ala | Asp | Lys | Ser | Ile | Arg | Ala | Asn | Gln | Ala | Leu | Val | 145 | 150 | 155 | 160 |
| Arg | Gln | Leu | Val | Ala | Ser | Tyr | Val | Asn | Asn | Arg | Glu | Asn | Ile | Ser | Ser | 165 | 170 | 175 | |
| Ile | Lys | Glu | Gln | Asn | Glu | Ile | Ala | His | Glu | Thr | Ile | Arg | Leu | Gln | Ser | 180 | 185 | 190 | |
| Ala | Phe | Glu | Val | Trp | Asp | Phe | Phe | Glu | Lys | Leu | Val | Ser | Tyr | Glu | His | 195 | 200 | 205 | |
| Ser | Ile | Tyr | Thr | Asn | Ile | Asn | Leu | Thr | Arg | Lys | Ile | Ser | Ile | Ile | Asn | 210 | 215 | 220 | |
| Ile | Ala | Leu | Ile | Ser | Lys | Thr | Gln | Ala | Asn | Ile | Glu | Ile | Ser | Ala | Gln | 225 | 230 | 235 | 240 |

(2) INFORMATION FOR SEQ ID NO:23853165_c1_11 - AA

Figure 209A - page 252

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 490 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 209

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: iron(II) transport system

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Trp | Asp | Glu | Ala | Lys | Lys | Glu | Gly | Ile | Asn | Ile | Asn | Thr | Glu | Lys | 1 | 5 | 10 | 15 |
| Leu | Ser | Gln | Glu | Leu | Gly | Val | Val | Cys | Val | Pro | Thr | Ser | Ala | Arg | Tyr | 20 | 25 | 30 | |
| Lys | Glu | Asp | Arg | Leu | Asn | Thr | Glu | Leu | Leu | Leu | Asp | Glu | Ile | Val | Arg | 35 | 40 | 45 | |
| Leu | Tyr | Ser | Gln | Asn | Thr | Thr | Asn | Asn | Glu | Asn | Ile | Lys | Val | Pro | Ser | 50 | 55 | 60 | |
| Gln | Ser | Phe | Lys | Glu | Ser | Leu | Lys | Tyr | Ser | Gln | Ser | Ala | Gln | Arg | Ile | 65 | 70 | 75 | 80 |
| Ala | Lys | Ser | Val | Ile | Ser | Glu | Asn | Lys | Gln | Asn | Ala | Ser | Phe | Glu | His | 85 | 90 | 95 | |
| Thr | Tyr | Lys | Ile | Asp | Lys | Ile | Phe | Asn | Ala | Pro | Ala | Leu | Trp | Asp | Phe | 100 | 105 | 110 | |
| His | Phe | Phe | Gly | Phe | Met | Phe | Ile | Ile | Phe | Ser | Leu | Ser | Phe | Leu | Ile | 115 | 120 | 125 | |
| Gly | Gly | Gly | Val | Gln | Lys | Ala | Leu | Glu | Glu | Gly | Phe | Lys | Ile | Leu | Ser | 130 | 135 | 140 | |
| Asp | Ser | Ile | Lys | Glu | Asn | Val | Ala | Asn | Glu | Asp | Leu | Ala | Ser | Leu | Val | 145 | 150 | 155 | 160 |
| Gly | Asp | Gly | Ile | Ile | Gly | Gly | Val | Gly | Ala | Thr | Val | Ser | Phe | Leu | Pro | 165 | 170 | 175 | |
| Leu | Ile | Val | Val | Leu | Tyr | Phe | Gly | Ile | Ser | Leu | Leu | Glu | Thr | Thr | Gly | 180 | 185 | 190 | |
| Tyr | Met | Ser | Arg | Val | Ala | Phe | Leu | Leu | Asp | Gly | Ile | Leu | His | Lys | Phe | 195 | 200 | 205 | |
| Gly | Leu | His | Gly | Lys | Ser | Phe | Ile | Pro | Leu | Ile | Thr | Gly | Phe | Gly | Cys | 210 | 215 | 220 | |
| Ser | Val | Pro | Ala | Tyr | Met | Ala | Thr | Arg | Thr | Leu | Gln | Asn | Tyr | Asn | Glu | 225 | 230 | 235 | 240 |

| | | | | | | | | | | | | | | | |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Arg | Leu | Ile | Thr | Leu 245 | Phe | Val | Ile | Gly | Phe 250 | Met | Ser | Cys | Ser | Ala 255 | Arg |
| Leu | Pro | Ile | Tyr 260 | Val | Leu | Phe | Val | Gly 265 | Ser | Phe | Phe | Pro | Ser 270 | Ser | Ser |
| Ala | Gly | Phe 275 | Val | Leu | Phe | Cys | Ile 280 | Tyr | Ile | Leu | Gly | Ala 285 | Val | Val | Ala |
| Leu | Val 290 | Met | Ala | Lys | Leu | Leu 295 | Lys | Leu | Ser | Val | Phe 300 | Lys | Gly | Gln | Thr |
| Glu 305 | Ser | Phe | Ile | Met | Glu 310 | Met | Pro | Lys | Tyr | Arg 315 | Phe | Pro | Ser | Trp | Arg 320 |
| Met | Val | Tyr | Phe 325 | Ser | Ile | Tyr | Thr | Lys | Ser 330 | Leu | Ser | Tyr | Leu | Lys 335 | Lys |
| Ala | Gly | Thr | Tyr 340 | Ile | Leu | Val | Gly | Ala 345 | Ile | Leu | Ile | Trp | Phe 350 | Met | Ser |
| Gln | Tyr | Pro 355 | Lys | Asn | Asp | Ala | Ala 360 | Met | Lys | Thr | Tyr | Lys 365 | Gln | Glu | Ser |
| Leu | Leu 370 | Val | Gln | Lys | Asn | Ala 375 | Asn | Leu | Ser | Ser | Glu 380 | Ala | Lys | Glu | Glu |
| Lys 385 | Leu | Lys | Glu | Leu | Lys 390 | Thr | Glu | Leu | Asp | Lys 395 | Lys | Asn | Leu | Lys | Asn 400 |
| Ser | Val | Val | Glu | Arg 405 | Gly | Gly | Ala | Tyr | Leu 410 | Glu | Lys | Val | Phe | Asn 415 | Pro |
| Met | Asp | Phe | Asp 420 | Trp | Arg | Leu | Ser | Val 425 | Ser | Leu | Val | Thr | Gly 430 | Phe | Met |
| Ala | Lys | Glu 435 | Val | Val | Val | Ser | Thr 440 | Leu | Gly | Val | Leu | Phe 445 | Ser | Leu | Gly |
| Asn | Gln 450 | Asn | Glu | Lys | Ser | Asp 455 | Ala | Phe | Arg | Glu | Ile 460 | Ile | Arg | Lys | Glu |
| Val 465 | Ser | Val | Pro | Ser | Gly 470 | Ile | Ala | Phe | Ile | Val 475 | Phe | Val | Met | Phe | Leu 480 |
| Tyr | Pro | Leu | Phe | Cys 485 | Ser | Asp | His | Tyr | Phe 490 | Trp | | | | | |

(2) INFORMATION FOR SEQ ID NO:23867207_c3_6-AA

Figure 210A - page 254

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 210

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | His | Lys | Ala | Lys | Val | Gly | Ile | Val | Phe | Gln | Ala | Leu | Leu | Gly |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Ile | Phe | Cys | Val | Phe | Leu | Leu | Leu | Phe | Tyr | Leu | Ser | Ala | Phe | Leu | Met |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Val | Ala | Phe | Lys | Asp | Thr | Lys | Arg | Met | Phe | Ile | Ser | Val | Leu | Ile | Gly |
| | | | 35 | | | | 40 | | | | | 45 | | | |
| Ser | Val | Val | Phe | Leu | Trp | Ser | Asp | Leu | Leu | Val | Phe | Val | Gly | Phe | Lys |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Asn | Ile | Ser | Phe | Val | Leu | Asp | Ile | Gly | Tyr | Glu | Ile | | | | |
| 65 | | | | | 70 | | | | | 75 | | | | | |

Figure 211A - page 255

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 196 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 211

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

[illegible]

(2) INFORMATION FOR SEQ ID NO:23880087_c3_16-AA

Figure 212A-page 256

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 212

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Pro | Phe | Leu | Lys | Asn | Trp | Ile | Trp | Ser | Leu | Lys | Met | Ala | Leu | Ser | |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | | |
| Ala | Ile | Ser | Gly | Ala | Ser | Gly | Val | Gly | Lys | Ser | Val | Leu | Ile | Ala | Ser | |
| | | | 20 | | | | | 25 | | | | | 30 | | | |
| Leu | Leu | Gly | Ala | Phe | Gly | Leu | Lys | Glu | Ser | Asn | Ala | Ser | Asn | Ile | Glu | |
| | | 35 | | | | | 40 | | | | | 45 | | | | |
| Val | Glu | Leu | Ile | Ala | Pro | Phe | Leu | Asp | Thr | Glu | Glu | Tyr | Gly | Ile | Phe | |
| | 50 | | | | | 55 | | | | | 60 | | | | | |
| Arg | Glu | Asp | Glu | His | Glu | Pro | Leu | Val | Ile | Ser | Val | Ile | Lys | Lys | Glu | |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 | |
| Lys | Thr | Arg | Tyr | Phe | Leu | Asn | Gln | Thr | Ser | Leu | Ser | Lys | Asn | Thr | Leu | |
| | | | | 85 | | | | | 90 | | | | | 95 | | |
| Lys | Ala | Leu | Leu | Lys | Gly | Leu | Ile | Lys | Arg | Leu | Ser | Asn | Asp | Arg | Phe | |
| | | | 100 | | | | | 105 | | | | | 110 | | | |
| Ser | Gln | Asn | Glu | Leu | Asn | Asp | Ile | Leu | Met | Leu | Ser | Leu | Leu | Asp | Gly | |
| | | 115 | | | | | 120 | | | | | 125 | | | | |
| Tyr | Ile | Gln | Asn | Lys | Asn | Lys | Arg | Leu | Ala | Pro | Phe | | | | | |
| | 130 | | | | | 135 | | | | | 140 | | | | | |

(2) INFORMATION FOR SEQ ID NO:23912707_c2_16:-AA

Figure 213A -page 257

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 213

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: ToxR-activated (tagE) gene [Vibrio cholerae] (inn

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Pro | Gln | Asn | Gln | Leu | Val | Ile | Thr | Ile | Ile | Asp | Glu | Ser | Gly | Ser | 1 | 5 | 10 | 15 |
| Lys | Gln | Leu | Lys | Phe | Ser | Lys | Asn | Leu | Lys | Arg | Asn | Leu | Ile | Ile | Ser | 20 | 25 | 30 | |
| Val | Val | Ile | Leu | Leu | Leu | Ile | Val | Gly | Leu | Gly | Val | Gly | Phe | Leu | Lys | 35 | 40 | 45 | |
| Phe | Leu | Ile | Ala | Lys | Met | Asp | Thr | Met | Thr | Ser | Glu | Arg | Asn | Ala | Val | 50 | 55 | 60 | |
| Leu | Arg | Asp | Phe | Arg | Gly | Leu | Tyr | Gln | Lys | Asn | Tyr | Ala | Leu | Ala | Lys | 65 | 70 | 75 | 80 |
| Glu | Ile | Lys | Asn | Lys | Arg | Glu | Glu | Leu | Phe | Ile | Val | Gly | Gln | Lys | Ile | 85 | 90 | 95 | |
| Arg | Gly | Leu | Glu | Ser | Leu | Ile | Glu | Ile | Lys | Lys | Gly | Ala | Asn | Gly | Gly | 100 | 105 | 110 | |
| Gly | His | Leu | Tyr | Asp | Glu | Val | Asp | Leu | Glu | Asn | Leu | Ser | Leu | Asn | Gln | 115 | 120 | 125 | |
| Lys | His | Leu | Ala | Leu | Met | Leu | Ile | Pro | Asn | Gly | Met | Pro | Leu | Lys | Thr | 130 | 135 | 140 | |
| Tyr | Ser | Ala | Ile | Lys | Pro | Thr | Lys | Glu | Arg | Asn | His | Pro | Ile | Lys | Lys | 145 | 150 | 155 | 160 |
| Ile | Lys | Gly | Val | Glu | Ser | Gly | Ile | Asp | Phe | Ile | Ala | Pro | Leu | Asn | Thr | 165 | 170 | 175 | |
| Pro | Val | Tyr | Ala | Ser | Ala | Asp | Gly | Ile | Val | Asp | Phe | Val | Lys | Thr | Arg | 180 | 185 | 190 | |
| Ser | Asn | Ala | Gly | Tyr | Gly | Asn | Leu | Val | Arg | Ile | Glu | His | Ala | Phe | Gly | 195 | 200 | 205 | |
| Phe | Ser | Ser | Ile | Tyr | Thr | His | Leu | Asp | His | Val | Asn | Val | Gln | Pro | Lys | 210 | 215 | 220 | |
| Ser | Phe | Ile | Gln | Lys | Gly | Gln | Leu | Ile | Gly | Tyr | Ser | Gly | Lys | Ser | Gly | 225 | 230 | 235 | 240 |

Asn Ser Gly Gly Glu Lys Leu His Tyr Glu Val Arg Phe Leu Gly Lys *Figure 213A - page 258*
 245 250 255

Ile Leu Asp Ala Glu Lys Phe Leu Ala Trp Asp Leu Asp His Phe Gln
 260 265 270

Ser Ala Leu Glu Glu Asn Lys Phe Ile Glu Trp Lys Asn Leu Phe Trp
 275 280 285

Val Leu Glu Asp Ile Val Gln Leu Gln Glu His Val Asp Lys Asp Thr
 290 295 300

Leu Lys Gly Gln
 305

(2) INFORMATION FOR SEQ ID NO:23912807_c1_7-AA

Figure 214A - page 259

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 338 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 214

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: phosphomannomutase

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ile | Thr | Gly | Ser | His | Asn | Pro | Lys | Glu | Tyr | Asn | Gly | Phe | Lys | Ile | 1 | 5 | 10 | 15 |
| Thr | Leu | Asn | Gln | Asn | Pro | Phe | Tyr | Gly | Lys | Asp | Ile | Gln | Ala | Leu | Lys | 20 | 25 | 30 | |
| Asn | Thr | Leu | Leu | Asn | Ala | Lys | His | Glu | Ile | Lys | Pro | Leu | Lys | Glu | Thr | 35 | 40 | 45 | |
| Pro | Glu | Lys | Val | Asn | Ala | Leu | Glu | Ala | Tyr | His | Arg | Tyr | Leu | Ile | Lys | 50 | 55 | 60 | |
| Asp | Phe | Lys | His | Leu | Lys | Asn | Leu | Lys | Tyr | Lys | Ile | Ala | Leu | Asp | Phe | 65 | 70 | 75 | 80 |
| Gly | Asn | Gly | Val | Gly | Ala | Leu | Gly | Leu | Glu | Pro | Ile | Leu | Lys | Ala | Leu | 85 | 90 | 95 | |
| Asn | Ile | Asp | Phe | Ser | Ser | Leu | Tyr | Ser | Asp | Pro | Asp | Gly | Asp | Phe | Pro | 100 | 105 | 110 | |
| Asn | His | His | Pro | Asp | Pro | Ser | Glu | Ala | Lys | Asn | Leu | Lys | Asp | Leu | Glu | 115 | 120 | 125 | |
| Lys | His | Met | Arg | Glu | Asn | Ala | Ile | Leu | Ile | Gly | Phe | Ala | Phe | Asp | Gly | 130 | 135 | 140 | |
| Asp | Ala | Asp | Arg | Ile | Ala | Met | Leu | Ser | Ser | His | His | Ile | Tyr | Ala | Gly | 145 | 150 | 155 | 160 |
| Asp | Glu | Leu | Ala | Ile | Leu | Phe | Ala | Lys | Arg | Leu | His | Ala | Gln | Gly | Ile | 165 | 170 | 175 | |
| Thr | Pro | Phe | Val | Ile | Gly | Glu | Val | Lys | Cys | Ser | Gln | Val | Met | Tyr | Asn | 180 | 185 | 190 | |
| Ala | Ile | Asn | Thr | Phe | Gly | Lys | Thr | Leu | Met | Tyr | Lys | Thr | Gly | His | Ser | 195 | 200 | 205 | |
| Asn | Leu | Lys | Ile | Lys | Leu | Lys | Glu | Thr | Asn | Ala | His | Phe | Ala | Ala | Glu | 210 | 215 | 220 | |
| Met | Ser | Gly | His | Ile | Phe | Phe | Lys | Glu | Arg | Tyr | Phe | Gly | Tyr | Asp | Asp | 225 | 230 | 235 | 240 |

[illegible]

(2) INFORMATION FOR SEQ ID NO:23915877_f1_2-AA

Figure 215A - page 261

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 206 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 215

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Lys | Asn | Leu | Gln | Lys | Lys | Asn | Pro | Lys | Lys | Ser | Unk | Pro | Gln |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Ala | Gln | Lys | Ala | Ile | Arg | Glu | Met | Lys | Met | Phe | Glu | Thr | Ile | Ala | Phe |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Tyr | Phe | Phe | Ala | Ile | Leu | Thr | Leu | Ser | Met | Ala | Leu | Val | Val | Ile | Thr |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Thr | Thr | Asn | Ile | Leu | Tyr | Ala | Ile | Thr | Ala | Leu | Ala | Ser | Ser | Met | Val |
| | | 50 | | | | 55 | | | | | 60 | | | | |
| Phe | Ile | Ser | Ala | Phe | Phe | Phe | Leu | Leu | Asp | Ala | Glu | Phe | Leu | Gly | Val |
| 65 | | | | 70 | | | | | 75 | | | | | 80 | |
| Val | Gln | Ile | Thr | Val | Tyr | Val | Gly | Ala | Val | Ile | Val | Met | Tyr | Ala | Phe |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| Gly | Met | Met | Phe | Phe | Asn | Ser | Ala | Ala | Glu | Val | Val | Glu | Arg | Lys | Gln |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Ser | Pro | Lys | Ile | Leu | Cys | Val | Leu | Ser | Phe | Gly | Val | Ala | Leu | Leu | Leu |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| Thr | Leu | Ile | Leu | Ser | Ala | Pro | Ser | Ile | Unk | Glu | Asn | Leu | Ser | Lys | Gln |
| | | | | | | 135 | | | | | 140 | | | | |
| Val | Asn | Ser | Asn | Ala | Ile | Asp | Ala | Gln | Unk | Pro | Asn | Ile | Lys | Ala | Ile |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 |
| Gly | Tyr | Val | Leu | Phe | Thr | Asn | Tyr | Leu | Ile | Pro | Phe | Glu | Ala | Ala | Ala |
| | | | | 165 | | | | | 170 | | | | | 175 | |
| Leu | Met | Leu | Leu | Val | Ala | Met | Val | Gly | Gly | Ile | Ala | Thr | Gly | Ile | Gln |
| | | | 180 | | | | | 185 | | | | | 190 | | |
| Lys | Ile | His | Gly | Lys | Asn | His | Thr | Gln | Phe | Ile | Lys | Glu | Ser | Leu | |
| | | 195 | | | | | 200 | | | | | 205 | | | |

(2) INFORMATION FOR SEQ ID NO:23945317_c2_15-AA

Figure 216A - page 262

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP216

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Ala | Ile | Leu | Ser | Ile | Leu | Lys | Leu | Glu | Ile | Lys | Ser | Tyr | Leu | 1 | 5 | 10 | 15 |
| Thr | Asn | Thr | Ser | Ala | Leu | Phe | Trp | Thr | Phe | Ile | Tyr | Pro | Ile | Leu | Met | 20 | 25 | 30 | |
| Leu | Leu | Leu | Leu | Ile | Phe | Val | Phe | Ser | Lys | Asn | Thr | Thr | Glu | Ile | Phe | 35 | 40 | 45 | |
| Tyr | Phe | Asn | Asn | Ile | Ile | Gly | Leu | Met | Gly | Leu | Leu | Ile | Ile | Ser | Ser | 50 | 55 | 60 | |
| Ala | Ile | Phe | Gly | Leu | Thr | Gln | Ala | Ile | Thr | Ser | Ser | Arg | Ser | His | Asn | 65 | 70 | 75 | 80 |
| Ile | Phe | Leu | Phe | Tyr | Met | Leu | Ser | Pro | Ala | Thr | Phe | Lys | Gln | Ile | Thr | 85 | 90 | 95 | |
| Leu | Ala | Leu | Ile | Ala | Ser | Arg | Leu | Ile | Val | Val | Ile | Leu | Tyr | Ala | Phe | 100 | 105 | 110 | |
| Ile | Phe | Ile | Val | Leu | Ser | Phe | Tyr | Ala | Leu | Asn | Ile | Ile | Thr | Ile | Leu | 115 | 120 | 125 | |
| Asn | Phe | Lys | Ala | Leu | Ile | Leu | Gly | Phe | Ile | Ser | Ile | Phe | Ser | Ser | Ala | 130 | 135 | 140 | |
| Leu | Phe | Cys | Phe | Cys | Leu | Ala | Ile | Phe | Val | Ala | Arg | Ile | Phe | Gln | Asn | 145 | 150 | 155 | 160 |
| Glu | Gln | Ser | Ile | Leu | Gly | Phe | Cys | Asn | Ile | Ile | Asn | Leu | Tyr | Ala | Leu | 165 | 170 | 175 | |
| Met | Ser | Cys | Asn | Val | Phe | Val | Pro | Leu | Glu | Tyr | Leu | Pro | Asn | Ile | Gly | 180 | 185 | 190 | |
| Gln | Leu | Phe | Ile | Lys | Thr | Ser | Ile | Phe | Tyr | Tyr | Leu | Asn | Gln | Leu | Leu | 195 | 200 | 205 | |
| Ile | Lys | Ala | Phe | Gln | Gly | Ile | Asp | Thr | Ile | Leu | Val | Leu | Ala | Thr | Ser | 210 | 215 | 220 | |
| Thr | Phe | Phe | Ile | Ile | Gly | Gly | Ile | Ile | Leu | Phe | Leu | Leu | Ser | Ala | Asn | 225 | 230 | 235 | 240 |

Arg Met Leu Leu Thr Pro Lys Glu Arg Met Arg
245 250

Figure 216A - page 263

Figure 217A - page 264

Lys Ser Lys His Arg
65

(2) INFORMATION FOR SEQ ID NO:24003758_c3_32-AA

Figure 218A - page 265

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 218

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: spoIIIE gene product

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ser | Arg | Ile | Leu | Gly | Leu | Ser | Asp | Asp | Leu | Ala | Met | Thr | Leu | Cys |
| 1 | | | | 5 | | | | 10 | | | | | 15 | | |
| Ala | Glu | Ser | Ile | Arg | Ile | Gln | Ala | Pro | Ile | Lys | Gly | Lys | Asp | Val | Val |
| | | | 20 | | | | 25 | | | | | | 30 | | |
| Gly | Ile | Glu | Ile | Pro | Asn | Ser | Gln | Ser | Gln | Ile | Ile | Tyr | Leu | Arg | Glu |
| | | 35 | | | | 40 | | | | | | 45 | | | |
| Ile | Leu | Glu | Ser | Glu | Leu | Phe | Gln | Lys | Ser | Ser | Ser | Pro | Leu | Thr | Leu |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Ala | Leu | Gly | Lys | Asp | Ile | Val | Gly | Asn | Pro | Phe | Ile | Thr | Asp | Leu | Lys |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 |
| Lys | Leu | Pro | His | Leu | Leu | Ile | Ala | Gly | Thr | Thr | Gly | Ser | Gly | Lys | Ser |
| | | | 85 | | | | | | 90 | | | | | 95 | |
| Val | Gly | Val | Asn | Ala | Met | Ile | Leu | Ser | Leu | Leu | Tyr | Lys | Lys | Pro | Pro |
| | | | 100 | | | | | 105 | | | | | 110 | | |

(2) INFORMATION FOR SEQ ID NO:24036302_f3_3-AA

Figure 219A-page 266

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 219.

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| Met | Asp | Glu | Unk | Leu | Val | Tyr | Gly | Val | Ile | Cys | Met | Pro | Ser | Gln | Val | 1 | 5 | 10 | 15 |
| Phe | Ala | Asn | Thr | Gly | Thr | Asn | Val | Ser | Ile | Ile | Phe | Phe | Gln | Lys | Thr | 20 | 25 | 30 | |
| Pro | Ser | Ala | Lys | Glu | Val | Ile | Leu | Ile | Asp | Ala | Ser | Lys | Leu | Gly | Glu | 35 | 40 | 45 | |
| Glu | Tyr | Thr | Glu | Asn | Lys | Asn | Lys | Lys | Thr | Arg | Leu | Arg | Pro | Ser | Asp | 50 | 55 | 60 | |
| Met | Asp | Leu | Ile | Leu | Glu | Thr | Phe | Gln | Asn | Lys | Ala | Pro | Lys | Ser | Asp | 65 | 70 | 75 | 80 |
| Phe | Cys | Ala | Leu | Val | Ser | Phe | Asp | Glu | Ile | Thr | Glu | Lys | Asn | Tyr | Ser | 85 | 90 | 95 | |
| Leu | Asn | Pro | Gly | Gln | Tyr | Phe | Thr | Ile | Glu | Asp | Thr | Ser | Glu | Thr | Ile | 100 | 105 | 110 | |
| Ser | Gln | Ala | Glu | Phe | Glu | Asn | Leu | Met | Gln | Gln | Tyr | Ser | Ser | Glu | Leu | 115 | 120 | 125 | |
| Ala | Ser | Leu | Phe | Asp | Glu | Ser | Gln | Asn | Leu | Gln | Gln | Glu | Ile | Leu | Glu | 130 | 135 | 140 | |
| Thr | Leu | Lys | Gly | Val | Arg | Phe | Glu | | | | | | | | | 145 | 150 | | |

(2) INFORMATION FOR SEQ ID NO:24039587_f1_3-AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 220

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Arg | Lys | Gly | Arg | Val | Met | Leu | Cys | Val | Phe | Asp | Ile | Glu | Thr | Ile |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Pro | Asn | Ile | Ser | Leu | Cys | Lys | Glu | His | Phe | Gln | Leu | Lys | Glu | Asp | Asp |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Ala | Leu | Lys | Ile | Cys | Glu | Trp | Ser | Phe | Glu | Lys | Gln | Lys | Glu | Lys | Ser |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Gly | Ser | Glu | Phe | Leu | Pro | Leu | Tyr | Leu | His | Glu | Ile | Ile | Ser | Ile | Ala |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Ala | Ser | Leu | Ala | Met | Ile | Thr | Gly | Asn | Leu | Ser | Lys | | | | |
| 65 | | | | | 70 | | | | | 75 | | | | | |

(2) INFORMATION FOR SEQ ID NO:24070250_c1_11 -AA

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 112 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP221

(iii) HYPOTHETICAL: YES

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: chemotaxis protein cheY

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Arg | Arg | Ile | Ile | Lys | Asn | Thr | Leu | Ser | Arg | Leu | Gly | Tyr | Glu | Asp |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Val | Leu | Glu | Ala | Glu | His | Gly | Val | Glu | Ala | Trp | Glu | Lys | Leu | Asp | Ala |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Asn | Ala | Asp | Thr | Lys | Val | Leu | Ile | Thr | Asp | Trp | Asn | Met | Pro | Glu | Met |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Asn | Gly | Leu | Asp | Leu | Val | Lys | Lys | Val | Arg | Ala | Asp | Asn | Arg | Phe | Lys |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Glu | Ile | Pro | Ile | Ile | Met | Ile | Thr | Thr | Glu | Gly | Gly | Lys | Ala | Glu | Val |
| 65 | | | | | 70 | | | | | 75 | | | | 80 | |
| Ile | Thr | Thr | Leu | Lys | Ala | Gly | Val | Asn | Asn | Tyr | Ile | Val | Lys | Pro | Phe |
| | | | | 85 | | | | 90 | | | | | | 95 | |
| Thr | Pro | Gln | Val | Leu | Lys | Glu | Lys | Leu | Glu | Val | Val | Leu | Gly | Thr | Asn |
| | | | 100 | | | | | 105 | | | | | 110 | | |

Asp

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 222

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: component of flagellum

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Glu | Glu | Gln | Glu | Asn | Thr | Ala | Gln | Gln | Pro | Gln | Lys | Lys | Ser | 1 | 5 | 10 | 15 |
| Lys | Ala | Leu | Leu | Phe | Val | Ile | Ile | Gly | Ser | Val | Leu | Val | Met | Leu | Leu | 20 | 25 | 30 | |
| Leu | Val | Gly | Val | Ile | Ile | Met | Leu | Leu | Met | Gly | Asn | Lys | Glu | Glu | Ser | 35 | 40 | 45 | |
| Lys | Glu | Asn | Ala | Ser | Lys | Asn | Thr | Gln | Glu | Val | Gln | Ala | Asn | Pro | Met | 50 | 55 | 60 | |
| Ala | Asn | Lys | Asn | Gln | Glu | Ala | Lys | Glu | Gly | Ser | Asn | Ile | Gln | Gln | Tyr | 65 | 70 | 75 | 80 |
| Leu | Val | Leu | Gly | Pro | Leu | Tyr | Ala | Ile | Asp | Ala | Pro | Phe | Ala | Val | Asn | 85 | 90 | 95 | |
| Leu | Val | Ser | Gln | Asn | Gly | Arg | Arg | Tyr | Leu | Lys | Ala | Ser | Ile | Ser | Leu | 100 | 105 | 110 | |
| Glu | Leu | Ser | Asn | Glu | Lys | Leu | Leu | Asn | Glu | Val | Lys | Val | Lys | Asp | Thr | 115 | 120 | 125 | |
| Ala | Ile | Lys | Asp | Thr | Ile | Ile | Glu | Ile | Leu | Ser | Ser | Lys | Ser | Val | Glu | 130 | 135 | 140 | |
| Glu | Val | Val | Thr | Asn | Lys | Gly | Lys | Asn | Lys | Leu | Lys | Asp | Glu | Ile | Lys | 145 | 150 | 155 | 160 |
| Ser | His | Leu | Asn | Ser | Phe | Leu | Ile | Asp | Gly | Phe | Ile | Lys | Asn | 165 | 170 | | | | |

| | | | | | | | | | | | | | | | |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Met 1 | Ala | Lys | Lys | Lys 5 | Ile | Ala | Ile | Ser | Cys 10 | Gly | Asp | Ile | Gln | Gly 15 | Val |
| Gly | Leu | Glu | Leu 20 | Ile | Leu | Lys | Ser | His 25 | Lys | Glu | Val | Ser | Ala 30 | Leu | Cys |
| Glu | Pro | Leu 35 | Tyr | Leu | Val | His | Ser 40 | Glu | Leu | Leu | Glu | Arg 45 | Ala | Asn | Gln |
| Leu | Leu 50 | Asp | Asn | Ala | Tyr | Glu 55 | Thr | Lys | Thr | Leu | Asn 60 | Ala | Ile | Ala | Ile |
| Asp 65 | Ala | Pro | Leu | Pro | Leu 70 | Leu | Asn | Ser | Ser | Thr 75 | Ile | Gly | Lys | Val | Ser 80 |
| Thr | Gln | Ser | Gly | Ala 85 | Tyr | Ser | Phe | Glu | Ser 90 | Phe | Lys | Lys | Ala | Cys 95 | Glu |
| Leu | Ala | Asp | Ser 100 | Lys | Glu | Val | Asp | Gly 105 | Ile | Cys | Thr | Leu | Pro 110 | Ile | Asn |
| Lys | Leu | Ala 115 | Trp | Gln | Gln | Ala | Gln 120 | Ile | Pro | Phe | Val | Gly 125 | His | Thr | Asp |
| Phe | Leu 130 | Lys | Gln | Arg | Tyr | Lys 135 | Asp | His | Gln | Ile | Ile 140 | Met | Met | Leu | Gly |
| Cys 145 | Ser | Lys | Leu | Phe | Val 150 | Gly | Leu | Phe | Ser | Asp 155 | His | Val | Pro | Leu | Ser 160 |
| Ala | Val | Ser | Gln | Leu 165 | Ile | Gln | Val | Lys | Ala 170 | Leu | Val | Lys | Phe | Leu 175 | Leu |
| Ala | Phe | Gln | Lys 180 | Ser | Thr | Gln | Ala | Lys 185 | Ile | Val | Gln | Val | Cys 190 | Gly | Phe |
| Asn | Pro | His 195 | Ala | Gly | Glu | Glu | Gly 200 | Leu | Phe | Gly | Glu | Glu 205 | Asp | Glu | Lys |
| Ile | Leu 210 | Lys | Ala | Ile | Gln | Glu 215 | Ser | Asn | Gln | Thr | Leu 220 | Gly | Phe | Glu | Cys |
| Phe 225 | Leu | Gly | Pro | Leu | Pro 230 | Ala | Asp | Ser | Ala | Phe 235 | Ala | Pro | Asn | Lys | Arg 240 |

Lys Ile Thr Pro Phe Tyr Val Ser Met Ser His Asp Val Gly Leu Ala
 245 250 255

Pro Leu Lys Ala Leu Tyr Phe Asp Glu Ser Ile Asn Val Ser Leu Asn
 260 265 270

Ala Pro Ile Leu Arg Ala Ser Thr Asp His Gly Thr Ala Phe Asp Ile
 275 280 285

Ala Tyr Gln Asn Lys Ala Asn His Lys Ser Tyr Leu Asn Ala Ile Lys
 290 295 300

Tyr Leu Ala
 305

(2) INFORMATION FOR SEQ ID NO:24104558_f1_1-AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 701 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 225

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: VirB4 homolog

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ala | Arg | Leu | Val | Val | Lys | Arg | Arg | Lys | Ile | Asp | Tyr | Lys | Gln | Ser | 1 | 5 | 10 | 15 |
| Ile | Gln | Ser | Asp | Ser | Gln | Tyr | Leu | Gln | Ala | Unk | Leu | Asn | Gln | Phe | Glu | 20 | 25 | 30 | |
| Asn | Lys | Glu | Val | Tyr | Glu | Asn | Gln | Tyr | Phe | Leu | Val | Leu | Glu | Ser | Thr | 35 | 40 | 45 | |
| His | Ser | Leu | His | Gly | Val | Leu | Glu | His | Lys | Lys | Lys | Ser | Phe | Met | His | 50 | 55 | 60 | |
| Ala | Asn | Arg | Glu | Asn | Phe | Lys | Asp | Ile | Leu | Ser | Tyr | Lys | Ala | His | Phe | 65 | 70 | 75 | 80 |
| Leu | Gln | Glu | Thr | Leu | Lys | Ser | Leu | Glu | Ile | Gln | Leu | Lys | Asn | Tyr | Ala | 85 | 90 | 95 | |
| Pro | Lys | Leu | Leu | Asn | Ser | Lys | Glu | Val | Leu | Asn | Phe | Tyr | Ala | Glu | Tyr | 100 | 105 | 110 | |
| Ile | Asn | Gly | Phe | Glu | Leu | Pro | Leu | Lys | Pro | Leu | Val | Gly | Gly | Tyr | Leu | 115 | 120 | 125 | |
| Ser | Asp | Ser | Tyr | Ile | Ala | Ser | Ser | Ile | Thr | Phe | Glu | Lys | Asp | Tyr | Phe | 130 | 135 | 140 | |
| Ile | Gln | Glu | Ser | Phe | Asn | Gln | Lys | Thr | Tyr | Asn | Arg | Leu | Ile | Gly | Ile | 145 | 150 | 155 | 160 |
| Lys | Ala | Tyr | Glu | Ser | Glu | Arg | Ile | Thr | Ser | Ile | Ala | Val | Gly | Ala | Leu | 165 | 170 | 175 | |
| Leu | Tyr | Gln | Glu | Thr | Pro | Leu | Asp | Ile | Ile | Phe | Ser | Ile | Glu | Pro | Met | 180 | 185 | 190 | |
| Ser | Val | Asn | Lys | Thr | Leu | Ser | Phe | Leu | Lys | Glu | Arg | Ala | Lys | Phe | Ser | 195 | 200 | 205 | |
| Met | Ser | Asn | Leu | Val | Lys | Asn | Glu | Leu | Leu | Glu | Tyr | Gln | Glu | Leu | Val | 210 | 215 | 220 | |
| Lys | Thr | Lys | Arg | Leu | Ser | Met | Gln | Lys | Phe | Ala | Leu | Asn | Val | Leu | Ile | 225 | 230 | 235 | 240 |

| | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Ala | Pro | Ser | Leu | Glu | Asp | Leu | Asp | Ala | Gln | Thr | Ser | Leu | Ile | Leu | 245 | 250 | 255 |
| Gly | Leu | Leu | Phe | Lys | Glu | Asn | Leu | Val | Gly | Val | Ile | Glu | Thr | Phe | Gly | 260 | 265 | 270 |
| Leu | Lys | Gly | Gly | Tyr | Phe | Ser | Phe | Phe | Pro | Glu | Arg | Ile | His | Leu | Asn | 275 | 280 | 285 |
| His | Arg | Leu | Arg | Phe | Leu | Thr | Ser | Lys | Ala | Leu | Ala | Cys | Leu | Met | Val | 290 | 295 | 300 |
| Phe | Glu | Arg | Gln | Asn | Leu | Gly | Phe | Lys | Ala | Asn | Ser | Trp | Gly | Asn | Ser | 305 | 310 | 315 |
| Pro | Leu | Ser | Val | Phe | Lys | Asn | Leu | Asp | Tyr | Ser | Pro | Phe | Leu | Phe | Asn | 325 | 330 | 335 |
| Phe | His | Asn | Gln | Glu | Val | Ser | His | Asn | Asn | Ala | Lys | Glu | Ile | Ala | Arg | 340 | 345 | 350 |
| Val | Asn | Gly | His | Thr | Leu | Val | Ile | Gly | Ala | Thr | Gly | Ser | Gly | Lys | Ser | 355 | 360 | 365 |
| Thr | Leu | Ile | Ser | Tyr | Leu | Met | Met | Ser | Ala | Leu | Lys | Tyr | Gln | Asn | Met | 370 | 375 | 380 |
| Arg | Leu | Leu | Ala | Phe | Asp | Arg | Met | Gln | Gly | Leu | Tyr | Ser | Phe | Thr | Glu | 385 | 390 | 395 |
| Phe | Phe | Lys | Gly | His | Tyr | His | Asp | Gly | Gln | Ser | Phe | Ser | Ile | Asn | Pro | 405 | 410 | 415 |
| Phe | Cys | Leu | Glu | Pro | Asn | Leu | Gln | Asn | Leu | Glu | Phe | Leu | Gln | Ser | Phe | 420 | 425 | 430 |
| Phe | Leu | Ser | Met | Leu | Asp | Leu | Ala | Pro | Ser | Arg | Asp | Lys | Glu | Ala | Leu | 435 | 440 | 445 |
| Glu | Asp | Met | Asn | Ala | Ile | Ser | Gly | Ala | Ile | Lys | Ser | Leu | Tyr | Glu | Thr | 450 | 455 | 460 |
| Leu | Tyr | Pro | Lys | Asp | Phe | Ser | Leu | Leu | Asp | Phe | Lys | Glu | Thr | Leu | Lys | 465 | 470 | 475 |
| Arg | Thr | Ser | Ser | Asn | Gln | Leu | Gly | Leu | Ser | Leu | Glu | Pro | Tyr | Leu | Asn | 485 | 490 | 495 |
| Asn | Pro | Leu | Phe | Asn | Ala | Leu | Asn | Asp | Ala | Phe | Asn | Ser | Asn | Ala | Phe | 500 | 505 | 510 |
| Leu | Asn | Val | Ile | Asn | Leu | Asp | Ala | Ile | Thr | Gln | Asn | Pro | Lys | Asp | Leu | 515 | 520 | 525 |
| Gly | Leu | Leu | Ala | Tyr | Tyr | Leu | Phe | Tyr | Lys | Ile | Leu | Glu | Glu | Ser | Arg | 530 | 535 | 540 |
| Lys | Asn | Asp | Ser | Gly | Phe | Leu | Val | Phe | Leu | Asp | Glu | Phe | Lys | Ser | Tyr | 545 | 550 | 555 |

Val Glu Asn Asp Leu Leu Asn Thr Lys Ile Asn Ala Leu Ile Thr Gln Figure 225A -page 275
565 570 575

Ala Arg Lys Ala Asn Gly Val Val Val Leu Ala Leu Gln Asp Ile Tyr
580 585 590

Gln Leu Ser Gly Val Lys Asn Ala His Ser Phe Leu Ser Asn Met Gly
595 600 605

Thr Leu Ile Leu Tyr Pro Gln Lys Asn Ala Arg Glu Leu Lys His Asn
610 615 620

Phe Asn Val Pro Leu Ser Glu Thr Glu Ile Ser Phe Leu Glu Asn Thr
625 630 635 640

Pro Leu Tyr Ala Arg Gln Val Leu Val Lys Asn Leu Gly Asn Gly Ser
645 650 655

Ser Asn Met Ile Asp Val Ser Leu Glu Gly Leu Gly Cys Tyr Leu Lys
660 665 670

Ile Phe Asn Ser Asp Ser Ser His Val Asn Lys Val Lys Ala Leu Gln
675 680 685

Lys Asp Tyr Pro Thr Glu Trp Arg Glu Lys Leu Leu Lys Ser
690 695 700

(2) INFORMATION FOR SEQ ID NO:24132293_f1_2-AA

Figure 226A - page 276

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 292 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 226

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: methyl-accepting chemotaxis protein; transmembran

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gln | Glu | Asp | Trp | Gln | Ala | Val | Gln | Asp | Thr | Ile | Lys | Val | Val | Ser | 1 | 5 | 10 | 15 |
| Asp | Val | Lys | Ala | Gly | Asn | Phe | Ala | Val | Arg | Ile | Thr | Ala | Glu | Pro | Ala | 20 | 25 | 30 | |
| Ser | Pro | Asp | Leu | Lys | Glu | Leu | Arg | Asp | Ala | Leu | Asn | Gly | Ile | Met | Unk | 35 | 40 | 45 | |
| Tyr | Leu | Gln | Glu | Ser | Val | Gly | Thr | His | Met | Pro | Ser | Ile | Phe | Lys | Ile | 50 | 55 | 60 | |
| Phe | Glu | Ser | Tyr | Ser | Gly | Leu | Asp | Phe | Arg | Gly | Arg | Ile | Gln | Asn | Ala | 65 | 70 | 75 | 80 |
| Ser | Gly | Arg | Val | Glu | Leu | Val | Thr | Asn | Ala | Leu | Gly | Gln | Glu | Ile | Gln | 85 | 90 | 95 | |
| Lys | Met | Leu | Glu | Thr | Ser | Ser | Asn | Phe | Ala | Lys | Asp | Leu | Ala | Asn | Asp | 100 | 105 | 110 | |
| Ser | Ala | Asn | Leu | Lys | Glu | Cys | Val | Gln | Asn | Leu | Glu | Lys | Ala | Ser | Asn | 115 | 120 | 125 | |
| Ser | Gln | His | Lys | Ser | Leu | Met | Glu | Thr | Ser | Lys | Thr | Ile | Glu | Asn | Ile | 130 | 135 | 140 | |
| Thr | Thr | Ser | Ile | Gln | Gly | Val | Ser | Ser | Gln | Ser | Glu | Ala | Met | Ile | Glu | 145 | 150 | 155 | 160 |
| Gln | Gly | Lys | Asp | Ile | Lys | Ser | Ile | Val | Glu | Ile | Ile | Arg | Asp | Ile | Ala | 165 | 170 | 175 | |
| Asp | Gln | Thr | Asn | Leu | Leu | Ala | Leu | Asn | Ala | Ala | Ile | Glu | Ala | Ala | Arg | 180 | 185 | 190 | |
| Ala | Gly | Glu | His | Gly | Arg | Gly | Phe | Ala | Val | Val | Ala | Asp | Glu | Val | Arg | 195 | 200 | 205 | |
| Lys | Leu | Ala | Glu | Arg | Thr | Gln | Lys | Ser | Leu | Ser | Glu | Ile | Glu | Ala | Asn | 210 | 215 | 220 | |
| Ile | Asn | Ile | Leu | Val | Gln | Ser | Ile | Ser | Asp | Thr | Ser | Glu | Ser | Ile | Lys | 225 | 230 | 235 | 240 |

[illegible]

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (xi) SEQUENCE DESCRIPTION: sodium/glutamate symport carrier protein

Leu Ala Tyr Ala
50

(2) INFORMATION FOR SEQ ID NO:24218968_f3_2: -A A

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 181 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 228

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: HYPOTHETICAL ABC TRANSPORTER

[illegible]

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 229

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ser | Leu | Ile | Lys | Val | Ser | Gly | Asp | Lys | Lys | Val | Ile | Glu | Val | Ser | 1 | 5 | 10 | 15 |
| Ile | Pro | Leu | Thr | Ser | Ile | Ser | Gly | Lys | Ala | Arg | Val | Lys | Ile | Arg | His | 20 | 25 | 30 | |
| Ala | Phe | Ser | Asp | Tyr | Gly | Ile | Ser | Thr | Ala | Thr | Arg | Lys | Ile | Pro | Phe | 35 | 40 | 45 | |
| Ser | Leu | Lys | His | Tyr | Val | Glu | Trp | Gln | Ile | Gly | Tyr | Asp | Val | Pro | Ile | 50 | 55 | 60 | |
| Lys | Asp | Lys | Glu | Lys | Phe | Glu | Leu | Thr | Thr | Leu | Lys | Asp | Glu | Lys | Tyr | 65 | 70 | 75 | 80 |
| His | Phe | Leu | Gly | Ala | Asn | Asn | Lys | Val | Lys | Thr | Leu | Tyr | Glu | Leu | Ser | 85 | 90 | 95 | |
| Glu | Met | Ile | Tyr | Tyr | Ala | Lys | Arg | Leu | Gly | Leu | Ile | Ser | Leu | Glu | Asn | 100 | 105 | 110 | |
| Leu | Glu | Asn | Thr | Leu | Lys | Phe | Leu | Glu | Lys | Gln | Lys | Gln | Phe | Ile | Glu | 115 | 120 | 125 | |
| Asp | Asn | Phe | Met | Ile | Thr | Arg | Glu | Arg | Phe | Arg | Ser | His | Gln | Phe | Gly | 130 | 135 | 140 | |
| Gly | Met | Asp | Phe | Glu | Leu | Ser | Arg | Ile | Ser | Tyr | Pro | Leu | Leu | Ile | His | 145 | 150 | 155 | 160 |
| Ser | Phe | Asp | Asp | Asn | Glu | Leu | Ser | Glu | Ile | Val | Ile | Lys | Glu | Gln | Gln | 165 | 170 | 175 | |
| Tyr | Gly | Ser | Lys | Thr | Gln | Ala | Met | Leu | Tyr | Phe | Cys | Phe | Ser | Ile | Leu | 180 | 185 | 190 | |
| Glu | Leu | Lys | Thr | Ala | Thr | Pro | Leu | Leu | Asn | Arg | Thr | Ala | Met | Pro | Lys | 195 | 200 | 205 | |
| Glu | His | Ala | Leu | Leu | Ile | Ile | His | Glu | Thr | Asn | Ala | Leu | Val | Phe | Leu | 210 | 215 | 220 | |
| Glu | Met | Leu | Lys | Ile | Phe | Gly | Leu | Leu | Ser | Gln | Val | His | His | Asn | Asp | 225 | 230 | 235 | 240 |

Val Leu Lys Ile Leu Glu Lys Ile Leu Gln Asn
245 250

(D) TOPOLOGY: linear

HPP 230

(A) ORGANISM: *Helicobacter pylori*

Asp Gly Ala Ser Ala Ile Ala Leu
35 40

(2) INFORMATION FOR SEQ ID NO:24222885_c3_10-AA

Figure 231A - page 283

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 231

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | |
|-----------|-----------|------------|------------|-----------|-----|-----------|------------|------------|-----------|-----------|-----------|-----------|------------|-----------|-----------|
| Val 1 | Phe | Val | Gly 5 | Leu | Tyr | His | Gly | Ala | Ser 10 | Ile | Phe | Asp | Leu | Lys 15 | Phe |
| Glu | Val | Tyr | Leu 20 | Thr | Met | Leu | Ile | Ser 25 | Leu | Met | Pro | Phe | Val 30 | Ala | Thr |
| Ile | Tyr | Ile 35 | Asn | Phe | Pro | Lys | Thr 40 | Thr | Glu | Thr | Ser | His 45 | Gly | Tyr | Ala |
| Arg | Trp 50 | Ala | Asn | Val | Lys | Asp 55 | Ile | Glu | Cys | Phe | Lys 60 | Ile | Phe | Ser | Lys |
| Glu 65 | Gly | Phe | Cys | Lys 70 | Val | Val | His | Arg | Leu | Gly 75 | Val | Gln | Phe | Asp | Asn 80 |
| Gly | Phe | Ile | Leu | Gly 85 | Lys | Phe | Gly | Phe | Pro 90 | Lys | Leu | Arg | Asn | Val 95 | Cys |
| Tyr | Asp | Lys | Pro 100 | Leu | Gly | Thr | Met | Ile 105 | Val | Ala | Pro | Pro | Gly 110 | Ala | Glu |
| Lys | Leu | His 115 | Val | Trp | Leu | Cys | Gln 120 | Ile | Tyr | | | | | | |

(2) INFORMATION FOR SEQ ID NO:24230058_f1_1-AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP232

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| Met | Lys | Arg | Leu | Ala | Val | Ala | Leu | Ile | Leu | Val | Leu | Gly | Val | Val | Trp | 1 | 5 | 10 | 15 |
| Gly | Lys | Ser | Leu | Pro | Lys | Trp | Ala | Lys | Asp | Cys | Ser | Lys | Glu | Met | Arg | 20 | 25 | 30 | |
| Ile | Glu | Lys | Thr | Gln | Thr | Lys | Asp | Glu | Lys | Ile | Leu | Val | Cys | Gly | Met | 35 | 40 | 45 | |
| Ser | Asp | Ile | Leu | Leu | Ser | Asp | Met | Asp | Tyr | Ser | Leu | Ser | Ser | Ala | Arg | 50 | 55 | 60 | |
| Gln | Asn | Ala | Leu | Glu | Lys | Val | Met | Glu | Ala | Phe | Lys | Gly | Asp | Arg | Ile | 65 | 70 | 75 | 80 |
| Glu | Ile | Lys | Ala | Gly | Glu | Leu | Lys | Ala | Thr | Phe | Ile | Asp | Thr | Asp | Lys | 85 | 90 | 95 | |
| Val | Tyr | Val | Leu | Leu | Arg | Ile | Thr | Lys | Lys | His | Val | Ala | Leu | Met | Asn | 100 | 105 | 110 | |
| Glu | | | | | | | | | | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:24238762_c3_33-AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 436 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 233

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: alpha-ketoglutarate permease

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asn | Pro | Gln | Ile | Gln | Pro | Ala | Thr | Lys | Lys | Pro | Leu | Lys | Ser | Leu | 1 | 5 | 10 | 15 |
| Leu | Ala | Ala | Ser | Ser | Gly | Asn | Leu | Val | Glu | Trp | Tyr | Asp | Phe | Tyr | Ala | 20 | 25 | 30 | |
| Tyr | Ala | Phe | Leu | Ala | Pro | Tyr | Phe | Ala | Lys | Glu | Phe | Thr | His | Thr | Asn | 35 | 40 | 45 | |
| Asp | Pro | Thr | Leu | Ala | Leu | Ile | Ser | Ala | Phe | Leu | Val | Phe | Met | Leu | Gly | 50 | 55 | 60 | |
| Phe | Phe | Met | Arg | Pro | Leu | Gly | Ser | Leu | Phe | Phe | Gly | Lys | Leu | Gly | Asp | 65 | 70 | 75 | 80 |
| Lys | Lys | Gly | Arg | Lys | Thr | Ser | Met | Val | Tyr | Ser | Ile | Ile | Leu | Met | Ala | 85 | 90 | 95 | |
| Leu | Gly | Ser | Phe | Met | Leu | Ala | Leu | Leu | Pro | Thr | Lys | Glu | Ile | Val | Gly | 100 | 105 | 110 | |
| Glu | Trp | Ala | Phe | Leu | Phe | Leu | Leu | Leu | Ala | Arg | Leu | Leu | Gln | Gly | Phe | 115 | 120 | 125 | |
| Ser | Val | Gly | Gly | Glu | Tyr | Gly | Val | Val | Ala | Thr | Tyr | Leu | Ser | Glu | Leu | 130 | 135 | 140 | |
| Gly | Lys | Asn | Gly | Lys | Lys | Gly | Phe | Tyr | Gly | Ser | Phe | Gln | Tyr | Val | Thr | 145 | 150 | 155 | 160 |
| Leu | Val | Gly | Gly | Gln | Leu | Leu | Ala | Ile | Phe | Ser | Leu | Phe | Ile | Val | Glu | 165 | 170 | 175 | |
| Asn | Val | Tyr | Thr | His | Glu | Gln | Ile | Ser | Ala | Phe | Ala | Trp | Arg | Tyr | Leu | 180 | 185 | 190 | |
| Phe | Ala | Leu | Glu | Gly | Ile | Leu | Ala | Leu | Leu | Ser | Leu | Phe | Leu | Arg | Asn | 195 | 200 | 205 | |
| Ile | Met | Glu | Glu | Thr | Met | Asp | Asn | Glu | Ala | Thr | Pro | Gln | Lys | Lys | Thr | 210 | 215 | 220 | |
| Asn | Val | Asn | Asn | Thr | Lys | Glu | Thr | His | Ile | Lys | Glu | Thr | Gln | Arg | Gly | 225 | 230 | 235 | 240 |

[illegible]

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 145 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

HPD 234

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

[illegible]

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 129 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 235

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Met Asn Ile Lys Ile Leu Lys Ile Leu Val Gly Gly Leu Phe Phe Leu
1 5 10 15

Ser Leu Asn Ala His Leu Trp Gly Lys Gln Asp Asn Ser Phe Leu Gly
20 25 30

Ile Gly Glu Arg Ala Tyr Lys Ser Gly Asn Tyr Ser Lys Ala Ala Ser
35 40 45

Tyr Phe Lys Lys Ala Cys Asn Asp Gly Val Ser Glu Gly Cys Thr Gln
50 55 60

Leu Gly Ile Ile Tyr Glu Asn Gly Gln Gly Thr Arg Ile Asp Tyr Lys
65 70 75 80

Lys Ala Leu Glu Tyr Tyr Lys Thr Ala Cys Gln Ala Asp Asp Arg Glu
85 90 95

Gly Cys Phe Gly Leu Gly Gly Leu Tyr Asp Glu Gly Leu Gly Thr Ala
100 105 110

Gln Asn Tyr Gln Glu Ala Leu Thr Leu Thr Gln Gly Met Arg Phe Lys
115 120 125

Thr Pro
130

(2) INFORMATION FOR SEQ ID NO:24298127_c3_12 -AA

Figure 23bA - page 289

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP236

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: phosphoglucomutase

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Asp | Ile | Ser | Ile | Phe | Arg | Glu | Tyr | Asp | Ile | Arg | Gly | Ile | Tyr | Pro | |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | | |
| Thr | Thr | Leu | Asp | Glu | Asn | Thr | Ala | Phe | Ser | Ile | Gly | Val | Glu | Leu | Gly | |
| | | | 20 | | | | | 25 | | | | | 30 | | | |
| Lys | Ile | Met | Arg | Glu | Tyr | Asp | Lys | Ser | Val | Phe | Val | Gly | His | Asp | Ala | |
| | | 35 | | | | | 40 | | | | | 45 | | | | |
| Arg | Val | His | Gly | Arg | Phe | Leu | Phe | Glu | Val | Leu | Ser | Ala | Gly | Leu | Gln | |
| | 50 | | | | | 55 | | | | | 60 | | | | | |
| Ser | Ser | Gly | Leu | Lys | Val | Tyr | Asp | Leu | Gly | Leu | Ile | Pro | Thr | Pro | Val | |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 | |
| Ala | Tyr | Phe | Ala | Ala | Phe | Asn | Glu | Ile | Asp | Asn | Ile | Gln | Trp | Pro | | |
| | | | | 85 | | | | | 90 | | | | | 95 | | |

(2) INFORMATION FOR SEQ ID NO:24328910_c3_16-AA

Figure 238A-page 291

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP238

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Phe | Lys | Lys | Met | Cys | Leu | Ser | Leu | Leu | Met | Ile | Ser | Gly | Val | Cys |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Val | Gly | Ala | Lys | Asp | Leu | Asp | Phe | Lys | Leu | Asp | Tyr | Arg | Ala | Thr | Gly |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Gly | Lys | Phe | Met | Gly | Lys | Met | Thr | Asp | Ser | Ser | Leu | Leu | Ser | Ile | Thr |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Ser | Met | Asn | Asp | Glu | Pro | Val | Val | Ile | Lys | Asn | Leu | Ile | Val | Asn | Arg |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Gly | Asn | Ser | Val | Glu | Ala | Thr | Lys | Lys | Val | Glu | Pro | Lys | Phe | Gly | Asp |
| 65 | | | | 70 | | | | | 75 | | | | | 80 | |
| Lys | Phe | Lys | Lys | Glu | Lys | Leu | Phe | Asp | His | Glu | Leu | Lys | Tyr | Ser | Gln |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| Gln | Ile | Phe | Tyr | Arg | Leu | Asp | Cys | Lys | Pro | Asn | Gln | Leu | Leu | Glu | Val |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Lys | Ile | Ile | Thr | Asp | Lys | Gly | Glu | Tyr | Tyr | His | Lys | Phe | Ser | Lys | |
| | | 115 | | | | | 120 | | | | | 125 | | | |

(2) INFORMATION FOR SEQ ID NO:24329712_c1_9-AA

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 501 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 239

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SULFATE TRANSPORT ATP-BINDING PROTEIN CYSA

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Thr | Leu | Lys | Pro | Tyr | Pro | Thr | Lys | Glu | Thr | Gly | Leu | Ala | Ser | Gln | 1 | 5 | 10 | 15 |
| Leu | Ser | Gly | His | Trp | Phe | Phe | Gln | Leu | Ser | Leu | Phe | Asn | Lys | Thr | Asn | 20 | 25 | 30 | |
| Phe | Asn | Pro | Asn | Lys | Ile | Trp | Ile | Pro | Leu | Glu | Phe | Asn | Lys | Arg | Ser | 35 | 40 | 45 | |
| Lys | Ile | Lys | Phe | Asp | Lys | Asp | Leu | Glu | Ile | Tyr | Phe | Asp | Ser | His | Glu | 50 | 55 | 60 | |
| Ser | Phe | Asn | Ile | Ser | Lys | Lys | Tyr | Leu | Gln | Glu | Ile | Asp | Gln | Glu | Ser | 65 | 70 | 75 | 80 |
| Leu | Lys | Lys | Ile | Lys | Gln | Ser | Lys | Asp | Phe | Phe | Ser | Ile | Gln | Lys | Ile | 85 | 90 | 95 | |
| Glu | Ser | Lys | His | Asp | Asn | Asn | Asp | Ile | Leu | Gln | Leu | Glu | Phe | Phe | Glu | 100 | 105 | 110 | |
| Asn | Asp | Thr | Ser | Phe | Leu | Phe | Ala | Lys | Gly | Ser | Phe | Ala | Glu | Ile | Leu | 115 | 120 | 125 | |
| Glu | Tyr | Asn | Met | Gln | Leu | Lys | Ile | Asp | Ser | Leu | Ile | Thr | Lys | Glu | Phe | 130 | 135 | 140 | |
| Asn | Lys | Leu | Leu | Ala | Ile | Val | Gln | Asp | Ser | Pro | Gln | Asp | Ser | Tyr | Gln | 145 | 150 | 155 | 160 |
| Leu | Lys | Ile | Arg | Val | Arg | His | Asn | Asn | Lys | Leu | Pro | Arg | Glu | Lys | Tyr | 165 | 170 | 175 | |
| Thr | Glu | His | Glu | Ile | Lys | Leu | Glu | Val | Tyr | Asp | Cys | Arg | Lys | Ser | His | 180 | 185 | 190 | |
| Asp | His | Asn | Glu | Pro | Ile | Ile | Leu | Ser | Gln | Gln | Ser | Thr | Gly | Phe | Gln | 195 | 200 | 205 | |
| Trp | Ala | Phe | Asn | Phe | Met | Phe | Gly | Phe | Leu | Tyr | Asn | Val | Gly | Ser | His | 210 | 215 | 220 | |
| Phe | Ser | Phe | Asn | His | Asn | Ile | Ile | Tyr | Val | Met | Asp | Glu | Pro | Ala | Thr | 225 | 230 | 235 | 240 |

[illegible]

(2) INFORMATION FOR SEQ ID NO:24395801_f2_3-AA

294

Figure 240A - page 294

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 41 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 240

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Val Tyr Phe Phe Leu Ala Leu Ser Gly Glu Lys Val Leu Leu Pro Val
1 5 10 15

Ile Gly Gly Leu Glu Lys Asn Ala Leu Glu Ala Gly Leu Leu Lys Gly
20 25 30

Asp Arg Ile Leu Leu Ser Thr Ile Lys Lys
35 40

(2) INFORMATION FOR SEQ ID NO:24396937_c2_11-AA

Figure 241A-page 295

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP241

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Asn | Phe | Lys | Leu | Ile | Asn | Phe | Phe | Thr | Gly | Gln | Asn | Asp | Ala | 1 | 5 | 10 | 15 |
| Gly | Lys | Thr | Asn | Leu | Leu | Glu | Ala | Leu | Tyr | Thr | Asn | Thr | Gly | Leu | Cys | 20 | 25 | 30 | |
| Asp | Pro | Thr | Ala | Asn | Gln | Val | Ser | Leu | Pro | Pro | Glu | His | Ala | Val | Asn | 35 | 40 | 45 | |
| Ile | Ser | Glu | Phe | Arg | Lys | Ile | Lys | Leu | Asp | Ala | Asp | Asn | Leu | Lys | Thr | 50 | 55 | 60 | |
| Phe | Phe | Tyr | Gln | Gly | Asn | Thr | Ala | Asn | Pro | Ile | Ser | Ile | Arg | Thr | Glu | 65 | 70 | 75 | 80 |
| Phe | Glu | His | Ala | Thr | Ile | Pro | Leu | Thr | Ile | Gln | Tyr | Pro | Thr | Gln | Thr | 85 | 90 | 95 | |
| Ser | Tyr | Ser | Lys | Asp | Ile | Asn | Leu | Asn | Ser | Asp | Asp | Ala | His | Met | Thr | 100 | 105 | 110 | |
| Asn | Leu | Ile | Asn | Thr | Thr | Ile | Thr | Lys | Pro | Gln | Leu | Gln | Phe | Ser | Tyr | 115 | 120 | 125 | |
| Asn | Pro | Ser | Leu | Ser | Pro | Met | Thr | Met | Thr | Tyr | Glu | Phe | Glu | Arg | Gln | 130 | 135 | 140 | |
| Asn | Leu | Gly | Leu | Ile | His | Ser | Asn | Leu | Asp | Lys | Ile | Ala | Gln | Thr | Tyr | 145 | 150 | 155 | 160 |
| Lys | Glu | Asn | Ala | Met | Phe | Ile | Pro | Ile | Glu | Leu | Ser | Ile | Val | Asn | Ser | 165 | 170 | 175 | |
| Leu | Lys | Ala | Leu | Glu | Asn | Leu | Gln | Leu | Ala | Ser | Lys | Glu | Lys | Glu | Leu | 180 | 185 | 190 | |
| Ile | Glu | Ile | Leu | Gln | Cys | Phe | Asn | Pro | Asn | Ile | Leu | Asn | Ala | Asn | Thr | 195 | 200 | 205 | |
| Ile | Arg | Lys | Ser | Val | Tyr | Ile | Gln | Ile | Lys | Asp | Glu | Asn | Thr | Pro | Leu | 210 | 215 | 220 | |
| Glu | Glu | Ser | Pro | Lys | Arg | Leu | Leu | Asn | Leu | Phe | Gly | Trp | Gly | Phe | Ile | 225 | 230 | 235 | 240 |

[illegible]

HPP 242

(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: YES

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Glu Ile Ile Pro Ser Ile Ser Ser Ala Glu Tyr Phe Lys Leu Tyr Asn
225 230 235 240

[illegible]

(Å) LENGTH: 114 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 243

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: Protein secretion secA subunit

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Unk | Ser | Val | Glu | Lys | Asp | Leu | Gln | Glu | Lys | Thr | Leu | Leu | Glu | Val |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |

Leu Pro Glu Ser Phe Ala Ile Thr Arg Glu Ala Ser Lys Arg Ile Leu
20 25 30

Lys Met Arg His Phe Asp Val Gln Leu Ile Gly Gly Met Val Leu Asn
35 40 45

Asp Gly Lys Ile Ala Glu Met Lys Thr Gly Glu Gly Lys Thr Leu Val
50 55 60

Ala Thr Leu Ala Val Ala Leu Asn Ala Met Lys Gly Glu Ser Val Tyr
65 70 75 80

Val Val Thr Val Asn Asp Tyr Leu Ala His Arg Asp Ser Lys Glu Met
85 90 95

Glu Pro Leu Tyr Gln Unk Leu Gly Tyr Unk Val Gly Thr Ile Thr Ala
100 105 110

Ser Val Arg
115

(2) INFORMATION FOR SEQ ID NO:24407533_c1_9-AA

Figure 244A- page 300

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP244

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Leu | Glu | Val | Val | Leu | Trp | Asp | Phe | Asp | Gly | Val | Ile | Phe | Asp | 1 | 5 | 10 | 15 |
| Ser | Met | His | Leu | Lys | Tyr | Glu | Gly | Phe | Lys | Ala | Leu | Phe | Gln | Lys | His | 20 | 25 | 30 | |
| Gly | Asn | Asp | Ser | Lys | Glu | Gly | Leu | Lys | Gln | Phe | Glu | Val | Tyr | His | Tyr | 35 | 40 | 45 | |
| Gln | Ser | Gly | Gly | Ile | Ser | Arg | Asn | Glu | Lys | Ile | Gln | Tyr | Phe | Tyr | Asn | 50 | 55 | 60 | |
| Glu | Ile | Leu | Lys | Thr | Pro | Ile | Ala | Gln | Glu | Glu | Ile | Asp | Ala | Leu | Ala | 65 | 70 | 75 | 80 |
| Leu | Glu | Phe | Gly | Ala | Ile | Ile | Glu | Gln | Lys | Leu | Phe | Asp | Arg | Gly | His | 85 | 90 | 95 | |
| Leu | Asn | Ser | Glu | Val | Met | Ala | Phe | Ile | Asp | Lys | His | Tyr | Gln | Asn | Tyr | 100 | 105 | 110 | |
| Ile | Phe | His | Ile | Ala | Ser | Ala | Ala | Leu | His | Ser | Glu | Leu | Gln | Val | Leu | 115 | 120 | 125 | |
| Cys | Glu | Phe | Leu | Gly | Ile | Thr | Lys | Tyr | Phe | Lys | Ser | Val | Glu | Gly | Ser | 130 | 135 | 140 | |
| Pro | Pro | Asp | Lys | Pro | Lys | Ile | Ile | Ala | Asn | Ile | Ile | Gln | Lys | Tyr | Ala | 145 | 150 | 155 | 160 |
| Tyr | Asp | Pro | Ser | Arg | Met | Leu | Met | Ile | Ala | Ile | Ala | Ser | Met | Ile | Met | 165 | 170 | 175 | |
| Lys | Ala | Leu | Arg | Leu | Ile | Lys | Trp | Arg | Phe | Trp | Ala | Ile | Thr | Ala | Arg | 180 | 185 | 190 | |
| Phe | | | | | | | | | | | | | | | | | | | |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 245

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Leu | Lys | Lys | Lys | Ile | Asp | Leu | His | Lys | Asp | Ser | Ile | Arg | Lys | Leu | |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | | |
| Phe | Phe | Tyr | Tyr | Phe | Ile | Pro | Leu | Val | Phe | Ser | Met | Ile | Ser | Leu | Ser | |
| | | | 20 | | | | | 25 | | | | | 30 | | | |
| Thr | Tyr | Ser | Met | Val | Asp | Asp | Met | Phe | Val | Gly | Lys | Lys | Leu | Gly | Lys | |
| | | 35 | | | | | 40 | | | | | 45 | | | | |
| Glu | Ala | Ile | Ala | Ala | Val | Asn | Ile | Ala | Trp | Pro | Ile | Phe | Pro | Gly | Leu | |
| | 50 | | | | | 55 | | | | | 60 | | | | | |
| Ile | Ala | Tyr | Glu | Leu | Leu | Phe | Gly | Phe | Gly | Ala | Ala | Ser | Ile | Val | Gly | |
| 65 | | | | | 70 | | | | 75 | | | | | | 80 | |
| Tyr | Phe | Leu | Gly | Gln | Asn | Lys | Thr | His | Arg | Ala | Arg | Leu | Val | Phe | Ser | |
| | | | | 85 | | | | | 90 | | | | | 95 | | |
| Ser | Val | Phe | Tyr | Phe | Val | Ala | Leu | Ser | Ala | Phe | Ile | Leu | Ser | Met | Ala | |
| | | | 100 | | | | | 105 | | | | | 110 | | | |
| Leu | Leu | Pro | Phe | Ser | Glu | Asn | Ile | Ala | Gln | Phe | Phe | Gly | Ser | Asn | Asp | |
| | | 115 | | | | | 120 | | | | | 125 | | | | |
| Ala | Leu | Leu | Asn | Met | Ser | Asn | Ala | Ile | Leu | Lys | Ser | Phe | | | | |
| | 130 | | | | | 135 | | | | | 140 | | | | | |

Figure 246A - page 302

(2) INFORMATION FOR SEQ ID NO:24409641_f3_3-AA

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 158 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 246

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | |
|------------|------------|-----------|------------|-----|------------|------------|------------|------------|-----------|------------|------------|------------|------------|-----------|-----------|
| Val 1 | Lys | Cys | Leu 5 | Leu | Ile | Lys | Lys | Ser 10 | Leu | Leu | Phe | Ala | Leu | Lys 15 | Pro |
| Leu | Pro | Asp 20 | Leu | Lys | Thr | Thr | Thr | Pro 25 | Ile | Leu | Ala | Pro | Met 30 | Ser | Val |
| Val | Ala 35 | Gly | Arg | Leu | Unk | Unk 40 | His | Leu | Val | Gln | His | Tyr 45 | Leu | Leu | Ala |
| Leu | Glu 50 | His | Val | Lys | Gly | Phe 55 | Met | Gly | Lys | Gly | Val 60 | Ile | Leu | Gly | Gly |
| Leu 65 | Ser | Gly | Ala | Gln | Arg 70 | Ala | Lys | Ile | Val | Val 75 | Ile | Gly | Gly | Gly | Val 80 |
| Val | Gly | Met | Glu 85 | Ser | Ala | Lys | Val | Leu | Unk 90 | Gln | Met | Gly | Unk | Lys 95 | Val |
| Thr | Ile | Leu | Glu 100 | Leu | Asp | Tyr | Ala | Lys 105 | Leu | Gln | Asn | His | Pro 110 | Tyr | Tyr |
| His | Leu 115 | Tyr | Asp | Leu | Glu | Val | Leu 120 | Ser | Val | Asn | Glu | Ala 125 | Asn | Ile | Ile |
| Gln | Ala 130 | Leu | Asn | Gly | Unk | Val 135 | Gly | Leu | Val | Gly | Ala 140 | Val | Leu | Val | Thr |
| Unk 145 | Ser | Gln | Thr | Pro | Lys 150 | Val | Unk | Leu | Arg | Arg 155 | His | Leu | Lys | Tyr | |

(2) INFORMATION FOR SEQ ID NO:24410643_f3_20-AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 247

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Ala | Lys | Ile | Val | Phe | Ser | Ser | Leu | Val | Ala | Phe | Gly | Val | Leu | 1 | 5 | 10 | 15 |
| Ser | Ala | Asn | Val | Glu | Gln | Phe | Gly | Ser | Phe | Phe | Asn | Glu | Ile | Lys | Lys | 20 | 25 | 30 | |
| Glu | Gln | Glu | Glu | Val | Ala | Ala | Lys | Glu | Asp | Ala | Leu | Lys | Ala | Arg | Lys | 35 | 40 | 45 | |
| Lys | Leu | Leu | Asn | Asn | Thr | His | Asp | Phe | Leu | Glu | Asp | Leu | Val | Phe | Arg | 50 | 55 | 60 | |
| Lys | Gln | Lys | Ile | Lys | Glu | Leu | Val | Asp | Tyr | Arg | Ala | Lys | Val | Leu | Leu | 65 | 70 | 75 | 80 |
| Asp | Leu | Glu | Asn | Lys | Tyr | Lys | Lys | Glu | Lys | Glu | Ala | Leu | Glu | Lys | Glu | 85 | 90 | 95 | |
| Thr | Arg | Gly | Lys | Ile | Leu | Thr | Ala | Lys | Ser | Lys | Ala | Tyr | Gly | Asp | Leu | 100 | 105 | 110 | |
| Glu | Gln | Ala | Leu | Lys | Asp | Asn | Pro | Leu | Tyr | Lys | Lys | Leu | Leu | Pro | Asn | 115 | 120 | 125 | |
| Pro | Tyr | Ala | Tyr | Val | Leu | Asn | Gln | Glu | Thr | Phe | Thr | Gln | Glu | Asp | Lys | 130 | 135 | 140 | |
| Glu | Arg | Leu | Ser | Tyr | Tyr | Tyr | Pro | Gln | Val | Lys | Thr | Ser | Ser | Ile | Phe | 145 | 150 | 155 | 160 |
| Lys | Lys | Thr | Thr | Ala | Thr | Thr | Lys | Asp | Lys | Ala | Gln | Ala | Leu | Leu | Gln | 165 | 170 | 175 | |
| Met | Gly | Val | Phe | Ser | Leu | Asp | Glu | Glu | Gln | Asn | Lys | Lys | Ala | Ser | Arg | 180 | 185 | 190 | |
| Leu | Ala | Leu | Ser | Tyr | Lys | Gln | Ala | Ile | Glu | Glu | Tyr | Ser | Asn | Asn | Ile | 195 | 200 | 205 | |
| Ser | Asn | Leu | Leu | Ser | Arg | Lys | Glu | Leu | Asp | Asn | Ile | Asp | Tyr | Tyr | Leu | 210 | 215 | 220 | |
| Gln | Leu | Glu | Arg | Asn | Lys | Phe | Asp | Ser | Lys | Ala | Lys | Asp | Ile | Ala | Gln | 225 | 230 | 235 | 240 |

| | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|
| Lys | Ala | Thr | Asn | Thr | Leu | Ile | Phe | Asn | Ser | Glu | Arg | Leu | Ala | Phe | Ser | | | |
| | | | | 245 | | | | | 250 | | | | | 255 | | | | |
| Met | Ala | Ile | Asp | Lys | Ile | Asn | Glu | Lys | Tyr | Leu | Arg | Gly | Tyr | Glu | Ala | | | |
| | | | 260 | | | | | 265 | | | | | 270 | | | | | |
| Phe | Ser | Asn | Leu | Leu | Lys | Asn | Val | Lys | Asp | Asp | Val | Glu | Leu | Asn | Thr | | | |
| | | 275 | | | | | 280 | | | | | 285 | | | | | | |
| Leu | Thr | Lys | Asn | Phe | Thr | Asn | Gln | Lys | Leu | Ser | Phe | Ala | Gln | Lys | Gln | | | |
| | 290 | | | | | 295 | | | | | 300 | | | | | | | |
| Lys | Leu | Cys | Leu | Leu | Val | Leu | Asp | Ser | Phe | Asn | Phe | Asp | Thr | Gln | Ser | | | |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 | | | |
| Lys | Lys | Ser | Ile | Leu | Lys | Lys | Thr | Asn | Glu | Tyr | Asn | Ile | Phe | Val | Asp | | | |
| | | | | 325 | | | | | 330 | | | | | 335 | | | | |
| Ser | Asp | Pro | Met | Met | Ser | Asp | Lys | Thr | Thr | Met | Gln | Lys | Glu | His | Tyr | | | |
| | | | 340 | | | | | 345 | | | | | 350 | | | | | |
| Lys | Ile | Phe | Asn | Phe | Phe | Lys | Thr | Val | Val | Ser | Ala | Tyr | Arg | Asn | Asn | | | |
| | | 355 | | | | | 360 | | | | | 365 | | | | | | |
| Val | Ala | Lys | Asn | Asn | Pro | Phe | Glu | | | | | | | | | | | |
| | 370 | | | | | 375 | | | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:24411011_c2_10 -AA

Figure 248A - page 305

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 248

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asp | Phe | Val | Gly | Phe | Glu | Asp | Leu | Lys | Cys | Lys | Asp | Lys | Glu | Asn | 1 | 5 | 10 | 15 |
| Ser | Gln | Lys | Val | Phe | Val | Ile | Arg | Asn | Asp | Lys | Leu | Gly | Asp | Phe | Ile | 20 | 25 | 30 | |
| Leu | Glu | Ile | Pro | Ala | Leu | Ile | Ala | Leu | Lys | His | Ala | Phe | Leu | Glu | Lys | 35 | 40 | 45 | |
| Gly | Val | Glu | Val | Tyr | Leu | Gly | Val | Val | Val | Pro | Ser | Tyr | Thr | Thr | Pro | 50 | 55 | 60 | |
| Ile | Ala | Leu | Glu | Phe | Pro | Phe | Ile | Asp | Glu | Val | Ile | Ile | Glu | Asp | Asn | 65 | 70 | 75 | 80 |
| His | Leu | Ala | Thr | Thr | His | Lys | Asn | Arg | Ser | Ile | Asp | Ala | Leu | Ile | Phe | 85 | 90 | 95 | |
| Leu | Phe | Ser | Asn | Phe | Lys | Asn | Ala | Lys | Leu | Ala | Phe | Ser | Leu | Arg | Lys | 100 | 105 | 110 | |
| Ser | Ile | Pro | Tyr | Ile | Leu | Ala | Pro | Lys | Thr | Lys | Ile | Tyr | Ser | Trp | Leu | 115 | 120 | 125 | |
| Tyr | Gln | Lys | Arg | Val | Arg | Gln | Asn | Arg | Ser | Leu | Cys | Leu | Lys | Thr | Glu | 130 | 135 | 140 | |
| Tyr | Glu | Tyr | Asn | Leu | Asp | Leu | Ile | His | Ala | Phe | Cys | Lys | Asp | Tyr | Asp | 145 | 150 | 155 | 160 |
| Leu | Pro | Asn | Ala | Gln | Leu | Lys | Lys | Ile | Ala | Trp | Lys | Leu | Lys | Asp | Lys | 165 | 170 | 175 | |
| Ser | Lys | Glu | Arg | Ser | Ile | Ile | Ala | Ser | Lys | Leu | Asn | Ala | Asn | Val | Asp | 180 | 185 | 190 | |
| Leu | Leu | Trp | Ile | Gly | Val | His | Met | His | Ser | Gly | Gly | Ser | Ser | Pro | Val | 195 | 200 | 205 | |
| Leu | Pro | Ala | Ser | His | Phe | Ile | Glu | Leu | Ile | Ala | Ile | Leu | His | Glu | Lys | 210 | 215 | 220 | |
| Leu | Ser | Cys | Glu | Ile | Ile | Leu | Ile | Cys | Gly | Pro | Gly | Glu | Arg | Lys | Ala | 225 | 230 | 235 | 240 |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Thr | Glu | Glu | Leu | Leu | Lys | Glu | Val | Pro | Phe | Ala | His | Leu | Tyr | Asp | Thr | |
| | | | | 245 | | | | | 250 | | | | | 255 | | |
| Ser | His | Ser | Leu | Val | Asp | Leu | Ala | Lys | Leu | Cys | Ala | Asn | Leu | Ser | Val | |
| | | | 260 | | | | | 265 | | | | | 270 | | | |
| Cys | Ile | Gly | Asn | Ala | Ser | Gly | Pro | Leu | His | Val | Asn | Ala | Leu | Phe | Asp | |
| | | 275 | | | | | 280 | | | | | 285 | | | | |
| Asn | Gln | Ser | Ile | Gly | Phe | Tyr | Pro | Asn | Glu | Leu | Thr | Ala | Ser | Ile | Ala | |
| | 290 | | | | | 295 | | | | | 300 | | | | | |
| Arg | Trp | Arg | Pro | Phe | Asn | Glu | Gln | Phe | Leu | Gly | Ile | Thr | Pro | Pro | Asn | |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 | |
| Gly | Ser | Asn | Asp | Met | Gly | Leu | Ile | Asp | Ile | Gln | Lys | Glu | Ser | Glu | Lys | |
| | | | | 325 | | | | | 330 | | | | | 335 | | |
| Ile | Met | Gly | Phe | Ile | Thr | Lys | Asn | Leu | Ser | His | His | Met | Gln | Glu | Arg | |
| | | | 340 | | | | | 345 | | | | | 350 | | | |

(2) INFORMATION FOR SEQ ID NO:24413512_c1_2: -AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 249

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | |
|-----------|-----------|-----------|----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| Val 1 | Gly | Val | Leu 5 | Ser | Leu | Lys | Ile | Glu | Ala 10 | Ile | Ser | Asn | Phe | Tyr 15 | Gly |
| Leu | Cys | Val 20 | Leu | Gly | Val | Leu | Leu | Ala 25 | Cys | Phe | Tyr | Leu | Leu 30 | Asp | Ala |
| Tyr | Tyr 35 | Leu | Met | Gln | Glu | Arg | Leu 40 | Phe | Arg | Glu | Gln | Tyr 45 | Gln | Trp | Leu |
| Ile | Lys 50 | Asn | Arg | Leu | Lys | Thr 55 | Asp | Glu | Arg | Leu | Phe 60 | Glu | Val | Phe | Pro |
| Ile 65 | His | Gln | Thr | Cys | Gln 70 | Ser | Thr | Gln | Phe | Leu 75 | Ser | Pro | Cys | Val | Arg 80 |
| Leu | Val | Phe | Ser | Pro 85 | Ile | Gly | Arg | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:24414687_f3_2-AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 250

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

[illegible]

(2) INFORMATION FOR SEQ ID NO:24415917_f1_2-AA

Figure 251A - page 309

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP251

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|----|----|----|
| Met | Lys | Lys | Thr | Thr | Leu | Phe | Val | Leu | Gly | Leu | Leu | Phe | Asn | Ser | Ser | 1 | 5 | 10 | 15 |
| Leu | Ser | Ala | Val | Asp | Gly | Ile | Ser | Gln | Thr | Glu | Pro | Ser | Ser | Leu | Asn | 20 | 25 | 30 | |
| Leu | Ala | Glu | Asp | Ser | Leu | Pro | Leu | Asn | His | Ser | Asn | Ala | Gln | Lys | Leu | 35 | 40 | 45 | |
| Ser | Leu | Lys | Asn | Ala | Trp | Asn | Arg | Val | Leu | Ser | Asn | His | Glu | Gly | Leu | 50 | 55 | 60 | |
| His | Ala | Gln | Asn | Thr | Pro | Leu | Ser | Glu | Arg | Val | Lys | 65 | 70 | 75 | | | | | |

(2) INFORMATION FOR SEQ ID NO:24416083_f3_16. AA

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 97 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 252

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Val Lys Lys Val Glu Ser Met Asn Val Val Pro Phe Ile Asp Ile Met
1 5 10 15

Leu Val Leu Leu Val Ile Val Leu Thr Thr Ala Ser Phe Val Gln Thr
20 25 30

Ser Lys Leu Pro Ile Ser Ile Pro Gln Val Asp Lys Asp Ser Thr Asp
35 40 45

Ser Lys Asp Val Leu Asp Lys Lys Gln Val Thr Ile Ala Ile Ser Asn
50 55 60

Lys Gly Ser Phe Tyr Phe Asp Asp Lys Glu Ile Ser Phe Glu Asn Leu
65 70 75 80

Lys His Lys Val Ser Thr Leu Ala Lys Asp Thr Pro Ile Val Phe Ala
85 90 95

Arg Arg

(2) INFORMATION FOR SEQ ID NO:24417212_f3_12-AA

Figure 253A-page 311

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 253

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

```

Met Gly Ser Tyr Thr Phe Pro Leu Ile Leu Lys Pro Ile Phe Ile Asn
1          5          10          15
Lys Val Pro Val Thr Ile Asp Phe Tyr Ala Asn Ala Asn Tyr Phe Leu
          20          25          30
Ile Tyr Gly Ala Leu Ala Asn Ala Val Val Gly Ser Ile Asn Ala Leu
          35          40          45
Asn Asp Glu Ile Arg Phe Lys Arg Asn Ala Gln Ile Glu Glu Ala Glu
          50          55          60
Leu Gly Thr Asp Gly Ile Lys Ile Lys Pro Ile Ala Leu Tyr Asn Pro
          65          70          75          80
Ser Glu Gly Tyr Leu Asn Tyr Ala Leu Ser Ser Val Phe Ile Phe Ile
          85          90          95
Leu His Gln Val Met Leu Ile Ala Ser Ser Met Phe Thr Ser Ser Arg
          100          105          110
Arg Leu Glu Leu Ala Leu Leu Asp Lys Lys Gln Ile Ala Leu Arg Leu
          115          120          125
Cys Ala Arg Leu Leu Val Phe Met Gly Ala Phe Ser Val Phe Val Leu
          130          135          140
Trp Tyr Phe Gly Ala Leu Phe Ser Phe Tyr Gly Ile Glu Arg His Gly
          145          150          155          160
Ser Ala

```

(2) INFORMATION FOR SEQ ID NO:24427340_f1_1-AA

Figure 254A - page 312

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 254

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: CELL DIVISION PROTEIN -- FUNCTIONAL HOMOLOG OF SR

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ile | Met | Thr | Lys | Leu | Asp | Gly | Thr | Ser | Lys | Gly | Gly | Ala | Ile | Leu |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Unk | Val | Leu | Tyr | Glu | Leu | Lys | Leu | Pro | Ile | Leu | Tyr | Leu | Gly | Met | Gly |
| | | | 20 | | | | | 25 | | | | | 30 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Lys | Glu | Asp | Asp | Leu | Ile | Ala | Phe | Asp | Glu | Glu | Arg | Phe | Ile | Glu |
| | | 35 | | | | | 40 | | | | | 45 | | | |

| | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Leu | Val | Asp | Ala | Val | Phe | Val | Glu | Gln |
| 50 | | | | | | 55 | | | |

Cys Ala
65

(2) INFORMATION FOR SEQ ID NO:2445812_c1_2-AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 256

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Ile | Ala | Ile | Lys | Asp | Leu | Leu | Ser | Ala | Tyr | Lys | Val | Val | Leu |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Pro | Leu | Asp | Lys | Ile | Ser | Met | Pro | Ser | Ser | Ala | Asp | Leu | Lys | Leu | Thr |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Leu | Gln | Phe | Leu | Lys | Asn | Thr | Ala | Pro | Leu | Phe | Ser | Val | Gln | Gly | Ser |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Val | Asn | Leu | Gln | Glu | Gly | Thr | Phe | Ser | Leu | Tyr | Asn | Ile | Pro | Leu | Tyr |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Thr | Gln | Ser | Ala | Gln | Ile | Asn | Leu | Asp | Ile | Ala | Gln | Glu | Tyr | Gln | Tyr |
| 65 | | | | 70 | | | | | | 75 | | | | 80 | |
| Ile | Tyr | Ile | Asp | Thr | Ile | His | Thr | Arg | Tyr | Ala | Asn | Met | Arg | Ile | |
| | | | | 85 | | | | | 90 | | | | | 95 | |

(A) LENGTH: 68 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Pro | Asp | Unk | Leu | His | Leu | His | Thr | Leu | Leu | Unk | Lys | Phe | Leu | Gln |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |

Gln Arg Ser Phe Asn Tyr Pro Asn Pro Leu Cys Ala Phe Ile Leu Ile
20 25 30

Leu Cys Asn Leu Pro Phe Ile Leu Ile Ser Val Leu Phe Arg Leu Asp
35 40 45

Ala Tyr Ala Leu Ile Val Ile Ser Leu Val Phe Ile Unk Cys Tyr Leu
50 55 60

Ile Gly Leu Leu Ile
65

(2) INFORMATION FOR SEQ ID NO:24492192_c2_9-AA

Figure 258A-page 316

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 258

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: ONE OF THE DIFFERENT ANTIGENIC SEROTYPES OF PROTE

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Asn | Glu | Leu | Lys | Asn | Ser | Lys | Gln | Val | Leu | Gly | Asn | Gly | Lys | Ala |
| 1 | | | | 5 | | | | 10 | | | | | | 15 | |
| Asp | Leu | Ser | Asn | Glu | Asn | Thr | Lys | Val | Arg | Gln | Thr | Lys | Thr | Asn | Leu |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Thr | Glu | Lys | Asn | Gln | Arg | Leu | Thr | Thr | Glu | Lys | Thr | Glu | Leu | Asn | Asn |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Lys | Ile | Thr | Gly | Leu | Ala | Thr | Glu | Lys | Glu | Arg | Leu | Ala | Ala | Asp | Lys |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Glu | Asn | Leu | Thr | Lys | Glu | Ser | Arg | Gln | Arg | Lys | Pro | Asn | | | |
| 65 | | | | | 70 | | | | | 75 | | | | | |

(2) INFORMATION FOR SEQ ID NO:24495312_c1_47 -AA

Figure 259A - page 317

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 259

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asp | Leu | Gln | Gln | Ile | Asp | Glu | Leu | Glu | Asn | Lys | Phe | Glu | Glu | Gln | 1 | 5 | 10 | 15 |
| Glu | Glu | Gln | Ala | Gln | Asp | Thr | Pro | Leu | Lys | Gln | Glu | Pro | Ser | Thr | Lys | 20 | 25 | 30 | |
| Glu | Val | Lys | Ile | Pro | Lys | Lys | Arg | Gly | Arg | Lys | Lys | Ser | Leu | Leu | Asp | 35 | 40 | 45 | |
| Glu | Asp | Lys | Lys | Lys | Ser | Phe | Asn | Ile | Ala | Phe | Ser | Pro | Cys | Val | Ile | 50 | 55 | 60 | |
| Lys | Glu | Leu | Asn | Glu | Phe | Leu | Leu | Glu | Phe | Gly | Ser | Phe | Lys | Glu | Thr | 65 | 70 | 75 | 80 |
| Arg | Ser | Thr | Phe | Ile | Glu | Glu | Ala | Leu | Ile | Arg | His | Leu | Lys | His | Arg | 85 | 90 | 95 | |
| Lys | Asn | Thr | Gln | Glu | Gln | Lys | Leu | Leu | Lys | Gln | Leu | Glu | Arg | Leu | Gln | 100 | 105 | 110 | |
| Asn | Lys | Glu | Lys | Gly | Ile | Met | Lys | Thr | Met | Asn | Leu | Asn | Glu | Phe | Phe | 115 | 120 | 125 | |
| Thr | His | Lys | Ile | Ile | Tyr | Lys | Asp | Thr | Pro | Leu | Lys | Phe | Lys | Asp | Thr | 130 | 135 | 140 | |
| Leu | Glu | Gln | Glu | Ile | Ser | Gln | Ala | Ser | Leu | Val | Glu | Lys | Leu | Ile | Leu | 145 | 150 | 155 | 160 |
| Ala | Asn | Ile | Leu | Ala | Asn | Met | Val | Phe | Ala | Lys | Ile | Ser | Asn | Glu | Asn | 165 | 170 | 175 | |

(2) INFORMATION FOR SEQ ID NO:24500088_c3_7-AA

Figure 260A -page 318

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 260

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| Met | Gly | Cys | Tyr | Gly | Ile | Gly | Ile | Ser | Arg | Leu | Leu | Ser | Val | Ile | Leu | 1 | 5 | 10 | 15 |
| Glu | Gln | Lys | Ser | Asp | Asp | Leu | Asp | Cys | Val | Trp | Thr | Lys | Asn | Thr | Ala | 20 | 25 | 30 | |
| Pro | Phe | Asp | Val | Val | Ile | Val | Val | Ser | Asn | Leu | Lys | Asp | Glu | Ala | Gln | 35 | 40 | 45 | |
| Lys | Lys | Leu | Ala | Phe | Glu | Val | Tyr | Glu | Arg | Leu | Leu | Gln | Lys | Gly | Val | 50 | 55 | 60 | |
| Asp | Ala | Leu | Leu | Asp | Asp | Arg | Asp | Ala | Arg | Phe | Gly | Ala | Lys | Met | Arg | 65 | 70 | 75 | 80 |
| Asp | Phe | Glu | Leu | Ile | Gly | Glu | Arg | Leu | Ala | Leu | Ile | Val | Gly | Lys | Gln | 85 | 90 | 95 | |
| Thr | Leu | Glu | Ser | Lys | Glu | Phe | Glu | Cys | Ile | Lys | Arg | Ala | Asn | Leu | Glu | 100 | 105 | 110 | |
| Lys | Gln | Thr | Ile | Lys | Asp | Ile | Gly | Ile | Arg | Arg | Lys | Asn | Phe | Arg | Asn | 115 | 120 | 125 | |
| Val | Ser | Glu | Arg | Ile | Arg | Gly | Gly | Asn | Gly | Lys | Asn | Ser | Asp | Trp | Leu | 130 | 135 | 140 | |

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 89 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 261

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: vacuolating cytotoxin of Hpylori

Met Glu Ile Gln Gln Thr His Arg Lys Ile Asn Arg Pro Leu Val Ser
1 5 10 15

Leu Val Leu Ala Gly Ala Leu Ile Ser Ala Ile Pro Gln Glu Ser His
20 25 30

Ala Ala Phe Phe Thr Thr Val Ile Ile Pro Ala Ile Val Gly Gly Ile
35 40 45

Ala Thr Gly Thr Ala Val Gly Thr Val Ser Gly Leu Leu Ser Trp Gly
50 55 60

Leu Lys Gln Ala Glu Glu Ala Asn Lys Thr Pro Asp Lys Pro Asp Lys
65 70 75 80

Val Trp Arg Ile Gln Ala Gly Lys Gly Leu
85 90

(2) INFORMATION FOR SEQ ID NO:24609431_c2_15 - AA

Figure 262 A - page 320

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 262

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Glu | Lys | Glu | Arg | Leu | Asn | Glu | Val | Ile | Leu | Glu | Glu | Glu | Asn |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Asn | Gly | Ser | Gly | Thr | Lys | Lys | Val | Phe | Leu | Ile | Val | Ala | Ile | Ala | Ile |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Ile | Ile | Leu | Ala | Val | Leu | Leu | Met | Val | Phe | Trp | Lys | Ser | Thr | Arg | Val |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Ala | Pro | Lys | Glu | Thr | Phe | Leu | Gln | Thr | Asp | Ser | Gly | Met | Gln | Lys | Ile |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Gly | Asn | Thr | Lys | Asp | Glu | Lys | Lys | Asp | Asp | Glu | Phe | Glu | Ser | Leu | Asn |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 |
| Met | Asp | Ser | Pro | Lys | Gln | Glu | Asp | Lys | Leu | Asp | Lys | Val | Val | Asp | Asn |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| Ile | Lys | Lys | Gln | Glu | Ser | Glu | Asn | Ser | Met | Pro | Ile | Gln | Thr | Asp | Gln |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Ala | Gln | Met | Glu | Met | Lys | Thr | Thr | Glu | Glu | Lys | Gln | Glu | Ser | Gln | Lys |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| Glu | Leu | Lys | Ala | Val | Glu | Pro | Ile | Pro | Met | Ser | Thr | Gln | Lys | Glu | Ser |
| | 130 | | | | | 135 | | | | | 140 | | | | |
| Gln | Ala | Val | Ala | Lys | Lys | Glu | Thr | Pro | His | Lys | Lys | Pro | Lys | Val | Ala |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 |
| Pro | Lys | Asp | Lys | Glu | Ala | His | Lys | Asp | Lys | Ala | Lys | His | Ala | Ala | Lys |
| | | | | 165 | | | | | 170 | | | | | 175 | |
| Glu | Pro | Lys | Val | Lys | Lys | Glu | Ala | Arg | Lys | Glu | Val | Ser | Lys | Lys | Ala |
| | | | 180 | | | | | 185 | | | | | 190 | | |
| Asn | Ser | Lys | Thr | Asn | Leu | Thr | Lys | Gly | His | Tyr | Leu | Gln | Val | Gly | Val |
| | | 195 | | | | | 200 | | | | | 205 | | | |
| Phe | Ala | His | Thr | Pro | Asn | Lys | Ala | Phe | Leu | Gln | Glu | Phe | Asn | Gln | Phe |
| | 210 | | | | | 215 | | | | | 220 | | | | |
| Pro | His | Lys | Ile | Glu | Asp | Arg | Gly | Ala | Thr | Lys | Arg | Tyr | Leu | Ile | Gly |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 |

Pro Tyr Lys Ser Lys Gln Glu Ala Leu Met His Ala Asp Glu Val Ser
245 250 255

Lys Lys Met Thr Lys Pro Val Val Ile Glu Val Arg
260 265

(2) INFORMATION FOR SEQ ID NO:24609593_f2_2-AA

Figure 263A - page 322

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 170 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 263

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: ferric enterobactin transport protein fepC

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Glu | Tyr | Tyr | Ala | Phe | Asn | Phe | Ser | Val | Leu | Asp | Phe | Val | Leu | Met | 1 | 5 | 10 | 15 |
| Gly | Lys | Ala | Thr | His | Leu | Asn | Leu | Phe | Ala | Met | Pro | Lys | Ala | Lys | His | 20 | 25 | 30 | |
| Ile | Lys | Glu | Ala | Thr | Ser | Val | Leu | Glu | Arg | Leu | Asp | Leu | Glu | Ser | Leu | 35 | 40 | 45 | |
| Lys | Asp | Gln | Gly | Ile | Asn | Asp | Leu | Ser | Gly | Gly | Gln | Arg | Gln | Met | Val | 50 | 55 | 60 | |
| Leu | Leu | Ala | Arg | Ser | Leu | Gln | Arg | Thr | Pro | Leu | Leu | Leu | Leu | Asp | 65 | 70 | 75 | 80 | |
| Glu | Pro | Thr | Ser | Ala | Leu | Asp | Leu | Lys | Asn | Gln | Ala | Leu | Phe | Phe | Asp | 85 | 90 | 95 | |
| Ala | Ile | Lys | Asp | Glu | Met | Lys | Lys | Arg | Glu | Leu | Ser | Val | Leu | Val | Asn | 100 | 105 | 110 | |
| Ile | His | Asp | Pro | Asn | Leu | Val | Ala | Arg | His | Ser | Thr | His | Val | Val | Met | 115 | 120 | 125 | |
| Leu | Lys | Asp | Lys | Lys | Leu | Phe | Leu | Gln | Ala | Ser | Thr | Pro | Ile | Ala | Met | 130 | 135 | 140 | |
| Thr | Ser | His | Asn | Leu | Ser | Ala | Leu | Tyr | Asp | Thr | Pro | Leu | Unk | Ala | Ile | 145 | 150 | 155 | 160 |
| Trp | His | Asp | Asp | Lys | Leu | Val | Val | Tyr | Ala | Leu | 165 | 170 | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:2461062_c1_30-AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 264

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

[illegible]

(2) INFORMATION FOR SEQ ID NO:24611590_f3_4-AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 265

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| Val | Val | Ile | Gln | Asp | Leu | Asn | Ala | Arg | Ile | Ala | Leu | Met | Lys | Leu | Leu | 1 | 5 | 10 | 15 |
| Phe | Gln | Asn | Val | Lys | Ser | Ala | Asn | Lys | Glu | Leu | Val | Phe | Cys | Asn | Lys | 20 | 25 | 30 | |
| Glu | Lys | Arg | Leu | Ile | Arg | Ser | Phe | Asp | Ala | Gln | Lys | Glu | Tyr | Gly | Ile | 35 | 40 | 45 | |
| Thr | Pro | Val | Glu | Asn | Ile | Leu | Ser | Val | Leu | Asp | Thr | Ala | Met | Asn | Pro | 50 | 55 | 60 | |
| Asn | Ser | Ala | Leu | Val | Ile | Asp | Asn | Leu | Asn | Glu | Ala | Lys | Glu | Leu | His | 65 | 70 | 75 | 80 |
| Asp | Lys | Val | Gly | Ala | Glu | Lys | Leu | Lys | Ser | Phe | Leu | Glu | Lys | Ala | Leu | 85 | 90 | 95 | |
| Asp | Asn | Glu | Gln | Tyr | Cys | Val | Ile | Phe | Ala | His | Asp | Phe | Arg | Gln | Ile | 100 | 105 | 110 | |
| Lys | Thr | Asn | Tyr | His | Phe | Asp | Lys | Leu | Lys | Glu | Leu | Leu | Asn | Asn | His | 115 | 120 | 125 | |
| Phe | Lys | Gln | Cys | Leu | Ala | Phe | Arg | Cys | Asn | Gly | Glu | Asn | Leu | Asn | Ala | 130 | 135 | 140 | |
| Ile | Lys | Ser | Asp | Leu | Pro | Ser | Thr | Unk | Gln | Thr | 145 | 150 | 155 | | | | | | |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 236 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 266

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Leu | Asn | Glu | Glu | Gln | Asn | Ser | Leu | Glu | Glu | Lys | Gly | Gly | Glu | Asn | 1 | 5 | 10 | 15 |
| Lys | Asn | Glu | Lys | Glu | Thr | Pro | Leu | Lys | Gly | Ile | His | Ser | Lys | Ile | Pro | 20 | 25 | 30 | |
| Ser | Leu | Lys | Gln | Ala | Leu | Glu | Gln | Thr | Ile | Ser | Lys | Ile | Lys | Ser | Ser | 35 | 40 | 45 | |
| Lys | Glu | Phe | Phe | Lys | Gln | Leu | Leu | His | Asn | Lys | Lys | Lys | Leu | Tyr | Ile | 50 | 55 | 60 | |
| Ala | Leu | Gly | Ile | Leu | Leu | Ser | Leu | Ile | Ala | Leu | Ile | Val | Ala | Leu | Ser | 65 | 70 | 75 | 80 |
| Leu | Leu | Leu | Gly | His | Lys | Lys | Glu | Asn | Lys | Gln | Thr | Ser | Leu | Gln | Thr | 85 | 90 | 95 | |
| Asn | Thr | Ala | Thr | Thr | Asn | Asn | Glu | Thr | Pro | Asn | Asp | Thr | Asn | Asn | Ala | 100 | 105 | 110 | |
| Glu | Ala | Glu | Gly | Gln | Ile | Glu | Asn | Leu | Asp | Leu | Pro | Asp | Leu | Ile | Gly | 115 | 120 | 125 | |
| Lys | Asp | Ser | Leu | Lys | Arg | Asn | Asp | Glu | Ser | Gln | Val | Asp | Ala | Met | Met | 130 | 135 | 140 | |
| Gln | Lys | Ala | Ser | Leu | Leu | Tyr | Glu | Gln | Gly | Gln | Lys | Asp | Glu | Ala | Leu | 145 | 150 | 155 | 160 |
| His | Leu | Phe | Asp | Lys | Ile | Ala | Ser | Phe | Ser | Gln | Gly | Ile | Ala | Ser | His | 165 | 170 | 175 | |
| Asn | Leu | Gly | Val | Ile | Lys | Phe | Lys | Glu | Lys | Asp | Phe | Asn | Gly | Ala | Leu | 180 | 185 | 190 | |
| Asp | Leu | Phe | Asp | Ser | Ser | Ile | Ala | Ser | Lys | Glu | Asn | Ala | Ser | Val | Ser | 195 | 200 | 205 | |
| Ala | Ile | Asp | Ala | Leu | Val | Thr | Ala | Tyr | His | Leu | Gln | Asp | Ala | Asp | Leu | 210 | 215 | 220 | |
| Tyr | Tyr | His | Tyr | Leu | Lys | Ile | Val | Lys | Arg | His | Phe | Val | 225 | 230 | 235 | | | | |

(2) INFORMATION FOR SEQ ID NO:24645837_f2_11-AA

Figure 267A - page 326

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 267

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|
| Met | Lys | Glu | Ser | Phe | Tyr | Ile | Glu | Gly | Met | Thr | Cys | Thr | Ala | Cys | Ser | | | |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | | | | |
| Ser | Gly | Ile | Glu | Arg | Ser | Leu | Gly | Arg | Lys | Ser | Phe | Val | Lys | Lys | Ile | | | |
| | | | 20 | | | | | 25 | | | | | 30 | | | | | |
| Glu | Val | Ser | Leu | Leu | Asn | Lys | Ser | Ala | Asn | Ile | Glu | Phe | Asn | Glu | Asn | | | |
| | | | 35 | | | | 40 | | | | | 45 | | | | | | |
| Glu | Thr | Asn | Leu | Asp | Glu | Ile | Phe | Lys | Leu | Ile | Glu | Lys | Leu | Gly | Tyr | | | |
| | | | 50 | | | 55 | | | | | 60 | | | | | | | |
| Ser | Pro | Lys | Lys | Thr | Leu | Ala | Glu | Glu | Lys | Lys | Glu | Phe | Phe | Ser | Pro | | | |
| 65 | | | | 70 | | | | | 75 | | | | | 80 | | | | |
| Asn | Val | Lys | Leu | Ala | Leu | Ala | Val | Ile | Phe | Thr | Leu | Phe | Val | Val | Tyr | | | |
| | | | | 85 | | | | 90 | | | | | | 95 | | | | |
| Leu | Ser | Met | Gly | Ala | Met | Leu | Ser | Pro | Ser | Leu | Leu | Pro | Glu | Ser | Leu | | | |
| | | | 100 | | | | | 105 | | | | | 110 | | | | | |
| Leu | Thr | Ile | Asn | His | His | Ser | Asn | Phe | Leu | Asn | Ala | Cys | Leu | Gln | Leu | | | |
| | | | 115 | | | | 120 | | | | | 125 | | | | | | |
| Ile | Gly | Ala | Leu | Ile | Val | Met | His | Leu | Gly | Arg | Asp | Phe | Tyr | Ile | Gln | | | |
| | | | 130 | | | 135 | | | | | 140 | | | | | | | |
| Gly | Phe | Lys | Ala | Leu | Trp | His | Arg | Gln | Pro | Asn | Met | Ser | Ser | Leu | Ile | | | |
| 145 | | | | | 150 | | | | | 155 | | | | 160 | | | | |
| Ala | Ile | Gly | Thr | Ser | Ala | Ala | Leu | Ile | Ser | Ala | Cys | Gly | Asn | Cys | Ile | | | |
| | | | | 165 | | | | | 170 | | | | | 175 | | | | |
| Trp | Phe | Ile | Pro | Ile | Ile | Ile | Pro | Ile | Ser | Gly | Leu | Met | Gly | Ile | Ile | | | |
| | | | 180 | | | | | 185 | | | | | 190 | | | | | |
| Ile | Leu | Lys | Ala | Cys | Ala | | | | | | | | | | | | | |
| | | | | 195 | | | | | | | | | | | | | | |

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 224 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 268

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(x1) SEQUENCE DESCRIPTION: HEAT SHOCK PROTEIN HTPX PRECURSOR

Met Asn Thr Ser Leu Leu Thr Gln Ala Gln Val Leu Ser Ser Lys Glu
1 5 10 15

Asn Gln Ile His Arg Leu Leu Leu Glu Leu Leu Glu Glu Ala Lys Leu
20 25 30

His Phe Glu Pro Lys Leu Tyr Ile Ile Asn Ala Pro Tyr Met Asn Ala
35 40 45

Phe Ala Ser Gly Trp Asp Glu Ser Asn Ser Leu Ile Ala Leu Thr Ser
50 55 60

Ala Leu Ile Glu Arg Leu Asp Arg Asp Glu Leu Lys Ala Val Ile Ala
65 70 75 80

His Glu Leu Ser His Ile Arg His Asn Asp Ile Arg Leu Thr Met Cys
85 90 95

Val Gly Ile·Leu Ser Asn Ile Met Leu Leu Val Ala Asn Phe Ser Val
100 105 110

Tyr Phe Phe Met Gly Asn Arg Lys Asn Ser Gly Ala Asn Leu Ala Arg
115 120 125

Met Ile Leu Trp Val Leu Gln Ile Ile Leu Pro Phe Leu Thr Leu Leu
130 135 140

Leu Gln Met Tyr Leu Ser Arg Thr Arg Glu Tyr Met Ala Asp Ser Gly
145 150 155 160

Ala Ala Phe Leu Met His Asp Asn Lys Pro Met Ile Arg Ala Leu Gln
165 170 175

Lys Ile Ser Asn Asp Tyr Thr Asn Asn Asp Tyr Lys Glu Ile Asp Lys
180 185 190

Asn Ser Thr Arg Ser Ala Ala Tyr Leu Phe Asn Ala Glu Met Phe Ser
195 200 205

Thr His Pro Ser Ile Lys Asn Arg Ile Gln Ser Leu Arg Lys Arg Val
210 215 220

Ile
225

(2) INFORMATION FOR SEQ ID NO:24708129_f2_4 -AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 269

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: penicillin-binding protein 2

| | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|
| Val | Gly | Ile | Val | Pro | Asp | Asn | Leu | Trp | Lys | Leu | Lys | Arg | Phe | Asn | Gln | | | |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | | | | |
| Asp | Trp | Arg | Val | Gly | Asp | Thr | Leu | Ile | Thr | Ala | Ile | Gly | Gln | Gly | Ser | | | |
| | | | 20 | | | | | 25 | | | | | 30 | | | | | |
| Phe | Leu | Ala | Thr | Pro | Leu | Gln | Val | Leu | Ala | Tyr | Thr | Gly | Leu | Ile | Ala | | | |
| | | 35 | | | | | 40 | | | | | 45 | | | | | | |
| Thr | Gly | Lys | Leu | Ala | Thr | Pro | His | Phe | Ala | Ile | His | Asn | Gln | Gln | Pro | | | |
| | 50 | | | | | 55 | | | | | 60 | | | | | | | |
| Leu | Lys | Asp | Pro | Leu | Asn | Arg | Phe | Ser | Lys | Lys | Glu | Ala | Pro | Ser | Leu | | | |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 | | | |
| Ala | Arg | Gly | His | Val | | | | | | | | | | | | | | |
| | | | | 85 | | | | | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:24798427_c2_35-AA

Figure 270A - page 329

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 495 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 270

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Phe | Asn | Ile | Lys | Arg | Thr | Phe | Leu | Ile | Thr | Ile | Ile | Ser | Phe | Phe | 1 | 5 | 10 | 15 |
| Leu | Ile | Val | Pro | Asn | Trp | Leu | Lys | Ala | Ile | Asp | Leu | Pro | Ile | Val | Ser | 20 | 25 | 30 | |
| Asn | Leu | Lys | Ile | Tyr | Gln | Thr | Val | Tyr | Cys | Met | Leu | Ile | Pro | Ser | Tyr | 35 | 40 | 45 | |
| Val | Leu | Thr | Asn | Lys | Ser | Phe | Ala | Asp | Ile | Leu | Thr | Gly | Tyr | Thr | Ser | 50 | 55 | 60 | |
| Ile | Gly | Ala | Ser | Gly | Ser | Gly | Lys | Ser | Ser | Gly | Gln | Gly | Val | Ile | Glu | 65 | 70 | 75 | 80 |
| Ala | Leu | Ser | Thr | Pro | Leu | Ala | Thr | Ser | Leu | Ala | Ala | Ser | Asn | Leu | Val | 85 | 90 | 95 | |
| Lys | Tyr | Leu | Asn | Thr | Leu | Gly | Pro | Leu | Trp | Gly | Ser | Ala | Trp | Ala | Ser | 100 | 105 | 110 | |
| Val | Ala | Thr | Ala | Ile | Gln | Gly | Phe | Ala | Leu | Thr | Pro | Ser | Ser | Gly | Cys | 115 | 120 | 125 | |
| Asn | Phe | Gly | Trp | Asn | Ala | Leu | Ile | Asn | Lys | Asn | Ile | Asp | Val | Ser | Met | 130 | 135 | 140 | |
| Asp | Ser | Val | Leu | Asp | Asn | Leu | Ser | Asn | Lys | Ile | Gln | Asn | Phe | Thr | Lys | 145 | 150 | 155 | 160 |
| Gly | Gly | Val | Glu | Asp | Asn | Val | Lys | Gly | Asn | Ile | Leu | Leu | Gln | Ile | Ile | 165 | 170 | 175 | |
| Gly | Ser | Ile | Thr | Ala | Gln | Ala | Ser | Thr | Asn | Ile | Thr | Ala | Asp | Gly | Leu | 180 | 185 | 190 | |
| Ile | Trp | Leu | Ile | Gly | Lys | Glu | Phe | Thr | Ala | Asn | Lys | Leu | Gln | Asn | Asn | 195 | 200 | 205 | |
| Thr | Ile | Ala | Met | Leu | Ala | Phe | Ala | Ala | Leu | Glu | Ser | Val | Val | Lys | Gly | 210 | 215 | 220 | |
| Ala | Asp | Ala | Ala | Val | Leu | Pro | Ala | Tyr | Gly | Val | Val | Asn | Leu | Pro | Asp | 225 | 230 | 235 | 240 |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Ile | Ile | Gly | Gln | Gly | Ser | Tyr | Leu | Asp | Phe | Val | Ser | Tyr | Leu | Ile |
| | | | 245 | | | | | | 250 | | | | | 255 | |
| Tyr | Ile | Val | Phe | Gly | Ile | Phe | Val | Phe | Ile | Ser | Phe | Met | Lys | Leu | Arg |
| | | | 260 | | | | | 265 | | | | | 270 | | |
| Asp | Ile | Ser | Asn | Gly | Ile | Gln | Ile | Asn | Ile | Gly | Phe | Glu | Tyr | Met | Arg |
| | | 275 | | | | | 280 | | | | | 285 | | | |
| Phe | Val | Gly | Gly | Thr | Leu | Phe | Lys | Met | Ala | Met | Val | Ser | Phe | Ile | Ala |
| | 290 | | | | | 295 | | | | | 300 | | | | |
| Tyr | Ala | Gly | Phe | Gly | Tyr | Leu | Tyr | Lys | Ile | Ser | Tyr | Ser | Ile | Tyr | Phe |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 |
| Gly | Leu | Ala | Gly | Ala | Phe | Gly | Leu | Asn | Gln | Val | Leu | Phe | Trp | Ala | Leu |
| | | | | 325 | | | | | 330 | | | | | 335 | |
| Asp | Leu | Val | Leu | Asn | Tyr | Thr | Val | Asn | Ser | Ile | Leu | Pro | Ala | Val | Arg |
| | | | 340 | | | | | 345 | | | | | 350 | | |
| Ala | Val | Phe | Ser | Asn | Val | Gly | Asn | Asn | Ala | Pro | Ser | Leu | Leu | Gln | Gly |
| | | 355 | | | | | 360 | | | | | 365 | | | |
| Leu | Gln | Val | Ala | Gly | Ile | Ser | Leu | Phe | Ala | Ile | Phe | Met | Gln | Val | Thr |
| | 370 | | | | | 375 | | | | | 380 | | | | |
| Ile | Ile | Met | Arg | Ile | Ser | Thr | Val | Val | Val | Lys | Pro | Leu | Ile | Ala | Gly |
| 385 | | | | | 390 | | | | | 395 | | | | | 400 |
| Ala | Phe | Ser | Gly | Ile | Val | Phe | Pro | Ile | Ala | Val | Cys | Leu | Ile | Val | Leu |
| | | | | 405 | | | | | 410 | | | | | 415 | |
| Asp | Trp | Phe | Lys | Asp | Ser | Met | Lys | Asn | Ile | Leu | Ile | Trp | Phe | Ile | Asn |
| | | | 420 | | | | | 425 | | | | | 430 | | |
| Asn | Leu | Phe | Ile | Leu | Val | Leu | Ala | Ile | Pro | Ile | Leu | Leu | Phe | Gly | Val |
| | | 435 | | | | | 440 | | | | | 445 | | | |
| Leu | Ala | Leu | Leu | Ala | Phe | Asn | Leu | Thr | Ile | Thr | Pro | Ser | Val | Ala | Ile |
| | 450 | | | | | 455 | | | | | 460 | | | | |
| Gln | Asn | Ile | Asn | Gln | Gly | Gly | Leu | Gly | Ile | Asp | Ser | Thr | Ile | Ala | Ser |
| 465 | | | | | 470 | | | | | 475 | | | | | 480 |
| Leu | Ile | Thr | Leu | Phe | Ile | Leu | Lys | Gly | Phe | Ile | Glu | Thr | Ile | Ile | Glu |
| | | | | 485 | | | | | 490 | | | | | 495 | |

(2) INFORMATION FOR SEQ ID NO:24803280_f3_7-AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 271

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| Met | Ala | Phe | Trp | Gln | Ala | Ile | Arg | Trp | Trp | Ile | Leu | Lys | Leu | Pro | Phe | 1 | 5 | 10 | 15 |
| Met | Met | Gly | Ala | Thr | Met | Met | Trp | Ile | Leu | Ser | Glu | Met | Ala | Phe | Lys | 20 | 25 | 30 | |
| Ile | Ala | Gly | Unk | Met | Ala | Phe | Lys | Glu | Ala | Ser | Arg | Ala | Ala | Asn | Pro | 35 | 40 | 45 | |
| Val | Leu | Leu | Glu | Pro | Met | Met | Lys | Val | Glu | Val | Glu | Val | Pro | Glu | Glu | 50 | 55 | 60 | |
| Tyr | Met | Gly | Asp | Val | Ile | Gly | Asp | Leu | Asn | Arg | Arg | Arg | Gly | Gln | Ile | 65 | 70 | 75 | 80 |
| Asn | Ser | Met | Asp | Asp | Arg | Leu | Gly | Leu | Lys | Ile | Val | Asn | Ala | Phe | Val | 85 | 90 | 95 | |
| Pro | Leu | Val | Glu | Met | Phe | Gly | Tyr | Ser | Thr | Asp | Leu | Arg | Ser | Ala | Thr | 100 | 105 | 110 | |
| Gln | Gly | Arg | Gly | Thr | Tyr | Ser | Met | Glu | Phe | Asp | His | Tyr | Gly | Glu | Val | 115 | 120 | 125 | |
| Pro | Ser | Asn | Ile | Ala | Lys | Glu | Ile | Val | Glu | Lys | Arg | Lys | Gly | 130 | 135 | 140 | | | |

(2) INFORMATION FOR SEQ ID NO:24806290_f1_1-AA

(A) LENGTH: 152 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 272

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Met Gln Asn Leu Pro Gly Met Ala Arg Ala Ala Met Leu Thr Thr Ser
1 5 10 15

Ser Ala Pro Ala Pro Glu Gly Glu Gly Ala Phe Arg Ala Met Lys Met
20 25 30

Ala Ser Glu Met Ala Lys Val Glu Val Gly Tyr Val Asn Ala His Gly
35 40 45

Thr Ser Thr His Tyr Asn Asp Trp Tyr Glu Ser Ile Ala Leu Lys Asn
50 55 60

Val Leu Ala Leu Lys Lys Lys Ser Leu Leu Leu Ala Pro Leu Lys Gly
65 70 75 80

Arg Leu Gly Leu Leu Gly Cys Cys Gly Val Arg Ser Arg Tyr Ser Ile
85 90 95

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Met | Unk | Gln | Gly | Ile | Leu | Pro | Pro | Thr | Ile | Asn | Gln | Glu | Thr |
| | | | 100 | | | | | 105 | | | | | 110 | | |

Pro Asp Pro Glu Cys Unk Leu Asp Tyr Ile Pro Asn Thr Ala Arg Glu
115 120 125

Lys Gln Val Asn Ala Val Met Ser Asn Ser Phe Gly Phe Gly Gly Thr
130 135 140

Asn Gly Val Val Ile Phe Lys Lys Ala
145 150

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 273

(vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| Met | Gln | Asn | Leu | Leu | Ile | Gln | Ala | Glu | Asn | Ala | Ile | Ala | Leu | Leu | Phe | 1 | 5 | 10 | 15 |
| Leu | Leu | Asn | Asp | Lys | Asn | Leu | Lys | Gly | Lys | Ile | Asp | Leu | Ile | Tyr | Ile | 20 | 25 | 30 | |
| Asp | Pro | Pro | Phe | Ala | Thr | Asn | Asn | His | Phe | Thr | Ile | Thr | Asn | Gly | Arg | 35 | 40 | 45 | |
| Ala | Thr | Thr | Ile | Ser | Asn | Ser | Lys | Asn | Gly | Asp | Ile | Ala | Tyr | Ser | Asp | 50 | 55 | 60 | |
| Lys | Val | Val | Gly | Met | Asp | Phe | Met | Glu | Phe | Leu | Lys | Gln | Arg | Leu | Val | 65 | 70 | 75 | |
| Leu | Leu | Lys | Glu | Leu | Leu | Ser | Glu | Gln | Gly | Ser | Ile | Tyr | Val | His | Thr | 85 | 90 | 95 | |
| Asp | Tyr | Lys | Ile | Gly | His | Tyr | Val | Lys | Val | Met | Leu | Asp | Glu | Ile | Phe | 100 | 105 | 110 | |
| Gly | Ile | Gln | Asn | Phe | Arg | Asn | Glu | Ile | Thr | Arg | Ile | Lys | Cys | Asn | Pro | 115 | 120 | 125 | |
| Lys | Asn | Phe | Lys | Arg | Ile | Gly | Tyr | Gly | Asn | Ile | Lys | Asp | Met | Ile | Leu | 130 | 135 | 140 | |
| Phe | Tyr | Ser | Lys | Gly | Lys | Asn | Pro | Ile | Phe | Asn | Glu | Pro | Lys | Ile | Pro | 145 | 150 | 155 | |
| Tyr | Thr | Pro | Gln | Asp | Leu | Glu | Lys | Arg | Phe | Pro | Lys | Ile | Asp | Lys | Asp | 165 | 170 | 175 | |
| Lys | Arg | Arg | Tyr | Thr | Thr | Val | Pro | Ile | His | Ala | Pro | Gly | Glu | Val | Glu | 180 | 185 | 190 | |
| Ser | Gly | Glu | Cys | Ser | Lys | Ala | Phe | Lys | Gly | Met | Leu | Pro | Pro | Lys | Gly | 195 | 200 | 205 | |
| Arg | His | Trp | Arg | Thr | Asp | Ile | Ala | Thr | Leu | Glu | Arg | Trp | Asp | Lys | Glu | 210 | 215 | 220 | |
| Gly | Leu | Ile | Glu | Tyr | Ser | Asn | Asn | Asn | Asn | Pro | Arg | Lys | Lys | Ile | Tyr | 225 | 230 | 235 | |

(2) INFORMATION FOR SEQ ID NO:24818802_f1_1-AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 274

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ile | Leu | Lys | Asn | Leu | Ile | Leu | Leu | Phe | Leu | Ala | Lys | Arg | Lys | Leu |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Ile | Phe | Ile | Glu | Ala | Asn | Phe | Tyr | Thr | Ile | Ser | Gly | Ser | Lys | Leu | Asn |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Glu | Val | Ala | Arg | Ser | Tyr | Gln | Asp | Leu | Ala | Leu | Lys | Phe | Glu | Ala | Phe |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Pro | Asn | Tyr | Glu | Phe | Ile | Trp | Ile | Thr | Asp | Gly | Ile | Gly | Trp | Leu | Asp |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Ala | Lys | Ser | Lys | Leu | Gln | Glu | Ala | Tyr | Lys | Ser | Val | Glu | Ile | Tyr | Asn |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 |
| Leu | Ser | Tyr | Val | Asn | Asp | Phe | Ile | Ser | Lys | Val | Gln | Lys | | | |
| | | | | 85 | | | | | 90 | | | | | | |

(2) INFORMATION FOR SEQ ID NO:24824087_f1_2-AA

Figure 275A-page 336

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 502 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 275

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: NA⁺/H⁺ ANTIporter [E.coli]

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Thr | Ser | Val | Val | Ile | Lys | Pro | His | Ala | Tyr | Gly | Glu | Gln | Val | Gln | 1 | 5 | 10 | 15 |
| Glu | Ile | Glu | Glu | Glu | Ser | Asp | Ser | Asp | Tyr | Glu | Lys | Asn | Asn | Asp | Gln | 20 | 25 | 30 | |
| Glu | Ala | Ile | Asn | Phe | Gly | Ile | Ala | Leu | His | Lys | Gly | Leu | Glu | Tyr | Gln | 35 | 40 | 45 | |
| Tyr | Ala | Tyr | Asn | Ile | Pro | Lys | Gln | Ser | Val | Leu | Glu | Tyr | Leu | Asn | Tyr | 50 | 55 | 60 | |
| His | Tyr | Gly | Phe | Tyr | Gly | Leu | Asp | Tyr | Gln | Ala | Leu | Glu | Glu | Ser | Leu | 65 | 70 | 75 | 80 |
| Glu | Leu | Phe | Glu | Asn | Asp | Ala | Gly | Ile | Gln | Ala | Leu | Phe | Lys | Asn | His | 85 | 90 | 95 | |
| Ala | Leu | Lys | Gly | Glu | Ala | Ala | Phe | Leu | Phe | Gln | Gly | Val | Val | Ser | Arg | 100 | 105 | 110 | |
| Ile | Asp | Val | Leu | Leu | Trp | Asp | Arg | Gly | Gln | Asn | Leu | Tyr | Val | Leu | Asp | 115 | 120 | 125 | |
| Tyr | Lys | Ser | Ser | Gln | Asn | Tyr | Gln | Gln | Ser | His | Lys | Ala | Gln | Val | Ser | 130 | 135 | 140 | |
| His | Tyr | Ala | Glu | Phe | Leu | Arg | Thr | Gln | Unk | Pro | His | Phe | Lys | Ile | Gln | 145 | 150 | 155 | 160 |
| Ala | Gly | Ile | Ile | Tyr | Ala | His | Lys | Arg | Leu | Leu | Glu | Lys | Unk | Trp | Val | 165 | 170 | 175 | |
| Glu | Asn | Lys | Asn | Unk | Unk | Val | Ser | Met | Asn | Leu | Lys | Lys | Thr | Glu | Asn | 180 | 185 | 190 | |
| Ala | Leu | Ser | Leu | Thr | Leu | Lys | Asn | Phe | Ile | Lys | Ser | Glu | Ser | Phe | Gly | 195 | 200 | 205 | |
| Gly | Ile | Phe | Leu | Phe | Leu | Asn | Ala | Val | Leu | Ala | Met | Val | Val | Ala | Asn | 210 | 215 | 220 | |
| Ser | Phe | Unk | Lys | Gln | Ser | Tyr | Phe | Ala | Leu | Trp | His | Thr | Pro | Phe | Gly | 225 | 230 | 235 | 240 |

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 87 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 276

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: flagellar biosynthetic protein fliQ

Met Glu Ser Gln Leu Met Lys Leu Ala Ile Glu Thr Tyr Lys Ile Thr
1 5 10 15

Leu Met Ile Ser Leu Pro Val Leu Leu Ala Gly Leu Val Val Gly Leu
20 25 30

Leu Val Ser Ile Phe Gln Ala Thr Thr Gln Ile Asn Glu Met Thr Leu
35 40 45

Ser Phe Val Pro Lys Ile Leu Ala Val Ile Gly Val Leu Ile Leu Thr
50 55 60

Met Pro Trp Met Thr Asn Met Leu Leu Asp Tyr Thr Lys Thr Leu Ile
65 70 75 80

Lys Leu Ile Pro Lys Ile Ile Gly
85

(2) INFORMATION FOR SEQ ID NO:25398250_c2_22: -AA

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 114 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 277

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

[illegible]

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 188 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 278

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | His | Ala | Glu | Leu | Gln | Lys | Ser | Ile | Asp | Glu | Asn | Leu | Glu | Val | Leu | 1 | 5 | 10 | 15 |
| Lys | Lys | Asn | His | Lys | His | Leu | Lys | Glu | Lys | Asn | Met | Pro | Leu | Pro | Phe | 20 | 25 | 30 | |
| Ile | Leu | Gly | Gly | Leu | Ala | Ile | Val | Ala | Ala | Gly | Tyr | Gly | Val | Lys | Lys | 35 | 40 | 45 | |
| Gly | Ile | Asp | Ala | Leu | Asp | Ala | Asp | Cys | Glu | Ala | Asp | Glu | Phe | Ile | Lys | 50 | 55 | 60 | |
| Lys | Ala | Glu | Ser | Leu | Lys | Glu | Glu | Ala | Thr | Lys | Lys | Ala | Glu | Ser | Ala | 65 | 70 | 75 | 80 |
| Glu | Ser | Asp | Cys | Arg | Arg | Ala | Phe | Met | Arg | Leu | Gly | Glu | Lys | Lys | Leu | 85 | 90 | 95 | |
| His | Val | Leu | Ser | His | Thr | Val | Ser | Asn | Phe | Leu | Asp | His | Phe | His | Arg | 100 | 105 | 110 | |
| Leu | Asn | Arg | Leu | Arg | Ile | Thr | Ile | Gly | Ile | Lys | Asp | Ile | Asp | Met | Gln | 115 | 120 | 125 | |
| Asp | Leu | Arg | Lys | Gln | Ile | Ser | Asn | Ala | Arg | Asn | Leu | Leu | Asn | Gln | Leu | 130 | 135 | 140 | |
| Asn | Thr | Asn | Gly | Ile | Asp | Gly | Arg | Leu | Cys | Ser | Gly | Ser | Asp | Cys | Arg | 145 | 150 | 155 | 160 |
| Leu | Trp | Trp | Phe | Arg | Arg | Ser | Gly | Phe | Thr | Ala | Gly | Asp | Thr | Val | Ala | 165 | 170 | 175 | |
| Val | Leu | Gly | Gly | Arg | His | Leu | Pro | Asn | Gly | Leu | Lys | Val | 180 | 185 | | | | | |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 259 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 279

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: flagellar distal capping protein homolog

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Glu | Asp | Leu | Pro | Phe | Ala | Ser | Asp | Ser | Gln | Phe | Thr | Tyr | Asn | 1 | 5 | 10 | 15 |
| Gly | Val | Ser | Ile | Thr | Arg | Pro | Thr | Asn | Glu | Val | Asn | Asp | Val | Ile | Ser | 20 | 25 | 30 | |
| Gly | Val | Asn | Ile | Thr | Leu | Glu | Gln | Thr | Thr | Glu | Pro | Asn | Lys | Pro | Ala | 35 | 40 | 45 | |
| Ile | Ile | Ser | Val | Ser | Arg | Asp | Asn | Gln | Ala | Ile | Ile | Asp | Ser | Leu | Lys | 50 | 55 | 60 | |
| Glu | Phe | Val | Lys | Ala | Tyr | Asn | Glu | Leu | Ile | Pro | Lys | Leu | Asp | Glu | Asp | 65 | 70 | 75 | 80 |
| Thr | Arg | Tyr | Asp | Ala | Asp | Thr | Lys | Ile | Ala | Gly | Ile | Phe | Asn | Gly | Val | 85 | 90 | 95 | |
| Gly | Asp | Ile | Arg | Ala | Ile | Arg | Ser | Ser | Leu | Asn | Asn | Val | Phe | Ser | Tyr | 100 | 105 | 110 | |
| Ser | Val | His | Thr | Asp | Asn | Gly | Val | Glu | Ser | Leu | Met | Lys | Tyr | Gly | Leu | 115 | 120 | 125 | |
| Ser | Leu | Asp | Asp | Lys | Gly | Val | Met | Ser | Leu | Asp | Glu | Ala | Lys | Leu | Ser | 130 | 135 | 140 | |
| Ser | Ala | Leu | Asn | Ser | Asn | Pro | Lys | Ala | Thr | Gln | Asp | Phe | Phe | Tyr | Gly | 145 | 150 | 155 | 160 |
| Ser | Asp | Ser | Lys | Asp | Met | Gly | Gly | Arg | Glu | Ile | His | Gln | Glu | Gly | Ile | 165 | 170 | 175 | |
| Phe | Ser | Lys | Phe | Asn | Gln | Val | Ile | Ala | Asn | Leu | Ile | Asp | Gly | Gly | Asn | 180 | 185 | 190 | |
| Ala | Lys | Leu | Lys | Ile | Tyr | Glu | Asp | Ser | Leu | Asp | Arg | Asp | Ala | Lys | Ser | 195 | 200 | 205 | |
| Leu | Thr | Lys | Asp | Lys | Glu | Asn | Ala | Gln | Glu | Leu | Leu | Lys | Thr | Arg | Tyr | 210 | 215 | 220 | |
| Asn | Ile | Met | Ala | Glu | Arg | Phe | Ala | Ala | Tyr | Asp | Ser | Gln | Ile | Ser | Lys | 225 | 230 | 235 | 240 |

Ala Asn Gln Lys Phe Asn Ser Val Gln Met Met Ile Asp Gln Ala Ala
245 250 255

Ala Lys Lys Asn
260

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 190 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP280

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Asn | Pro | Gln | Ala | Asn | Val | Leu | Lys | Leu | Phe | Leu | Asn | Gln | Val | 1 | 5 | 10 | 15 |
| Ala | Asp | Gln | Lys | Tyr | Ile | Asp | Met | Asn | Asp | Glu | Lys | Asn | Tyr | Asp | Pro | 20 | 25 | 30 | |
| Arg | Glu | Pro | Glu | Pro | Pro | Tyr | Gly | Thr | Lys | Gly | Ala | Leu | Asp | Glu | Ile | 35 | 40 | 45 | |
| Ile | Arg | Thr | Asp | Ala | Arg | Ser | Trp | Ala | Asn | Thr | Pro | Asp | Asp | Glu | Phe | 50 | 55 | 60 | |
| Gly | Ser | Ile | Met | Ser | Ser | Phe | Lys | Arg | Phe | Met | Tyr | Val | Tyr | Lys | Asp | 65 | 70 | 75 | 80 |
| Pro | Lys | Val | Arg | Glu | Ala | Thr | Ser | Lys | Met | Ser | Phe | Asp | Tyr | Glu | Glu | 85 | 90 | 95 | |
| Leu | Arg | Thr | Gly | Asn | Ile | Ser | Ile | Tyr | Ile | Val | Ile | Ala | Gln | Ile | Asp | 100 | 105 | 110 | |
| Ile | Gly | Thr | Leu | Ser | Ser | Leu | Val | Arg | Ala | Phe | Leu | Glu | Ser | Ile | Ala | 115 | 120 | 125 | |
| Lys | Asn | Leu | Met | Val | Lys | Glu | Ser | Ser | Lys | Pro | Glu | Glu | Arg | Ile | Phe | 130 | 135 | 140 | |
| Ile | Ile | Ala | Asp | Glu | Phe | Val | Arg | Phe | Gly | Lys | Leu | Pro | Phe | Leu | Leu | 145 | 150 | 155 | 160 |
| Glu | Met | Pro | Ala | Leu | Cys | Arg | Ser | Tyr | Asn | Val | Val | Pro | Leu | Phe | Ile | 165 | 170 | 175 | |
| Thr | Gln | Asp | Tyr | Ala | Met | Ile | Arg | Asn | Thr | Ile | Ala | Met | Met | Ile | 180 | 185 | 190 | | |

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 350 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 281

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ile | Ser | Glu | Ile | Ile | Lys | Phe | Gln | Leu | Lys | Gly | Ile | Lys | Met | Ile | 1 | 5 | 10 | 15 |
| Arg | Leu | Lys | Gly | Leu | Asn | Lys | Thr | Leu | Lys | Thr | Ser | Leu | Leu | Ala | Gly | 20 | 25 | 30 | |
| Val | Leu | Leu | Gly | Ala | Thr | Ala | Pro | Leu | Met | Ala | Lys | Pro | Leu | Leu | Ser | 35 | 40 | 45 | |
| Asp | Glu | Asp | Leu | Leu | Lys | Arg | Val | Lys | Leu | His | Asn | Ile | Lys | Glu | Asp | 50 | 55 | 60 | |
| Thr | Leu | Thr | Ser | Cys | Asn | Ala | Lys | Val | Asp | Gly | Ser | Gln | Tyr | Leu | Asn | 65 | 70 | 75 | 80 |
| Ser | Gly | Trp | Asn | Leu | Ser | Lys | Glu | Phe | Pro | Gln | Glu | Tyr | Arg | Glu | Lys | 85 | 90 | 95 | |
| Ile | Phe | Glu | Cys | Val | Glu | Glu | Glu | Lys | His | Lys | Gln | Ala | Leu | Asn | Leu | 100 | 105 | 110 | |
| Ile | Asn | Lys | Glu | Asp | Thr | Glu | Asp | Lys | Glu | Glu | Leu | Ala | Lys | Lys | Ile | 115 | 120 | 125 | |
| Lys | Glu | Ile | Lys | Glu | Lys | Ala | Lys | Val | Leu | Arg | Gln | Lys | Phe | Met | Ala | 130 | 135 | 140 | |
| Phe | Glu | Met | Lys | Glu | His | Ser | Lys | Glu | Phe | Pro | Asn | Lys | Lys | Gln | Leu | 145 | 150 | 155 | 160 |
| Gln | Thr | Met | Leu | Glu | Asn | Ala | Phe | Asp | Asn | Gly | Ala | Glu | Ser | Phe | Ile | 165 | 170 | 175 | |
| Asp | Asp | Trp | His | Glu | Arg | Phe | Gly | Gly | Ile | Ser | Arg | Glu | Asn | Thr | Tyr | 180 | 185 | 190 | |
| Lys | Ala | Leu | Gly | Ile | Lys | Glu | Tyr | Ser | Asp | Glu | Gly | Lys | Ile | Leu | Ala | 195 | 200 | 205 | |
| Phe | Gly | Glu | Arg | Ser | Tyr | Ile | Arg | Gln | Tyr | Lys | Lys | Asp | Phe | Glu | Glu | 210 | 215 | 220 | |
| Ser | Thr | Tyr | Asp | Thr | Arg | Gln | Thr | Leu | Ser | Ala | Met | Ala | Asn | Met | Ser | 225 | 230 | 235 | 240 |

| | | | | | | | | | | | | | | | |
|------------|------------|------------|------------|------------|------------|------------|-----|------------|------------|------------|------------|------------|------------|------------|------------|
| Gly | Glu | Asn | Asp | Tyr 245 | Lys | Ile | Thr | Trp | Leu 250 | Lys | Pro | Lys | Tyr | Gln 255 | Leu |
| His | Ser | Ser | Asn 260 | Asn | Ile | Lys | Pro | Leu 265 | Met | Ser | Asn | Thr | Glu 270 | Leu | Leu |
| Asn | Met | Ile 275 | Glu | Leu | Thr | Asn 280 | Ile | Lys | Lys | Glu | Tyr | Val 285 | Met | Gly | Cys |
| Asn | Met 290 | Glu | Ile | Asp | Gly | Ser 295 | Lys | Tyr | Pro | Ile | His 300 | Lys | Asp | Trp | Gly |
| Phe 305 | Phe | Gly | Lys | Ala | Lys 310 | Val | Pro | Glu | Thr | Trp 315 | Arg | Asn | Lys | Ile | Trp 320 |
| Glu | Cys | Ile | Lys | Asn 325 | Lys | Val | Lys | Ser | Tyr 330 | Asp | Asn | Thr | Thr | Ala 335 | Glu |
| Ile | Gly | Ile | Val 340 | Trp | Lys | Lys | Asn | Thr 345 | Tyr | Ser | Ile | Ser | His 350 | His | |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 282

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: flagellar motor switch protein flmM

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Ala | Asp | Ile | Leu | Ser | Gln | Glu | Glu | Ile | Asp | Ala | Leu | Leu | Glu | Val | |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | | |
| Val | Asp | Glu | Asn | Val | Asp | Ile | Gln | Asn | Val | Gln | Lys | Lys | Asp | Ile | Ile | |
| | | | 20 | | | | | 25 | | | | | 30 | | | |
| Pro | Gln | Arg | Ser | Val | Thr | Leu | Tyr | Asp | Phe | Lys | Arg | Pro | Asn | Arg | Val | |
| | | | 35 | | | | 40 | | | | | 45 | | | | |
| Ser | Lys | Glu | Gln | Leu | Arg | Ser | Phe | Arg | Ser | Ile | His | Asp | Lys | Met | Ala | |
| | 50 | | | | | 55 | | | | | 60 | | | | | |
| Arg | Asn | Leu | Ser | Ser | Gln | Val | Ser | Ser | Ile | Met | Arg | Ser | Ile | Val | Glu | |
| 65 | | | | | 70 | | | | 75 | | | | | | 80 | |
| Ile | Gln | Leu | His | Ser | Val | Asp | Gln | Met | Thr | Tyr | Gly | Glu | Phe | Leu | Met | |
| | | | | 85 | | | | | 90 | | | | | 95 | | |
| Ser | Leu | Pro | Ser | Pro | Thr | Ser | Phe | Asn | Val | Phe | Ser | Met | Lys | Pro | Met | |
| | | | 100 | | | | | 105 | | | | | 110 | | | |
| Gly | Gly | Thr | Gly | Val | Leu | Glu | Ile | Asn | Pro | Ser | Ile | Ala | Phe | Pro | Met | |
| | | | 115 | | | | 120 | | | | | 125 | | | | |
| Ile | Asp | Arg | Leu | Leu | Gly | Gly | Lys | Gly | Ser | Ala | Tyr | Asp | Gln | Asn | Arg | |
| | 130 | | | | | 135 | | | | | 140 | | | | | |
| Glu | Phe | Ser | Asp | Ile | Glu | Leu | Asn | Leu | Leu | Asp | Thr | Ile | Leu | Arg | Gln | |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 | |
| Val | Met | Gln | Ile | Leu | Lys | Glu | Val | Trp | Ser | Pro | Val | Val | Glu | Met | Tyr | |
| | | | | 165 | | | | | 170 | | | | | 175 | | |
| Pro | Thr | Ile | Asp | Ala | Lys | Glu | Ser | Ser | Ala | Asn | Val | Val | Gln | Ile | Val | |
| | | | 180 | | | | | 185 | | | | | 190 | | | |
| Ala | Gln | Asn | Glu | Ile | Ser | Ile | Met | Val | Val | Leu | Glu | Ile | Ile | Ile | Gly | |
| | | | 195 | | | | 200 | | | | | 205 | | | | |
| His | Ser | Arg | Gly | Met | Met | Asn | Ile | Cys | Tyr | Pro | Val | Ile | Ser | Ile | Glu | |
| | 210 | | | | | 215 | | | | | 220 | | | | | |
| Ser | Ile | Leu | Ser | Lys | Met | Gly | Ser | Arg | Asp | Phe | Met | Leu | Ser | Glu | Thr | |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Ser | Lys | Lys | Ser | Arg | Asn | Lys | Glu | Leu | Gln | Ala | Leu | Leu | Ser | Gly |
| | | | | 245 | | | | | 250 | | | | | 255 | |
| Val | Ser | Val | Asp | Met | Met | Val | Phe | Leu | Gly | Ala | Val | Glu | Leu | Ser | Leu |
| | | | 260 | | | | | 265 | | | | | 270 | | |
| Lys | Glu | Met | Leu | Asp | Leu | Asp | Val | Gly | Asp | Thr | Ile | Arg | Leu | Asn | Lys |
| | | 275 | | | | | 280 | | | | | 285 | | | |
| Val | Ala | Asn | Asp | Glu | Val | Ser | Val | Tyr | Val | His | Lys | Lys | Lys | Arg | Tyr |
| | 290 | | | | | 295 | | | | | 300 | | | | |
| Leu | Ala | Ser | Val | Gly | Phe | Gln | Gly | Tyr | Arg | Lys | Thr | Ile | Gln | Ile | Lys |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 |
| Glu | Val | Val | Tyr | Ser | Glu | Lys | Glu | Arg | Thr | Lys | Glu | Ile | Leu | Glu | Met |
| | | | | 325 | | | | | 330 | | | | | 335 | |
| Leu | Glu | Glu | Gln | Arg | Arg | Arg | Gln | Ser | Trp | Ala | Met | Leu | Trp | Ser | |
| | | | 340 | | | | | 345 | | | | | 350 | | |

(2) INFORMATION FOR SEQ ID NO:25595387_c2_15-AA

Figure 283A - page 348

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 304 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP283

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Arg | Ile | Val | Phe | Met | Gly | Thr | Pro | Ser | Phe | Ala | Glu | Val | Ile | Leu | 1 | 5 | 10 | 15 |
| Arg | Ala | Leu | Val | Glu | Asn | Glu | Asp | Lys | Lys | Ile | Glu | Val | Val | Gly | Leu | 20 | 25 | 30 | |
| Phe | Thr | Gln | Arg | Asp | Lys | Pro | Phe | Gly | Arg | Lys | Lys | Glu | Leu | Lys | Ala | 35 | 40 | 45 | |
| Pro | Glu | Thr | Lys | Thr | Tyr | Ile | Leu | Glu | Asn | His | Leu | Asn | Ile | Pro | Ile | 50 | 55 | 60 | |
| Phe | Gln | Pro | Gln | Ser | Leu | Lys | Glu | Pro | Glu | Val | Gln | Ile | Leu | Lys | Gly | 65 | 70 | 75 | 80 |
| Leu | Lys | Pro | Asp | Phe | Ile | Val | Val | Val | Ala | Tyr | Gly | Lys | Ile | Leu | Pro | 85 | 90 | 95 | |
| Lys | Glu | Val | Leu | Thr | Ile | Ala | Pro | Cys | Ile | Asn | Leu | His | Ala | Ser | Leu | 100 | 105 | 110 | |
| Leu | Pro | Lys | Tyr | Arg | Gly | Ala | Ser | Pro | Ile | His | Glu | Met | Ile | Leu | Asn | 115 | 120 | 125 | |
| Asp | Asp | Arg | Ile | Tyr | Gly | Ile | Ser | Thr | Met | Leu | Met | Asp | Leu | Glu | Leu | 130 | 135 | 140 | |
| Asp | Ser | Gly | Asp | Ile | Leu | Glu | Ser | Ala | Ser | Phe | Leu | Arg | Glu | Asp | Tyr | 145 | 150 | 155 | 160 |
| Leu | Asp | Leu | Asp | Ala | Leu | Ser | Leu | Lys | Leu | Ala | Arg | Met | Gly | Ala | Thr | 165 | 170 | 175 | |
| Leu | Leu | Leu | Ser | Thr | Leu | Lys | Asn | Phe | His | Ser | Ile | Thr | Arg | Lys | Pro | 180 | 185 | 190 | |
| Gln | Asp | His | Met | Gln | Ala | Ser | Phe | Cys | Lys | Lys | Ile | Ala | Lys | Ala | Asp | 195 | 200 | 205 | |
| Gly | Leu | Val | Gly | Phe | Lys | Asp | Ala | Lys | Asn | Leu | Phe | Leu | Lys | Ser | Leu | 210 | 215 | 220 | |
| Ala | Phe | Lys | Ser | Trp | Pro | Glu | Ile | Phe | Leu | Glu | Asn | Ser | Leu | Lys | Leu | 225 | 230 | 235 | 240 |

Leu Glu Val Glu Leu Val Glu Asn Glu Lys Ser His Lys Glu Gly Glu
245 250 255

Ile Leu Ala Ile Asp Glu Arg Gly Val Leu Val Gly Cys Leu Lys Gly
260 265 270

Ser Val Arg Ile Ala Arg Leu Gln Ala Val Gly Lys Lys Pro Leu Lys
275 280 285

Ala Lys Asp Tyr Leu Asn Gly Arg Arg Leu Lys Val Gly Gly Ile Leu
290 295 300

Thr
305

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 189 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPD 284

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: PHOSPHO-N-ACETYLMURAMOYL-PENTAPEPTIDE-TRANSFERASE

Met Pro Thr Met Leu Ala Val Gly Phe Trp Val Leu Val Phe Leu Ser
1 5 10 15

Thr Ser Asn Ala Val Asn Leu Thr Asp Gly Leu Asp Gly Leu Ala Ser
20 25 30

Val Pro Ser Ile Phe Thr Leu Leu Ser Leu Ser Ile Phe Val Tyr Val
35 40 45

Ala Gly Asn Ala Glu Phe Ser Lys Tyr Leu Leu Tyr Pro Lys Val Ile
50 55 60

Asp Val Gly Glu Leu Phe Val Ile Ser Leu Ala Leu Val Gly Ser Leu
65 70 75 80

Phe Gly Phe Leu Trp Tyr Asn Cys Asn Pro Ala Ser Val Phe Met Gly
85 90 95

Asp Ser Gly Ser Leu Ala Ile Gly Gly Phe Ile Ala Tyr Asn Ala Ile
100 105 110

```
Val Ser His Asn Glu Ile Leu Leu Val Leu Met Gly Ser Ile Phe Val
      115                                120                125
```

Ile Glu Thr Leu Ser Val Ile Leu Gln Val Gly Ser Tyr Lys Thr Arg
130 135 140

Lys Lys Arg Leu Phe Leu Met Ala Pro Ile His His His Phe Glu Gln
145 150 155 160

Lys Gly Trp Ala Glu Asn Lys Val Ile Val Arg Phe Trp Ile Ile Ser
165 170 175

Met Leu Ser Asn Leu Val Ala Leu Leu Ser Leu Lys Val Cys
180 185 190

(2) INFORMATION FOR SEQ ID NO:25625192_c2_3 - AA

HPP 285

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Leu Met Arg Ile Leu Thr Pro Pro Leu
115 120

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 488 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 286

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Arg | Phe | Glu | Asn | Phe | Ile | Asn | Arg | Leu | Ala | Phe | Tyr | Met | Ala | Thr | 1 | 5 | 10 | 15 |
| Gly | Ser | Gly | Lys | Thr | Ile | Val | Ile | Ile | Lys | Leu | Val | Glu | Leu | Leu | Ser | 20 | 25 | 30 | |
| Val | Ala | Met | Gly | Met | Gly | Leu | Ile | Pro | Lys | Lys | Asn | Ile | Met | Phe | Phe | 35 | 40 | 45 | |
| Ser | Ala | Asn | Glu | His | Leu | Ile | Lys | Gln | Phe | Glu | Lys | Glu | Ile | Glu | Lys | 50 | 55 | 60 | |
| Tyr | Asn | Arg | Asn | Lys | Asp | Tyr | Ser | Lys | Gln | Ile | Asp | Phe | Lys | Asn | Leu | 65 | 70 | 75 | 80 |
| Lys | Ser | Val | Lys | Asn | Lys | Asp | Phe | Tyr | Arg | Ala | Pro | Lys | Asp | Ser | Leu | 85 | 90 | 95 | |
| Met | Lys | Glu | Ile | Ala | Leu | Phe | Tyr | Tyr | Arg | Ala | Asp | Leu | Met | Ser | Asp | 100 | 105 | 110 | |
| Glu | Glu | Ser | Lys | Glu | Asn | Leu | Leu | Asn | Tyr | Lys | Asp | Cys | Trp | Asp | Asn | 115 | 120 | 125 | |
| Gly | Glu | Asn | Tyr | Val | Ile | Leu | Asp | Glu | Ala | His | Lys | Gly | Asn | Lys | Thr | 130 | 135 | 140 | |
| Glu | Ser | Lys | Arg | Gln | Ala | Ile | Phe | Ser | Leu | Leu | Ser | Leu | Lys | Gly | Phe | 145 | 150 | 155 | 160 |
| Leu | Phe | Asn | Phe | Ser | Ala | Thr | Phe | Thr | Glu | Glu | Ser | Asp | Leu | Ile | Thr | 165 | 170 | 175 | |
| Ala | Val | Tyr | Asn | Leu | Ser | Val | Gly | Glu | Trp | Val | Lys | Leu | Gly | Tyr | Gly | 180 | 185 | 190 | |
| Lys | Glu | Ser | Val | Leu | Leu | Lys | Lys | Asn | Asn | Leu | Asn | Ala | Phe | Lys | Glu | 195 | 200 | 205 | |
| Leu | Lys | Asp | Leu | Asn | Asp | Arg | Glu | Lys | Glu | Ile | Ala | Leu | Leu | Lys | Ala | 210 | 215 | 220 | |
| Leu | Leu | Leu | Leu | Gly | Met | Gln | Lys | Arg | Tyr | Lys | Val | Glu | Gly | Tyr | Phe | 225 | 230 | 235 | 240 |

| | | | | | | | | | | | | | | | |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| His | Asp | Pro | Leu | Met 245 | Leu | Val | Phe | Thr | His 250 | Ser | Val | Asn | Met | Glu 255 | Asn |
| Ser | Asp | Ala | Unk 260 | Ile | Phe | Phe | Lys | Thr 265 | Leu | Ala | Arg | Val | Ile 270 | Glu | Asn |
| Asp | Asp | Glu 275 | Ser | Asp | Phe | Ser | Lys 280 | Ala | Lys | Asp | Asp | Leu 285 | Leu | Glu | Glu |
| Leu | Lys 290 | Asn | Pro | Glu | Phe | Leu 295 | Phe | Ser | Asp | Gly | Lys 300 | Asp | Lys | Glu | Lys |
| Asp 305 | Tyr | Lys | Ile | Glu | Val 310 | Phe | Lys | Glu | Ser | Leu 315 | Lys | Gly | Met | Asp | Phe 320 |
| Lys | Gly | Leu | Lys | Glu 325 | Ala | Val | Phe | Tyr | Ala 330 | Ser | Asn | Gly | His | Ile 335 | Glu |
| Val | Ile | Ile | Asn 340 | Pro | Lys | Asn | Asn | Gln 345 | Glu | Ile | Ala | Phe | Lys 350 | Leu | Asn |
| Thr | Ser | Asp 355 | Lys | Val | Phe | Cys | Leu 360 | Ile | Arg | Ile | Gly | Asp 365 | Ile | Thr | Glu |
| Trp | Ile 370 | Arg | Glu | Lys | Leu | Lys 375 | Ser | Val | Lys | Val | Val 380 | Ser | Lys | Asn | Leu |
| Ser 385 | Phe | Lys | Glu | Glu | Ser 390 | Tyr | Phe | Ser | Gln | Ile 395 | Asp | Lys | Ser | Ser | Ile 400 |
| Asn | Ile | Leu | Val | Gly 405 | Ser | Arg | Ala | Phe | Asp 410 | Thr | Gly | Trp | Asp | Ser 415 | Thr |
| Arg | Pro | Ser | Val 420 | Ile | Leu | Phe | Leu | Asn 425 | Ile | Gly | Leu | Asp | Asp 430 | Asp | Ala |
| Lys | Lys | Leu 435 | Val | Lys | Gln | Ser | Phe 440 | Gly | Arg | Gly | Val | Arg 445 | Ile | Glu | Ser |
| Val | Lys 450 | Asn | Gln | Arg | Gln | Arg 455 | Leu | Ala | Tyr | Leu | Glu 460 | Ile | Asp | Glu | Ala |
| Ile 465 | Lys | Glu | Gln | Ala | Glu 470 | Thr | Lys | Arg | Cys | Asn 475 | Ala | Gly | Asn | Ala | Phe 480 |
| Cys | Asp | Thr | Tyr | Gln 485 | Pro | Cys | Lys | Pro | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:259665 c2_17-AA

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 146 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP287

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Met Arg Phe Tyr Phe Lys Phe Leu Trp Leu Leu Gly Ile Phe Leu Ile
1 5 10 15

Phe Tyr Phe Leu Asp Ile Lys Gly Ser Ser Ser Tyr Ile Ser Asp Arg
20 25 30

Val Lys Ser Ala Leu Met Ser Ala Lys Asn Ser Leu Leu Asp Asn Val
35 40 45

Gln Ala Tyr Phe Phe Gln Ala Gln Asn Ile Lys Glu Phe Gln Lys Glu
50 55 60

Arg Leu Ile Leu Glu Ala Leu Lys Leu Glu Asn Ala Glu Phe Glu Arg
65 70 75 80

Ala Leu Asn Ser Ile Tyr Pro Leu Glu Asn Pro Lys Met Thr Tyr Thr
85 90 95

Pro Leu Met Thr Ser Phe Ile Asn Leu Glu Asp Thr His Ser Val Ser
100 105 110

Leu Asn Pro Ile Val Asn Leu Glu Glu Asn Lys Ile Tyr Gly Leu Val
115 120 125

Ser His Asn Gln Ala Ile Gly Ile Ala Val Leu Glu Lys Gly Arg Leu
130 135 140

Asn Gly Phe
145

(2) INFORMATION FOR SEQ ID NO:25976418_f2_4-AA

Figure 288A-page 355

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 288

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Phe | Leu | Phe | Tyr | Leu | Ile | Gly | Arg | Lys | Ile | Leu | Lys | Lys | Pro | Lys | 1 | 5 | 10 | 15 |
| Asp | Ala | Leu | Tyr | Val | Val | Leu | Thr | Tyr | Ala | Leu | Leu | Pro | Gly | Val | Asn | 20 | 25 | 30 | |
| Leu | Phe | Ala | Ile | Leu | Leu | Ala | Lys | Ser | Val | Leu | Val | Leu | Ser | Leu | Gly | 35 | 40 | 45 | |
| Leu | Leu | Ile | Ser | Tyr | Leu | Tyr | Ile | Lys | Thr | Gln | Lys | Ile | Pro | Tyr | Leu | 50 | 55 | 60 | |
| Thr | Leu | Ser | Ala | Cys | Ala | Phe | Leu | Asp | Gly | Ala | Phe | Ile | Pro | Leu | Leu | 65 | 70 | 75 | 80 |
| Leu | Gly | Val | Phe | Ala | Tyr | Ala | Leu | Arg | Lys | Thr | Ala | Ile | Leu | Arg | Ala | 85 | 90 | 95 | |
| Arg | Ser | Leu | Leu | Trp | Trp | Phe | Tyr | Cys | Asp | His | Ala | Leu | Phe | Ser | Gly | 100 | 105 | 110 | |
| Asp | Phe | Asn | Lys | Gly | Leu | Pro | Ser | Gly | Tyr | Phe | Ile | Asp | Thr | Cys | Leu | 115 | 120 | 125 | |
| Glu | Leu | Met | Leu | Leu | Tyr | Ser | Pro | Leu | Leu | Phe | Leu | Tyr | Tyr | Pro | Tyr | 130 | 135 | 140 | |
| Thr | Leu | Tyr | Lys | Ala | Leu | Leu | Asp | Lys | Lys | Pro | Trp | Leu | Leu | Ala | Phe | 145 | 150 | 155 | 160 |
| Val | Ala | Arg | Ala | Thr | Gly | Phe | Cys | Leu | Trp | | | | | | | 165 | 170 | | |

(2) INFORMATION FOR SEQ ID NO:25992137_c3_17:-AA

Figure 289A - page 356

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 289

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: N-ACETYLMURAMOYL-L-ALANINE AMIDASE CWLB PRECURSOR

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|----|
| Val | Asn | Leu | Met | Asp | Tyr | Phe | Ser | Lys | Ser | Leu | Phe | Leu | Asn | Ser | Leu | 1 | 5 | 10 | 15 |
| Asn | Thr | Gln | Arg | Leu | Ile | Val | Ser | Asn | Lys | Leu | Ala | Ile | Asp | Val | Gln | 20 | 25 | 30 | |
| Tyr | Gly | Met | Leu | Gln | Ser | Val | Arg | Lys | Asn | Tyr | Pro | Asp | Val | Val | Asp | 35 | 40 | 45 | |
| Gly | Gly | Val | Arg | Glu | Gly | Pro | Phe | Trp | Val | Leu | Ala | Gly | Ala | Leu | Met | 50 | 55 | 60 | |
| Pro | Ser | Ile | Leu | Ile | Glu | Ile | Gly | Tyr | Asn | Ser | His | Ala | Ile | Glu | Ser | 65 | 70 | 75 | 80 |
| Lys | Arg | Ile | Gln | Ser | Lys | Pro | Tyr | Gln | Lys | Ile | Leu | Ala | Lys | Gly | Ile | 85 | 90 | 95 | |
| Ala | Asp | Gly | Ile | Asp | Ser | Phe | Phe | Ser | Lys | Asn | Asp | | | | | 100 | 105 | | |

(2) INFORMATION FOR SEQ ID NO:25995917_c1_15 - AA

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 212 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 290

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

[illegible]

(2) INFORMATION FOR SEQ ID NO:26052137_c2_8-AA

(A) LENGTH: 81 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 291

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Val Ala Val Gly Asn Leu Phe Ser Glu His Leu Tyr Asp Leu Arg Asn
1 5 10 15

Glu Thr Met Thr Asn Leu Ile Gly Phe Leu Leu Val Leu Ala Ser Ile
20 25 30

Trp Val Phe Phe Leu Ala Leu Gly Val Leu Leu Gly Lys Met Leu Val
35 40 45

Phe Ser Gly Leu Gly Ile Ile Asp Lys Ala Leu Gly Phe Ile Phe Ser
50 55 60

Cys Leu Lys Thr Phe Leu Val Leu Ser Phe Ile Leu Tyr Ala Leu Ser
65 70 75 80

Lys Met

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 311 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 292

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: flagellar basal body L-ring protein

| | | | | | | | | | | | | | | | |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Met 1 | Lys | Ser | Asp | Lys 5 | Pro | Phe | Leu | Glu | Arg 10 | Tyr | Phe | Tyr | Asp | Pro 15 | Thr |
| Leu | Leu | Gln | Lys 20 | Gly | Leu | Ile | Phe | Ala 25 | Leu | Tyr | Pro | Phe | Ser 30 | Leu | Ile |
| Tyr | Gln | Cys 35 | Ile | Ala | Thr | Ile | Lys 40 | Arg | Lys | Thr | Ala | Lys 45 | Lys | His | Asp |
| Phe | Lys 50 | Ile | Pro | Ile | Ile | Ser 55 | Ile | Gly | Asn | Leu | Ile 60 | Ala | Gly | Gly | Ser |
| Gly 65 | Lys | Thr | Pro | Phe | Ile 70 | Leu | Glu | Ile | Ala | Pro 75 | Arg | Tyr | Gln | Glu | Val 80 |
| Ala | Val | Val | Ser | Arg 85 | Gly | Tyr | Gln | Arg | Asp 90 | Ser | Lys | Gly | Leu | Val 95 | Val |
| Val | Ser | Val | Lys 100 | Gly | Asn | Ile | Leu | Val 105 | Pro | Gln | Lys | Thr | Ala 110 | Gly | Asp |
| Glu | Ala | Tyr 115 | Leu | Leu | Ala | Leu | Asn 120 | Leu | Lys | Gln | Ala | Ser 125 | Val | Ile | Val |
| Ser | Glu 130 | Lys | Arg | Glu | Leu | Gly 135 | Val | Leu | Lys | Ala | Leu 140 | Glu | Leu | Gly | Ser |
| Lys 145 | Ile | Val | Phe | Leu | Asp 150 | Asp | Gly | Phe | Arg | Phe 155 | Asn | Phe | Asn | Gln | Phe 160 |
| Asn | Ala | Leu | Leu | Lys 165 | Pro | Lys | Val | Pro | Pro 170 | Tyr | Tyr | Pro | Phe | Cys 175 | Leu |
| Pro | Ser | Gly | Leu 180 | Tyr | Arg | Glu | Asn 185 | Ile | Lys | Ser | Tyr | Lys | Glu 190 | Ala | His |
| Leu | Val | Ile 195 | Thr | Glu | Asp | Lys | Asp 200 | Tyr | Gln | Arg | Ile | Thr 205 | Ser | Ile | Thr |
| Asn | Pro 210 | Thr | Lys | Arg | Met | Leu 215 | Leu | Val | Thr | Ala | Ile 220 | Ala | Asn | Pro | Ser |
| Arg 225 | Leu | Asp | Ala | Phe | Leu 230 | Pro | Lys | Glu | Val | Val 235 | Lys | Lys | Leu | Tyr | Phe 240 |

| | | | | | | | | | | | | | | | |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|-----|------------|------------|------------|------------|-----|
| Arg | Asp | His | Ala | Pro 245 | Phe | Asp | Leu | Lys | Leu 250 | Leu | Glu | Lys | Glu | Phe 255 | Tyr |
| Gln | Asn | Asn | Ala 260 | Thr | Ser | Leu | Leu | Val 265 | Thr | Ser | Lys | Asp | Leu 270 | Val | Lys |
| Leu | Gln | Asp 275 | Cys | Lys | Leu | Pro | Leu 280 | Ser | Val | Leu | Asp | Leu 285 | Lys | Leu | Glu |
| Ile | Cys 290 | Pro | Lys | Val | Leu | Glu 295 | Glu | Ile | Asp | Arg | Tyr 300 | Ile | Leu | Ser | Tyr |
| Pro 305 | Cys | Asn | Ile | Lys | Glu 310 | His | Leu | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:26258562_c2_4: -AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 296

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: probable cadmium-transporting ATPase

Val Ile Thr Asn Asp Ser Leu Ser Ser Leu Val Lys Val Leu Ala Ile
1 5 10 15

Ala Lys Lys Thr Lys Ser Ile Thr Trp Gln Asn Ile Leu Phe Ala Leu
20 25 30

Gly Ile Lys Ala Val Phe Ile Val Leu Gly Leu Met Gly Val Ala Ser
35 40 45

Leu Trp Glu Ala Val Phe Gly Asp Val Gly Val Thr Leu Leu Ala Leu
50 55 60

Ala Asn Ser Ile Ala Arg
65 70

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 88 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

HPP 297

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Helicobacter pylori*

[illegible]

(2) INFORMATION FOR SEQ ID NO:26301059_c2_3: -AA

366
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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP298

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Phe | Glu | Pro | Val | Ile | Ala | Tyr | Lys | Leu | Phe | His | Ser | Phe | Val | Ile |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Leu | Gly | Cys | Ala | Ile | Glu | Thr | Leu | Thr | Thr | Lys | Cys | Val | Glu | Gly | Ile |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Thr | Ala | Asn | Glu | Lys | Ile | Cys | His | Asp | Tyr | Val | Phe | Asn | Ser | Ile | Gly |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Ile | Val | Thr | Ala | Leu | Asn | Pro | His | Ile | Gly | Tyr | Glu | Lys | Ser | Ala | Met |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Ile | Ala | Lys | Glu | Ala | Leu | Lys | Ser | Asp | Arg | Ser | Ile | Tyr | Asp | Ile | Ala |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 |
| Leu | Glu | Lys | Lys | Ile | Leu | Thr | Lys | Glu | Gln | Leu | Asp | Asp | Ile | Phe | Lys |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| Pro | Glu | Asn | Met | Leu | Arg | Thr | His | Ala | Phe | Lys | Lys | His | Lys | Asp | |
| | | | 100 | | | | | 105 | | | | | | 110 | |

(2) INFORMATION FOR SEQ ID NO:26306340_f2_3: -AA

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 64 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP299

(iii) HYPOTHETICAL: YES

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met Leu Arg Leu Leu Ala Gln Lys Ser Ala Ile Lys Leu Ile Leu Ile
1 5 10 15
Pro Pro Ser Ala Asn Ala Leu Gly Ile Ala Ser Ile Cys Glu Leu Ser
20 25 30
Glu Glu Val Phe Glu His Glu Lys Ile Val Gly Ile Arg Ala Gln Gly
35 40 45
Asp Phe Thr Ile Asn Ser Asp Asp Arg Gly Phe Trp Glu Arg Arg Cys
50 55 60
Gln
65

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP300

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Lys | Leu | Leu | Leu | Leu | Leu | Glu | His | Lys | Ile | Val | Lys | Ile | Gly | 1 | 5 | 10 | 15 |
| Leu | Ile | Ile | Val | Ile | Val | Leu | Val | Gly | Phe | Phe | Leu | Phe | Tyr | Glu | Gln | 20 | 25 | 30 | |
| Glu | Ile | Lys | Glu | Lys | Ala | Val | Asn | Val | Ser | Gln | Gly | Lys | Phe | Pro | Thr | 35 | 40 | 45 | |
| Ser | Ser | Tyr | Leu | Phe | Gln | Ala | Tyr | Glu | Gly | Ile | Lys | Asn | Lys | Ile | Asp | 50 | 55 | 60 | |
| Thr | Ile | Asn | Gln | Val | Lys | Pro | Asn | Asp | Glu | Thr | Lys | Ser | Val | Asn | Glu | 65 | 70 | 75 | 80 |
| Asn | Ile | Glu | Lys | Thr | Gln | Lys | Asp | Leu | Asp | Asp | Phe | Asn | Ala | Leu | Val | 85 | 90 | 95 | |
| Gln | Lys | Leu | Pro | Asn | Leu | Pro | Lys | Asp | Phe | Asn | Lys | Thr | Leu | Ile | Lys | 100 | 105 | 110 | |
| Pro | Gln | Ser | Pro | Phe | Phe | Asn | Tyr | Asn | Thr | Ala | Asn | Glu | Asp | Glu | Lys | 115 | 120 | 125 | |
| Asn | Arg | Leu | Val | Ile | Leu | Ala | Ser | Arg | Ile | Ser | Ser | Gln | Lys | Glu | Thr | 130 | 135 | 140 | |
| Gln | Pro | Pro | Ile | Ser | Ile | Lys | Asn | Ser | Val | Ser | His | Ile | Lys | Ser | Lys | 145 | 150 | 155 | 160 |
| Glu | Lys | Arg | Glu | Leu | Glu | Lys | Glu | Trp | Ala | Lys | Pro | Ser | Val | Ser | Phe | 165 | 170 | 175 | |
| Gly | Ser | Phe | Ser | Leu | Leu | Ser | Ser | Ser | Ser | Ser | Phe | Ser | Ser | Phe | Glu | 180 | 185 | 190 | |
| Val | Ser | Phe | Leu | Ser | Arg | Gly | Ile | Gly | Leu | Asp | Cys | Glu | Lys | Leu | Lys | 195 | 200 | 205 | |
| Ser | Phe | Leu | Lys | Ala | Phe | Ser | Ser | Ser | Leu | Phe | Ser | Leu | Leu | Ser | Ser | 210 | 215 | 220 | |
| Leu | Phe | Cys | His | Pro | Leu | Ser | Leu | Phe | Cys | Ser | Leu | Ile | Gly | Leu | Ile | 225 | 230 | 235 | 240 |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe | Cys | Phe | Ser | Lys | Phe | Ser | Arg | Glu | Leu | Val | Asn | Ala | Ser | Asn | Asn |
| | | | | 245 | | | | | 250 | | | | | 255 | |
| | | | | | | | | | | | | | | | |
| Ser | Leu | Glu | Phe | Ser | Ser | Leu | Ser | Arg | Leu | Gly | Ser | | | | |
| | | | 260 | | | | | 265 | | | | | | | |

Figure 301A - page 370

| | | | | | | | | | | | | | | | |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Val 1 | Thr | Glu | Ser | Tyr 5 | Gly | Tyr | Lys | Lys | Ile 10 | Thr | Lys | Tyr | Leu | Ile 15 | Ala |
| His | Lys | Met | Pro 20 | Ser | Gly | Met | Gln | Gly 25 | Phe | Phe | Phe | Asn | Thr 30 | Arg | Arg |
| Glu | Ile | Phe 35 | Lys | Asp | Lys | Arg | Val 40 | Arg | Glu | Ala | Leu | Phe 45 | Tyr | Ala | Phe |
| Asp | Phe 50 | Glu | Trp | Ala | Asn | Lys 55 | Asn | Leu | Phe | Phe | Ser 60 | Gln | Tyr | Lys | Arg |
| Thr 65 | Thr | Ser | Phe | Phe | Ser 70 | Asn | Ser | Ile | Tyr | Ala 75 | Ser | Pro | Pro | Leu | Pro 80 |
| Ser | Pro | Glu | Glu | Lys 85 | Ala | Leu | Leu | Ala | Pro 90 | Tyr | Glu | Lys | Ser | Leu 95 | Asp |
| Glu | Arg | Val | Phe 100 | Lys | Glu | Pro | Tyr | Ile 105 | Val | Pro | Arg | Thr | Asp 110 | Gly | Pro |
| Asp | Val | Leu 115 | Gly | Tyr | Asn | Leu | Arg 120 | Glu | Asn | Leu | Lys | Tyr 125 | Ala | Gln | Lys |
| Leu 130 | Leu | Glu | Ser | Ala | Gly | Phe 135 | Ser | Tyr | Lys | Asn | Met 140 | Arg | Leu | Val | Asp |
| Lys 145 | Asn | Asn | Lys | Pro | Phe 150 | Ser | Phe | Thr | Leu | Leu 155 | Leu | Asn | Ser | Pro | Ala 160 |
| Phe | Glu | Arg | Leu | Ala 165 | Leu | Ala | Phe | Ala | Lys 170 | Asn | Leu | Arg | Val | Leu 175 | Gly |
| Ile | Glu | Met | Lys 180 | Ile | Gln | Arg | Val | Asp 185 | Leu | Ser | Gln | Tyr | Val 190 | Asn | Arg |
| Ile | Lys | Ser 195 | Tyr | Asp | Phe | Asp | Met 200 | Ile | Val | Gly | Val | Ile 205 | Gly | Gln | Ser |
| Ser | Phe 210 | Pro | Gly | Asn | Glu | Gln 215 | His | Phe | Tyr | Phe | Ala 220 | Leu | | | |

HPP 302

(A) LENGTH: 99 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: UDP-N-ACETYLMURAMYL-TRYPEPTIDE SYNTHETASE

Met Gly Ala Ile Ala Ser Cys Tyr Ala His Gln Ile Ile Leu Thr Ser
1 5 10 15

Asp Asn Pro Arg Ser Glu Asn Glu Glu Asp Ile Ile Lys Asp Ile Leu
20 25 30

Lys Gly Ile Asn Asn Ser Ser Lys Val Ile Val Glu Lys Asp Arg Lys
35 40 45

Lys Ala Ile Leu Asn Ala Leu Glu Asn Leu Lys Asp Asp Glu Val Leu
50 55 60

Leu Ile Leu Gly Lys Gly Asp Glu Asn Ile Gln Ile Phe Lys Asp Lys
65 70 75 80

Thr Ile Phe Phe Ser Asp Gln Glu Val Val Lys Asp Tyr Tyr Leu Asn
85 90 95

Leu Lys Gln Gly
100

(2) INFORMATION FOR SEQ ID NO:26380318_f3_8:-AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP303

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: FLAGELLAR MOTOR SWITCH PROTEIN F

| | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|
| Val | Met | Asp | Lys | Leu | Thr | Lys | Ser | Leu | Gln | Thr | Gln | Lys | Asn | Phe | Ala | | | |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | | | | |
| Tyr | Leu | Gly | Lys | Ile | Lys | Pro | Gln | Gln | Leu | Ala | Asp | Phe | Ile | Ile | Asn | | | |
| | | | 20 | | | | | 25 | | | | | 30 | | | | | |
| Glu | His | Pro | Gln | Thr | Ile | Ala | Leu | Ile | Leu | Ala | His | Met | Glu | Unk | Pro | | | |
| | | | 35 | | | | 40 | | | | | 45 | | | | | | |
| Asn | Ala | Ala | Glu | Thr | Leu | Ser | Tyr | Phe | Pro | Asp | Glu | Met | Lys | Ala | Glu | | | |
| | | | 50 | | | 55 | | | | | 60 | | | | | | | |
| Ile | Ser | Ile | Arg | Met | Ala | Asn | Phe | Arg | Arg | Asn | Ile | Ala | Pro | Ser | Gly | | | |
| 65 | | | | 70 | | | | | | 75 | | | | | 80 | | | |

(2) INFORMATION FOR SEQ ID NO:26423583_f2_3: -AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP304

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Arg | Tyr | Phe | Arg | Ser | Ala | Phe | Leu | Leu | Phe | Phe | Met | Thr | Leu | Phe | 1 | 5 | 10 | 15 |
| Phe | Val | Ser | Cys | Ser | Lys | His | Pro | Phe | Ser | Lys | Gln | Thr | Pro | Lys | Thr | 20 | 25 | 30 | |
| Lys | Glu | Arg | Ile | Arg | Gln | Glu | Glu | Ala | Asn | Lys | Lys | Arg | Glu | Glu | Thr | 35 | 40 | 45 | |
| Leu | Asn | Ala | Leu | Arg | Gln | Phe | Arg | Leu | Ile | Tyr | Ile | Asn | Thr | Pro | Val | 50 | 55 | 60 | |
| Phe | Arg | Phe | Tyr | Asp | Tyr | Gly | Thr | Ile | Lys | Thr | Asp | Lys | Asp | His | Asn | 65 | 70 | 75 | 80 |
| Thr | Glu | Val | Thr | Leu | Tyr | Lys | Leu | Ser | Gln | Lys | Val | Gly | Asp | Ile | Tyr | 85 | 90 | 95 | |
| Met | Thr | Lys | Arg | Ser | Ile | Cys | Phe | Ser | Gln | Lys | Cys | Ser | Ala | Lys | Trp | 100 | 105 | 110 | |
| Ile | Ala | Ala | Arg | Asp | Leu | Phe | Gly | Lys | Val | Ser | Tyr | Gly | Asp | Leu | Phe | 115 | 120 | 125 | |
| Asp | Asp | Ile | Val | Leu | Gly | Arg | Asp | Ile | Phe | Lys | Gly | Leu | Gly | Lys | Arg | 130 | 135 | 140 | |
| His | Leu | Thr | Pro | Glu | Tyr | Val | Ile | Gln | Arg | Phe | Gln | Lys | Ser | Gly | Glu | 145 | 150 | 155 | 160 |
| Ile | Ile | Leu | Tyr | Glu | Arg | Lys | Asn | Gly | Leu | Ile | Ser | Phe | Gln | Asn | Leu | 165 | 170 | 175 | |
| Thr | Gln | Lys | Ile | Ala | Ile | Arg | Ile | Glu | Pro | Tyr | Glu | Pro | Ser | Leu | Gln | 180 | 185 | 190 | |
| Asp | Leu | Glu | Asp | Asn | Glu | Asn | Ala | Asp | Ser | Glu | Leu | Gln | 195 | 200 | 205 | | | | |

-AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 305

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: flagellar hook polypeptide

Met Arg Ile Glu Glu Asn Gly Val Ile Ser Leu Ala Phe Ser Asn Gly
1 5 10 15

Val Val Glu Pro Val Ala Arg Ile Gly Ile Unk Ala Phe Thr Asn Asp
20 25 30

Gln Gly Leu Arg Lys Ile Gly Gly Asn Leu Tyr Glu Met Gln Glu Gly
35 40 45

Thr Ile Asn Gly Glu Asn Arg Pro Leu Unk Gly Asn Pro Ile Leu Gly
50 55 60

Trp Asp Glu Glu Gly Lys Leu Lys Phe Gly Lys Ile Arg His Lys Tyr
65 70 75 80

Leu Glu Thr Ser Asn Val Asn Ala Gly Asn Ala Leu Thr Asn Leu Ile
85 90 95

Leu Met Gln Arg Gly Tyr Ser Met Asn Ala Arg Ala Phe Gly Ala Gly
100 105 110

Asp Asp Met Ile Lys Glu Ala Ile Ser Leu Lys Lys
115 120

(2) INFORMATION FOR SEQ ID NO:26614041_f3_3-AA

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- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 92 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP306

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: vacuolating cytotoxin - Helicobacter pylori

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Glu | Ala | Arg | Tyr | Tyr | Tyr | Gly | Asp | Thr | Ser | Tyr | Phe | Tyr | Leu | His |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Val | Gly | Val | Leu | Gln | Glu | Phe | Ala | His | Phe | Gly | Ser | Asn | Asp | Val | Ala |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Ser | Leu | Asn | Thr | Phe | Lys | Ile | Asn | Ala | Ala | Arg | Ser | Pro | Leu | Ser | Thr |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Tyr | Ala | Arg | Ala | Met | Met | Gly | Gly | Glu | Leu | Gln | Leu | Ala | Lys | Glu | Val |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Phe | Leu | Asn | Leu | Gly | Val | Val | Tyr | Leu | His | Asn | Leu | Ile | Ser | Asn | Ala |
| 65 | | | | 70 | | | | | 75 | | | | | 80 | |
| Ser | His | Phe | Ala | Ser | Asn | Leu | Gly | Met | Arg | Tyr | Ser | Phe | | | |
| | | | | 85 | | | | | 90 | | | | | | |

(2) INFORMATION FOR SEQ ID NO:26758437_c3_6: -AA

Figure 307A - page 376

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 307

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| Met | Lys | Asn | Leu | Arg | His | Phe | Arg | Lys | Leu | Ile | Ala | Phe | Leu | Gly | Phe | 1 | 5 | 10 | 15 |
| Ser | Pro | Leu | Leu | Leu | Gln | Ala | Asp | Met | Thr | Thr | Phe | Phe | Asn | Ser | Ile | 20 | 25 | 30 | |
| Glu | Gln | Gln | Leu | Thr | Ser | Pro | Thr | Ala | Lys | Gly | Ile | Leu | Met | Val | Ile | 35 | 40 | 45 | |
| Phe | Leu | Gly | Leu | Ala | Ile | Phe | Ile | Trp | Lys | Asn | Leu | Asp | Arg | Trp | Lys | 50 | 55 | 60 | |
| Glu | Ile | Leu | Met | Thr | Val | Leu | Ala | Leu | Lys | Glu | Val | Pro | Met | Gln | Tyr | 65 | 70 | 75 | 80 |
| Phe | Ile | Pro | Ala | Ser | Asn | Leu | Lys | Glu | Ile | Ser | Ser | Lys | Glu | Lys | Phe | 85 | 90 | 95 | |
| Leu | Trp | Leu | Asn | Ala | Lys | Ser | Phe | Leu | Leu | Ser | Gly | Phe | Val | Pro | Phe | 100 | 105 | 110 | |
| Ile | Met | Ile | Pro | Trp | Leu | Asp | Ile | Leu | Asn | Ser | Phe | Val | Leu | Tyr | Val | 115 | 120 | 125 | |
| Cys | Phe | Leu | Leu | Ile | Phe | Ser | Ile | Ala | Glu | Phe | Phe | Asp | Glu | Asp | Ile | 130 | 135 | 140 | |

(2) INFORMATION FOR SEQ ID NO:272058_c3_26: - AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 308

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

[illegible]

(2) INFORMATION FOR SEQ ID NO:2738378_f3_6: AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP309

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Gly | Gly | Ile | Val | Ala | Asn | Met | Asn | Asp | Leu | Ser | Thr | Tyr | Met | Val |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Glu | Asn | Leu | Leu | Met | Gly | Leu | Tyr | Leu | Phe | Ser | Ser | Ala | Leu | Asp | Leu |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Gly | Val | Lys | Lys | Ala | Ile | Asn | Leu | Ala | Ser | Ser | Cys | Ala | Tyr | Pro | Lys |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Tyr | Ala | Pro | Asn | Pro | Leu | Lys | Glu | Ser | Asp | Leu | Leu | Asn | Gly | Ser | Leu |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Glu | Pro | Thr | Asn | Glu | Gly | Tyr | Ala | Leu | Pro | Asn | Ser | Leu | Unk | | |
| 65 | | | | | 70 | | | | | 75 | | | | | |

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 176 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 310

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Lys | Arg | Lys | His | Val | Ser | Lys | Lys | Val | Phe | Asn | Val | Ile | Ile | 1 | 5 | 10 | 15 |
| Leu | Phe | Val | Ala | Val | Phe | Thr | Leu | Leu | Val | Val | Ile | His | Lys | Thr | Leu | 20 | 25 | 30 | |
| Ser | Asn | Gly | Ile | His | Ile | Gln | Asn | Leu | Lys | Ile | Gly | Lys | Leu | Gly | Ile | 35 | 40 | 45 | |
| Ser | Glu | Leu | Tyr | Leu | Lys | Leu | Asn | Asn | Lys | Leu | Ser | Leu | Glu | Val | Glu | 50 | 55 | 60 | |
| Arg | Val | Asp | Leu | Ser | Ser | Phe | Phe | His | Gln | Lys | Pro | Thr | Lys | Lys | Arg | 65 | 70 | 75 | 80 |
| Leu | Glu | Val | Ser | Asp | Leu | Ile | Lys | Asn | Ile | Arg | Tyr | Gly | Ile | Trp | Ala | 85 | 90 | 95 | |
| Val | Ser | Tyr | Phe | Glu | Lys | Leu | Lys | Val | Lys | Glu | Ile | Ile | Leu | Asp | Asp | 100 | 105 | 110 | |
| Lys | Asn | Lys | Ala | Asn | Ile | Phe | Phe | Asp | Gly | Asn | Lys | Tyr | Glu | Unk | Arg | 115 | 120 | 125 | |
| Ile | Ser | Arg | Asn | Gln | Arg | Gly | Ile | Phe | Pro | Arg | Arg | Arg | Leu | Lys | Ile | 130 | 135 | 140 | |
| Ser | Ser | Leu | Lys | Ser | Ser | Ile | Cys | Phe | Leu | Lys | Met | Leu | Lys | Ser | Lys | 145 | 150 | 155 | 160 |
| Trp | Met | Ala | Thr | Pro | Thr | Ile | Unk | Pro | Lys | Pro | Gly | Lys | Trp | Arg | Ser | 165 | 170 | 175 | |

Ile

(A) LENGTH: 257 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Val Ser Cys Trp Gly Ala Ser Lys Lys Arg Phe Leu Gly Phe Cys Val
1 5 10 15

Trp Gly Arg Cys Val Tyr Ala Gly Gly Leu Met Ala Glu Gln Asp Pro
20 25 30

Lys Glu Leu Ile Phe Ser Gly Ile Thr Ile Tyr Thr Asp Lys Asn Phe
35 40 45

Thr Arg Ala Lys Lys Tyr Phe Glu Lys Ala Cys Lys Ser Asn Asp Ala
50 55 60

Asp Gly Cys Ala Ile Leu Arg Glu Val Tyr Ser Ser Gly Lys Ala Ile
65 70 75 80

Ala Arg Glu Asn Ala Arg Glu Ser Ile Glu Lys Ala Leu Glu His Thr
85 90 95

Ala Thr Ala Lys Val Cys Lys Leu Asn Asp Ala Glu Lys Cys Lys Asp
100 105 110

Leu Ala Glu Phe Tyr Phe Asn Val Asn Asp Leu Lys Asn Ala Leu Glu
115 120 125

Tyr Tyr Ser Lys Ser Cys Lys Leu Asn Asn Val Glu Gly Cys Met Leu
130 135 140

Ser Ala Thr Phe Tyr Asn Asp Met Ile Lys Gly Leu Lys Lys Asp Lys
145 150 155 160

Lys Asp Leu Glu Tyr Tyr Ser Lys Ala Cys Glu Leu Asn Asn Gly Gly
165 170 175

Gly Cys Ser Lys Leu Gly Gly Asp Tyr Phe Phe Gly Glu Gly Val Thr
180 185 190

Lys Asp Phe Lys Lys Ala Phe Glu Tyr Ser Ala Lys Ala Cys Glu Leu
195 200 205

Asn Asp Ala Lys Gly Cys Tyr Ala Leu Ala Ala Phe Tyr Asn Glu Gly
210 215 220

Lys Gly Val Ala Lys Asp Glu Lys Gln Thr Thr Glu Asn Leu Glu Lys
225 230 235 240

Ser Cys Lys Leu Gly Leu Lys Glu Ala Cys Asp Ile Leu Lys Glu Gln
245 250 255

Lys Gln

(2) INFORMATION FOR SEQ ID NO:2855006_f2_4: -AA

Figure 312A - page 382

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 312

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Val | Ala | Leu | Thr | Leu | Gly | Ala | Arg | Gly | Gly | Val | Tyr | Leu | Cys | Gly | Gly | |
| 1 | | | | 5 | | | | 10 | | | | | 15 | | | |
| Ile | Ile | Pro | Arg | Phe | Ile | Asp | Tyr | Phe | Lys | Thr | Ser | Pro | Phe | Arg | Ala | |
| | | | 20 | | | | | 25 | | | | | 30 | | | |
| Arg | Phe | Glu | Thr | Lys | Gly | Arg | Met | Gly | Ala | Phe | Leu | Ala | Ser | Ile | Pro | |
| | | 35 | | | | | 40 | | | | | 45 | | | | |
| Val | His | Val | Val | Met | Lys | Lys | Thr | Pro | Gly | Leu | Asp | Gly | Ala | Gly | Ile | |
| | 50 | | | | | 55 | | | | | 60 | | | | | |
| Ala | Leu | Glu | Asn | Tyr | Leu | Leu | His | Asp | Arg | Ile | | | | | | |
| 65 | | | | | 70 | | | | | 75 | | | | | | |

(2) INFORMATION FOR SEQ ID NO:289077_f2_24-AA

Figure 313A-page 383

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 313

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Gly | Leu | Thr | Met | Lys | Lys | Leu | Val | Phe | Ser | Met | Leu | Leu | Cys | 1 | 5 | 10 | 15 |
| Cys | Lys | Ser | Val | Phe | Ala | Glu | Gly | Glu | Thr | Pro | Leu | Ile | Val | Asn | Asp | 20 | 25 | 30 | |
| Pro | Glu | Thr | His | Val | Ser | Gln | Ala | Thr | Ile | Ile | Gly | Lys | Met | Val | Asp | 35 | 40 | 45 | |
| Ser | Ile | Lys | Arg | Tyr | Glu | Glu | Ile | Ile | Ser | Lys | Ala | Gln | Ala | Gln | Val | 50 | 55 | 60 | |
| Asn | Gln | Leu | Gln | Lys | Val | Asn | Asn | Met | Ile | Asn | Thr | Thr | Asn | Ser | Leu | 65 | 70 | 75 | 80 |
| Ile | Ser | Ser | Ser | Ala | Ile | Thr | Leu | Ala | Asn | Pro | Met | Gln | Val | Leu | Gln | 85 | 90 | 95 | |
| Asn | Ala | Gln | Tyr | Gln | Ile | Glu | Ser | Ile | Arg | Tyr | Asn | Tyr | Glu | Asn | Leu | 100 | 105 | 110 | |
| Lys | Gln | Ser | Ile | Glu | Asn | Trp | Asn | Ala | Gln | Asn | Leu | Leu | Arg | Asn | Lys | 115 | 120 | 125 | |
| Tyr | Leu | Gln | Gln | Gln | Cys | Pro | Trp | Leu | Asn | Val | Asn | Ala | Leu | Thr | Asn | 130 | 135 | 140 | |
| Asn | Lys | Ile | Val | Asn | Leu | Lys | Asp | Leu | Asn | Asn | Leu | Ile | Thr | Lys | Asn | 145 | 150 | 155 | 160 |
| Gly | Glu | Gln | Thr | Gln | Thr | Ala | Arg | Asp | Val | Gln | Asn | Leu | Ile | Gln | Ser | 165 | 170 | 175 | |
| Ile | Ser | Gly | Ser | Gly | Tyr | Gly | Asn | Met | Gln | Ser | Leu | Ala | Gly | Glu | Leu | 180 | 185 | 190 | |
| Ser | Gly | Arg | Ala | Trp | Gly | Glu | Met | Leu | Cys | Lys | Met | Val | Asn | Asp | Ser | 195 | 200 | 205 | |
| Asn | Tyr | Glu | Ser | Glu | Gln | Ala | Leu | Leu | Ala | Thr | Gly | Asn | Asn | Pro | Glu | 210 | 215 | 220 | |
| Glu | Gln | Lys | Arg | Arg | Phe | Leu | Leu | Arg | Val | Lys | Lys | Lys | Val | Asn | Asp | 225 | 230 | 235 | 240 |

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Lys | Gln | Leu | Lys | Asp | Lys | Leu | Asp | Pro | Phe | Leu | Lys | Arg | Leu | Asp | 245 | 250 | 255 | |
| Val | Leu | Gln | Thr | Glu | Phe | Gly | Val | Thr | Asp | Pro | Thr | Ala | Asn | His | Asn | 260 | 265 | 270 | |
| Lys | Gln | Gly | Ile | His | Tyr | Cys | Thr | Glu | Asn | Lys | Glu | Thr | Gly | Lys | Cys | 275 | 280 | 285 | |
| Asp | Pro | Ile | Lys | Asn | Val | Phe | Arg | Thr | Thr | Arg | Leu | Asp | Asn | Glu | Leu | 290 | 295 | 300 | |
| Glu | Gln | Glu | Ile | Gln | Thr | Leu | Thr | Leu | Asp | Leu | Ile | Lys | Ala | Ser | Asn | 305 | 310 | 315 | 320 |
| Lys | Asp | Ala | Gln | Ser | Gln | Ala | Tyr | Ala | Asn | Phe | Asn | Gln | Arg | Ile | Lys | 325 | 330 | 335 | |
| Leu | Leu | Thr | Leu | Lys | Tyr | Leu | Lys | Glu | Ile | Thr | Asn | Gln | Met | Leu | Phe | 340 | 345 | 350 | |
| Leu | Asn | Gln | Thr | Met | Ala | Met | Gln | Ser | Glu | Ile | Met | Thr | Asp | Asp | Tyr | 355 | 360 | 365 | |
| Phe | Arg | Gln | Asn | Asn | Asp | Gly | Phe | Gly | Glu | Lys | Glu | Asn | His | Ile | Asp | 370 | 375 | 380 | |
| Glu | Gln | Leu | Thr | Gln | Lys | Arg | Ile | Asn | Glu | Arg | Glu | Arg | Ala | Arg | Ile | 385 | 390 | 395 | 400 |
| Tyr | Phe | Gln | Asn | Pro | Asn | Val | Lys | Phe | Asp | Gln | Phe | Gly | Phe | Pro | Ile | 405 | 410 | 415 | |
| Phe | Ser | Ile | Trp | Asp | | | | | | | | | | | | 420 | | | |

A A

Ile

(2) INFORMATION FOR SEQ ID NO:2915903_f1_2: -AA

Figure 315A - page 386

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 315

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| Met | Gln | Leu | Ser | Pro | Leu | Gln | Ser | Ala | Leu | Leu | Tyr | Phe | Arg | Tyr | Phe | 1 | 5 | 10 | 15 |
| Ile | Tyr | Pro | Glu | Lys | Lys | Thr | Arg | Ser | Phe | Asp | Leu | Ser | Asp | Leu | Ile | 20 | 25 | 30 | |
| Phe | Ile | Val | Met | Val | Phe | Leu | Val | Leu | Ala | Leu | Gly | Leu | Leu | Met | Ser | 35 | 40 | 45 | |
| Glu | Glu | Ile | Ser | Ile | Ser | Tyr | Asn | Glu | Ala | Lys | Asp | Phe | Phe | Tyr | Ser | 50 | 55 | 60 | |
| Asp | Ala | Trp | Phe | Val | Lys | Ile | Ala | Gln | Lys | Ser | Val | Ala | Ile | Leu | Arg | 65 | 70 | 75 | 80 |
| Pro | Lys | Arg | Phe | Gly | Phe | Lys | Ile | Ala | Phe | Phe | Asp | Arg | Ser | Arg | His | 85 | 90 | 95 | |
| Gln | His | Val | Phe | Ile | Leu | Pro | His | Arg | Ala | Lys | Asp | Phe | Lys | Lys | Ala | 100 | 105 | 110 | |

(2) INFORMATION FOR SEQ ID NO:291700_f3_4: -AA

Figure 316A -page 387

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 206 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 316

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: weak vacA similarity

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Gly | Cys | Unk | Arg | Met | Lys | Gln | Thr | Phe | Trp | Unk | Leu | Ser | Trp | Gly | 1 | 5 | 10 | 15 |
| Glu | Lys | Ser | Gln | Lys | Val | Cys | Val | His | Arg | Pro | Trp | Tyr | Ala | Ile | Trp | 20 | 25 | 30 | |
| Ser | Cys | Asp | Lys | Trp | Glu | Glu | Lys | Thr | Gln | Gln | Phe | Thr | Gly | Asn | Gln | 35 | 40 | 45 | |
| Leu | Ile | Thr | Lys | Thr | Trp | Ala | Gly | Gly | Asn | Ala | Ala | Asn | Tyr | Tyr | His | 50 | 55 | 60 | |
| Ser | Gln | Asn | Asn | Gln | Asp | Ile | Thr | Ala | Asn | Leu | Lys | Asn | Asp | Asn | Gly | 65 | 70 | 75 | 80 |
| Thr | Tyr | Phe | Leu | Ser | Gly | Leu | Tyr | Asn | Tyr | Thr | Gly | Gly | Glu | Tyr | Asn | 85 | 90 | 95 | |
| Gly | Gly | Asn | Leu | Asp | Ile | Glu | Leu | Gly | Ser | Asn | Ala | Thr | Phe | Asn | Leu | 100 | 105 | 110 | |
| Gly | Ala | Ser | Ser | Gly | Asn | Ser | Phe | Thr | Ser | Trp | Tyr | Pro | Asn | Gly | His | 115 | 120 | 125 | |
| Thr | Asp | Val | Thr | Phe | Ser | Ala | Gly | Thr | Ile | Asn | Val | Asn | Asn | Ser | Val | 130 | 135 | 140 | |
| Glu | Val | Gly | Asn | Arg | Val | Gly | Ser | Gly | Ala | Gly | Thr | His | Thr | Gly | Thr | 145 | 150 | 155 | 160 |
| Ala | Thr | Leu | Asn | Leu | Asn | Ala | Asn | Lys | Val | Thr | Ile | Asn | Ser | Asn | Ile | 165 | 170 | 175 | |
| Ser | Ala | Tyr | Lys | Thr | Ser | Gln | Val | Asn | Val | Gly | Asn | Ala | Asn | Ser | Val | 180 | 185 | 190 | |
| Ile | Thr | Ile | Asn | Ser | Val | Ser | Leu | Asn | Gly | Glu | Thr | Cys | Ser | Leu | 195 | 200 | 205 | | |

(2) INFORMATION FOR SEQ ID NO:29298130_c2_16: - AA

Figure 317A - page 388

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 317

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: FLAGELLAR BASAL-BODY ROD PROTEIN

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Arg | Ser | Leu | Tyr | Ser | Ala | Thr | Ser | Gly | Met | Leu | Ala | Gln | Gln | 1 | 5 | 10 | 15 |
| Thr | His | Ile | Asp | Thr | Thr | Ser | Asn | Asn | Ile | Ala | Asn | Val | Asn | Thr | Thr | 20 | 25 | 30 | |
| Gly | Phe | Lys | Lys | Ser | Arg | Ala | Asp | Phe | Asn | Asp | Leu | Phe | Tyr | Gln | Ala | 35 | 40 | 45 | |
| Met | Gln | Tyr | Ala | Gly | Thr | Asn | Thr | Ser | Asn | Thr | Thr | Leu | Ser | Pro | Asp | 50 | 55 | 60 | |
| Gly | Met | Glu | Val | Gly | Leu | Gly | Val | Arg | Pro | Ser | Ala | Ile | Thr | Lys | Met | 65 | 70 | 75 | 80 |
| Phe | Ser | Gln | Gly | Ser | Pro | Lys | Glu | Thr | Glu | Asn | Asn | Leu | Asp | Ile | Ala | 85 | 90 | 95 | |
| Ile | Thr | Gly | Lys | Gly | Phe | Phe | Gln | Val | Gln | Leu | Pro | Asp | Gly | Thr | Thr | 100 | 105 | 110 | |
| Ala | Tyr | Thr | Arg | Ser | Gly | Asn | Phe | Lys | Leu | Asp | Glu | Gln | Gly | Asn | Leu | 115 | 120 | 125 | |
| Val | Thr | Ser | Glu | Gly | Tyr | Leu | Leu | Ile | Pro | Gln | Ile | Thr | Leu | Pro | Glu | 130 | 135 | 140 | |
| Asp | Thr | Thr | Gln | Val | Asn | Ile | Gly | Val | Asp | Gly | Thr | Val | Ser | Val | Thr | 145 | 150 | 155 | 160 |
| Gln | Gly | Leu | Gln | Thr | Thr | Ser | Asn | Val | Ile | Gly | Gln | Ile | Thr | Leu | Ala | 165 | 170 | 175 | |
| Asn | Phe | Val | Asn | Pro | Ala | Gly | Leu | His | Ser | Met | Gly | Asp | Asn | Leu | Phe | 180 | 185 | 190 | |
| Ser | Ile | Thr | Asn | Ala | Ser | Gly | Asp | Ala | Ile | Val | Gly | Asn | Pro | Asp | Ser | 195 | 200 | 205 | |
| Gln | Gly | Leu | Gly | Lys | Leu | Arg | Gln | Gly | Phe | Leu | Glu | Leu | Ser | Asn | Val | 210 | 215 | 220 | |
| Arg | Leu | Val | Glu | Glu | Met | Thr | Asp | Leu | | | | | | | | 225 | 230 | | |

(2) INFORMATION FOR SEQ ID NO:29302003_f1_1:-AA

389
Figure 318A - page 389

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 77 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 318

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Tyr | Ala | Leu | Met | Val | Ala | Phe | Phe | Ala | Tyr | Met | Ser | Tyr | Cys | Leu |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Gly | Tyr | Gln | Phe | Ser | Lys | Phe | Val | Ser | Lys | Asn | Asn | Ile | Ser | Ser | Leu |
| | | | 20 | | | | | | 25 | | | | 30 | | |
| Ser | Ser | Leu | Leu | Ser | Ser | Cys | Val | Arg | Val | Val | Ser | Val | Leu | Ile | Leu |
| | | | 35 | | | | 40 | | | | | 45 | | | |
| Ser | Leu | Ser | Ser | Leu | Glu | Leu | Arg | Tyr | Phe | Ser | Pro | Leu | Thr | Ile | Ile |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Thr | Met | His | Phe | Ala | Leu | Thr | Leu | Ile | Ile | Leu | Phe | Phe | Phe | | |
| 65 | | | | | 70 | | | | | 75 | | | | | |

(2) INFORMATION FOR SEQ ID NO:29386577_f3_10: -AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 319

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Arg | Ser | Trp | Met | Lys | Lys | Lys | Tyr | Phe | Thr | Leu | Leu | Leu | Gln | Ser | 1 | 5 | 10 | 15 |
| Ser | Val | Val | Leu | Ala | Val | Phe | Ile | Gly | Cys | Ser | Ser | Thr | Arg | Asn | His | 20 | 25 | 30 | |
| Thr | Phe | Ser | Ala | Leu | Ser | Asn | Gln | Glu | Asn | Thr | Asp | Asp | Lys | Leu | Pro | 35 | 40 | 45 | |
| Val | Val | His | Ser | Ile | Lys | Thr | Ile | Asn | Asp | Val | Ser | Ser | Val | Gly | Phe | 50 | 55 | 60 | |
| Glu | Trp | Ser | Lys | Val | Ala | Asp | Thr | Tyr | Asp | Ile | Asp | Gly | Phe | Val | Leu | 65 | 70 | 75 | 80 |
| Tyr | Arg | Leu | Lys | Lys | Asp | Ser | Lys | Leu | Lys | Arg | Ile | Ala | Thr | Ile | Lys | 85 | 90 | 95 | |
| Asn | Pro | Tyr | Ala | Thr | His | Tyr | Tyr | Asp | Glu | Gly | Leu | Glu | Thr | Glu | Ser | 100 | 105 | 110 | |
| Ser | Tyr | Thr | Tyr | Gln | Leu | Ala | Thr | Tyr | Lys | Gly | Asp | Lys | Ile | Ser | Lys | 115 | 120 | 125 | |
| Leu | Ser | Glu | Pro | Ile | Leu | Val | Lys | Thr | Ser | Phe | Ile | Asn | Pro | Val | Glu | 130 | 135 | 140 | |
| Ser | Val | Phe | Ala | Ser | Leu | Glu | Tyr | Pro | Lys | Ser | Val | Lys | Val | Phe | Trp | 145 | 150 | 155 | 160 |
| Ser | Pro | His | Pro | Asn | Pro | Ser | Val | Ser | Lys | Tyr | Ile | Ile | Gln | Arg | Gln | 165 | 170 | 175 | |
| Asn | Lys | Asp | Gly | Lys | Phe | Leu | Asn | Val | Gly | Ala | Val | Lys | Asn | Arg | Leu | 180 | 185 | 190 | |
| Phe | Val | Glu | Phe | Phe | Asp | Lys | Asp | Leu | Glu | Asp | Gly | Gln | Lys | Tyr | Arg | 195 | 200 | 205 | |
| Tyr | Gln | Ile | Ile | Ala | Glu | Asn | Phe | Met | Gly | Asp | Lys | Ser | Arg | Pro | Ser | 210 | 215 | 220 | |
| Val | Ile | Val | Glu | Gly | Lys | Thr | Lys | Asp | Leu | Pro | Lys | Glu | Ile | Ala | Asn | 225 | 230 | 235 | 240 |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Val | Arg | Val | Ser | Gln | Asn | Leu | Thr | Arg | Gln | Ile | Glu | Leu | Ser | Trp | Asp | |
| | | | | 245 | | | | | 250 | | | | | 255 | | |
| Lys | Ser | Pro | Glu | Glu | Asp | Val | Ile | Ala | Tyr | Arg | Ile | Tyr | Ala | Ser | Asn | |
| | | | 260 | | | | | 265 | | | | | 270 | | | |
| Asn | Arg | Asn | Asp | Lys | Tyr | Lys | Phe | Ile | Ala | Gln | Thr | Thr | Asn | Thr | Ser | |
| | | 275 | | | | | 280 | | | | | 285 | | | | |
| Tyr | Val | Asp | Lys | Ile | Glu | Lys | Asp | Asn | Leu | Thr | Arg | Tyr | Tyr | Lys | Val | |
| | 290 | | | | | 295 | | | | | 300 | | | | | |
| Val | Ala | Val | Asp | Lys | Thr | His | Leu | Glu | Gly | Ala | Leu | Pro | Lys | Glu | Pro | |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 | |
| Ala | Met | Gly | Glu | Thr | Ser | Asp | Arg | Pro | Glu | Ala | Pro | Ile | Ile | Thr | Lys | |
| | | | | 325 | | | | | 330 | | | | | 335 | | |
| Gly | Thr | Ile | Gln | Asp | Ser | Ser | Ala | Leu | Ile | Gln | Trp | Glu | Asn | Asn | Pro | |
| | | | 340 | | | | | 345 | | | | | 350 | | | |
| Ser | Pro | Lys | Ile | Ala | Thr | Tyr | Ala | Val | Tyr | Arg | Phe | Glu | Ala | Asn | Ser | |
| | | 355 | | | | | 360 | | | | | 365 | | | | |
| Lys | Thr | Pro | Leu | Arg | Phe | Gly | Asn | Ile | Thr | Gln | Asn | Gln | Phe | Val | Asp | |
| | 370 | | | | | 375 | | | | | 380 | | | | | |
| Lys | Asp | Met | Lys | Val | Gly | Val | Ala | Tyr | Arg | Tyr | Gln | Val | Val | Ser | Val | |
| 385 | | | | | 390 | | | | | 395 | | | | | 400 | |

- AA

(D) TOPOLOGY: linear

HPP 320

(A) ORGANISM: *Helicobacter pylori*

| | | | | | | | | | | | | | | | |
|-----------|-----------|-----------|----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| Met 1 | Gln | Asn | Gly 5 | Tyr | Tyr | Ala | Ala | Thr | Gly 10 | Ala | Met | Ala | Thr | Gln 15 | Phe |
| Asn | Arg | Leu 20 | Asp | Leu | Thr | Ser | Asn | Asn 25 | Leu | Ala | Asn | Leu | Asn 30 | Thr | Asn |
| Gly | Phe | Lys 35 | Arg | Asp | Asp | Ala | Ile 40 | Thr | Gly | Asp | Phe | Leu 45 | Arg | Leu | Tyr |
| Gln | Glu 50 | Tyr | Arg | Glu | Gln | Leu 55 | Pro | Leu | Glu | Asp | Gln 60 | Thr | Lys | Ala | Ser |
| Ala 65 | Lys | Tyr | Leu | Asn | Arg 70 | Thr | Ser | Ile | Val | Cys 75 | Leu | Phe | Tyr | Gln | Lys 80 |
| Ser | Ile | His | Arg | Lys 85 | Leu | Gly | Ser | Val | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:29458178_c3_41:- AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP321

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| Met | Leu | Pro | Thr | Lys | Thr | Arg | Ile | Arg | Asp | Pro | Asn | Lys | Gln | Glu | Leu | 1 | 5 | 10 | 15 |
| Thr | Gln | Pro | Lys | Ile | Lys | Gly | Leu | Ser | Met | Gly | Lys | Ile | Leu | Ala | Ser | 20 | 25 | 30 | |
| Leu | Leu | Gly | Gly | Gly | Thr | Asn | Leu | Phe | Thr | Gly | Leu | Ser | Ser | Asp | Leu | 35 | 40 | 45 | |
| Phe | Ser | Met | Ile | Leu | Asn | Phe | Leu | Phe | Phe | Leu | Met | Leu | Met | Met | Gly | 50 | 55 | 60 | |
| Leu | Asn | Glu | Ala | Leu | Gly | Lys | Lys | Phe | Asn | Leu | Pro | Met | Asp | Asn | Ile | 65 | 70 | 75 | 80 |
| Lys | Asn | Phe | Met | Ala | Glu | Val | Leu | Lys | Asn | Gly | Phe | Asp | Ser | Ile | Lys | 85 | 90 | 95 | |
| Asn | Met | Gly | Ser | Ala | Leu | Val | Gly | Asn | Gly | Phe | Gly | Ser | Ser | Lys | Ser | 100 | 105 | 110 | |
| Asp | Lys | Thr | Thr | Asn | Lys | Met | Ser | Val | Pro | Gln | Val | Arg | Leu | 115 | 120 | 125 | | | |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 194 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 322

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: IRON(III) DICITRATE TRANSPORT PROTEIN FECA PRECUR

Val Gly Ala Met Pro Thr Ile Gln Ile Arg Asp Phe Gly Ala Gly Gly
1 5 10 15

Ser Gly His Ser Asp Ala Thr Leu Met Leu Val Asn Gly Ile Pro Val
20 25 30

Tyr Met Ala Pro Tyr Ala His Ile Glu Leu Asp Ile Phe Pro Val Thr
35 40 45

Phe Gln Ala Ile Asp Arg Ile Asp Val Ile Lys Gly Gly Gly Ser Val
50 55 60

Gln Tyr Gly Pro Asn Thr Tyr Gly Gly Ile Val Asn Ile Ile Thr Lys
65 70 75 80

Pro Ile Pro Asn Gln Trp Glu Asn Gln Ala Ala Glu Arg Asn Thr Tyr
85 90 95

Trp Ala Lys Ala Arg Asn Ala Gly Phe Ala Ala Pro His Asp Lys Thr
100 105 110

Gly Asp Pro Ser Phe Ile Lys Ser Leu Gly Asn Asn Leu Leu Tyr Asn
115 120 125

Thr Tyr Val Arg Ser Gly Gly Met Ile Asn Lys His Val Gly Ile Gln
130 135 140

Arg Lys Leu Thr Gly Leu Glu Ala Lys Ala Leu Gly Thr Ile Ala Pro
145 150 155 160

Leu Val Phe Gln Thr Ile Gly Trp Met Gly Ser Met Thr Ser Met Lys
165 170 175

Ala Met Gly Leu Lys Pro Ile Thr Asn Thr Thr Ile Leu Ala Ile Asp
180 185 190

Gln Pro Gly
195

(2) INFORMATION FOR SEQ ID NO:29500075_f3_2: -AA

Figure 323A - page 395

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 323

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: OXYGEN-INSENSITIVE NAD(P)H NITROREDUCTASE

Met Ala Asn Met Met Met Ala Ala Ala Met Leu Gly Ile Asp Ser Cys
1 5 10 15

Pro Ile Glu Gly Tyr Asp Gln Glu Lys Val Glu Ala Tyr Leu Glu Glu
20 25 30

Lys Gly Tyr Leu Asn Thr Ala Glu Phe Gly Val Ser Val Met Ala Ser
35 40 45

Phe Gly Tyr Arg Asn Gln Glu Ile Thr Pro Lys Thr Arg Trp Lys Thr
50 55 60

Glu Val Ile Tyr Glu Val Ile Glu
65 70

(2) INFORMATION FOR SEQ ID NO:29531590_c3_20: -AA

396
Figure 324A-page 396

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 324

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Gly | Leu | Val | Leu | Met | Val | Leu | Leu | Ala | Ser | Tyr | Glu | Ser | Phe |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Val | Ser | Lys | Leu | Asp | Lys | Val | Asp | Ala | Ser | Glu | Ile | Thr | Trp | Leu | Lys |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| His | Thr | Asp | Phe | Asn | Ala | Leu | Lys | Leu | Lys | Val | Ser | Leu | Ser | Ile | Val |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Ala | Ile | Ser | Ala | Ile | Phe | Leu | Leu | Lys | Arg | Tyr | Met | Ser | Leu | Glu | Asp |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Val | Leu | Ser | Ser | Ile | Pro | Lys | Asp | Thr | Pro | Leu | Ser | His | Asn | Pro | Ile |
| 65 | | | | 70 | | | | | 75 | | | | | 80 | |
| Phe | Trp | Gln | Val | Val | Ile | His | Leu | Val | Phe | Val | Cys | Ser | Ala | Leu | Leu |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| Thr | Ala | Val | Thr | Asn | Asn | Ile | Ala | Phe | Ser | Gln | Lys | Glu | Arg | His | |
| | | | 100 | | | | | 105 | | | | | 110 | | |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 325

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| Met | Ile | Thr | Ile | Val | Ile | Ala | Lys | Ala | Gly | Asn | Ile | Val | Lys | Unk | Asp | 1 | 5 | 10 | 15 |
| Ile | Phe | Thr | His | Ile | Ser | Asp | Ile | Lys | Met | Gly | Leu | Ile | Lys | Gly | Gly | 20 | 25 | 30 | |
| Gln | Trp | Gly | Val | Ile | Gly | Leu | Gly | Asn | Ile | Gly | Lys | Arg | Val | Ala | Lys | 35 | 40 | 45 | |
| Leu | Ala | Gln | Ala | Phe | Gly | Ala | Lys | Val | Val | Tyr | Phe | Ser | Pro | Lys | Asp | 50 | 55 | 60 | |
| Lys | Lys | Glu | Glu | Tyr | Glu | Arg | Leu | Ser | Leu | Glu | Glu | Leu | Leu | Lys | Thr | 65 | 70 | 75 | 80 |
| Ser | Gly | Ile | Ile | Ser | Ile | His | Ala | Pro | Leu | Asn | Glu | Ser | Thr | Arg | Asp | 85 | 90 | 95 | |
| Leu | Ile | Ala | Leu | Lys | Glu | Leu | Gln | Ser | Leu | Lys | Asp | Gly | Ala | Ile | Leu | 100 | 105 | 110 | |
| Ile | Asn | Val | Gly | Arg | Gly | Gly | Ile | Val | Asn | Glu | Lys | Unk | Leu | Ala | Unk | 115 | 120 | 125 | |
| Unk | Leu | Glu | Thr | Thr | Asp | Leu | Tyr | Tyr | Ala | Ser | Asp | Val | Phe | 130 | 135 | 140 | | | |

(2) INFORMATION FOR SEQ ID NO:29843937_f2_4: -AA

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 62 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 326

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: vacuolating cytotoxin of Hpylori

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Asn | Phe | Asn | Ala | Lys | Asn | Ile | Ser | Ile | Asp | Asn | Leu | Val | Glu | Ile |
| 1 | | | | 5 | | | | 10 | | | | | | 15 | |
| Asn | Asn | Arg | Val | Gly | Ser | Gly | Ala | Gly | Arg | Lys | Ala | Ser | Ser | Thr | Val |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Leu | Thr | Leu | Gln | Ala | Ser | Glu | Gly | Ile | Thr | Unk | Ser | Lys | Asn | Ala | Glu |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Ile | Ser | Leu | Tyr | Asp | Gly | Ala | Thr | Unk | Ile | Trp | Leu | Gln | Thr | Gly | |
| 50 | | | | | | 55 | | | | | 60 | | | | |

(2) INFORMATION FOR SEQ ID NO:29844512_c1_14: -AA

Figure 327A - page 399³⁹⁹

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 327

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Arg | Thr | Leu | Ile | Leu | Ser | Leu | Leu | Lys | His | Ala | Ile | Leu | Met | Gly |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Met | Leu | Leu | Lys | Glu | Cys | Gln | Glu | Lys | Leu | Lys | Arg | Ser | Leu | Asn | Leu |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Ser | Ala | Asn | His | Cys | Val | Leu | Ser | Ala | Gly | Tyr | Gly | Ala | Ser | Ser | Ala |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Ile | Lys | Lys | Phe | Gln | Glu | Ile | Leu | Gly | Val | Cys | Ile | Pro | Ser | Lys | Thr |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Lys | Lys | Asn | Leu | Glu | Pro | Tyr | Leu | Lys | Asp | Met | Ala | Leu | Lys | Arg | Val |
| 65 | | | | | 70 | | | | 75 | | | | | 80 | |
| Ile | Val | Gly | Pro | Tyr | Glu | His | His | Ser | Asn | Glu | Val | Ser | Trp | Arg | Glu |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| Gly | Leu | Cys | Glu | Val | Val | Arg | Ile | Pro | Leu | Asn | Glu | His | Gly | Leu | Leu |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Asp | Leu | Glu | Ile | Leu | Glu | Gln | Thr | Leu | Lys | Lys | Thr | Pro | Asn | Ser | Leu |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| Val | Ser | Val | Ser | Ala | Ala | Ser | Asn | Val | Thr | Gly | Ile | Leu | Thr | Pro | Leu |
| | 130 | | | | | 135 | | | | | 140 | | | | |
| Lys | Glu | Val | Ser | Ser | Leu | Cys | Lys | Glu | Tyr | Arg | Ala | Ile | Leu | Ala | Leu |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 |
| Asp | Leu | Ala | Asn | Phe | Ser | Ala | His | Ala | Asn | Pro | Lys | Asp | Cys | Glu | Tyr |
| | | | 165 | | | | | | 170 | | | | | 175 | |
| Gln | Thr | Gly | Phe | Tyr | Ala | Pro | His | Lys | Leu | Leu | Gly | Gly | Val | Gly | Gly |
| | | | 180 | | | | | 185 | | | | | 190 | | |
| Cys | Gly | Leu | Leu | Gly | Ile | Ser | Lys | Asp | Leu | Ile | Asp | Thr | Gln | Ile | Pro |
| | | 195 | | | | | 200 | | | | 205 | | | | |
| Thr | Ser | Phe | Ser | Ala | Gly | Gly | Val | Ile | Lys | Tyr | Ala | Asn | Arg | Thr | Arg |
| | 210 | | | | | 215 | | | | | 220 | | | | |
| His | Glu | Phe | Ile | Asp | Glu | Leu | Pro | Leu | Arg | Glu | Glu | Phe | Gly | Thr | Pro |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 |

Figure 327A - page 400

Gly Leu Leu Gln Phe Tyr Arg Ser Ala Leu Ala Tyr Gln Leu Arg Asp
245 250 255

Glu Cys Gly Leu Asp Phe Ile His Lys Lys Glu Asn Asn Leu Leu Arg
260 265 270

Val Leu Val Tyr Gly Leu Lys Asp Leu Pro Ala Ile Asn Ile Tyr Gly
275 280 285

Asn Leu Thr Ala Ser Arg Val Gly Val Val Thr Phe Asn Ile Gly Gly
290 295 300

Ile Ser Pro Tyr Asp Leu
305 310

(2) INFORMATION FOR SEQ ID NO:30078126_f3_7: -AA

Figure 328A- page 401

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 328

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: glycerolphosphate auxotrophy in plsB background

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| Val | Asp | Val | Val | Val | Cys | Asp | Gly | Phe | Met | Gly | Asn | Val | Val | Leu | Lys | 1 | 5 | 10 | 15 |
| Thr | Thr | Glu | Gly | Val | Ala | Ser | Ala | Ile | Gly | Ser | Ile | Phe | Lys | Asp | Glu | 20 | 25 | 30 | |
| Ile | Lys | Ser | Ser | Phe | Lys | Ser | Lys | Met | Gly | Ala | Leu | Met | Leu | Lys | Asn | 35 | 40 | 45 | |
| Ala | Phe | Gly | Ile | Leu | Lys | Gln | Lys | Thr | Asp | Tyr | Ala | Glu | Tyr | Gly | Gly | 50 | 55 | 60 | |
| Ala | Pro | Leu | Leu | Gly | Val | Asn | Lys | Ser | Val | Ile | Ile | Ser | His | Gly | Lys | 65 | 70 | 75 | 80 |
| Ser | Asn | Ala | Arg | Ala | Val | Glu | Cys | Ala | Ile | Tyr | Gln | Ala | Ile | Ser | Ala | 85 | 90 | 95 | |
| Val | Glu | Ser | Gln | Val | Cys | Leu | Arg | Ile | Thr | Gln | Ala | Phe | Glu | Ser | Leu | 100 | 105 | 110 | |
| Lys | Ser | Gln | Ser | Phe | Glu | Ser | Gln | Ser | Asp | Gln | Gln | Asp | Ala | 115 | 120 | 125 | | | |

(2) INFORMATION FOR SEQ ID NO:30081291_f3_2: - AA

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 68 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP329

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Met Gln Pro Asp Tyr Val Leu Val Ile Unk Pro Gly Leu Val Phe Ile
1 5 10 15

Glu Asn Ile Phe Ala Asn Glu Lys Glu Unk Thr Unk Tyr Ile Ile Thr
20 25 30

Ser Tyr Leu Asn Lys Glu Glu Leu Phe Glu Lys Lys Pro Glu Leu Lys
35 40 45

Thr Arg Lys Val Phe Gly Gly Leu Phe Lys Asn Leu Tyr Gly Asn Leu
50 55 60

Lys Thr Pro Tyr Pro
65

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 168 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 330

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|-----------|------------|------------|------------|------------|-----------|------------|
| Val 1 | Ala | Cys | Asn | Thr 5 | Ala | Ser | Ala | Leu | Ala 10 | Leu | Glu | Glu | Met | Gln 15 | Lys |
| Tyr | Ser | Lys | Ile 20 | Pro | Ile | Val | Gly | Val 25 | Ile | Glu | Pro | Ser | Ile 30 | Leu | Ala |
| Ile | Lys | Arg 35 | Gln | Val | Glu | Asp | Lys 40 | Asn | Ala | Pro | Ile | Leu 45 | Val | Leu | Gly |
| Thr | Lys 50 | Ala | Thr | Ile | Gln | Ser 55 | Asn | Ala | Tyr | Asp | Asn 60 | Ala | Leu | Lys | Gln |
| Gln 65 | Gly | Tyr | Leu | Asn | Ile 70 | Ser | His | Leu | Ala | Thr 75 | Ser | Leu | Phe | Val | Pro 80 |
| Leu | Ile | Glu | Glu | Ser 85 | Ile | Leu | Glu | Gly | Glu 90 | Leu | Leu | Glu | Thr | Cys 95 | Met |
| His | Tyr | Tyr | Phe 100 | Thr | Pro | Leu | Glu | Ile 105 | Leu | Pro | Glu | Val | Ile 110 | Ile | Leu |
| Gly | Cys | Thr 115 | His | Phe | Pro | Leu | Ile 120 | Ala | Gln | Lys | Ile | Glu 125 | Gly | Tyr | Phe |
| Met | Gly 130 | His | Phe | Ala | Leu | Pro 135 | Thr | Pro | Pro | Leu | Leu 140 | Ile | His | Ser | Gly |
| Asp 145 | Ala | Ile | Val | Glu | Tyr 150 | Leu | Gln | Gln | Lys | Tyr 155 | Ala | Leu | Lys | Asn | Asn 160 |
| Ala | Cys | Thr | Phe | Pro 165 | Lys | Val | Glu | Phe | | | | | | | |

(i) SEQUENCE CHARACTERISTICS:

(Å) LENGTH: 103 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP331

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | |
|-----------|-----------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----|
| Met 1 | Arg | Lys | Glu 5 | Lys | Ile | Met | Thr | Asn 10 | Phe | Glu | Lys | Ile | Ile | Ala 15 | Gln |
| Asn | Arg | Leu 20 | Lys | Thr | Asn | Ala | Val 25 | Leu | Thr | Thr | Tyr | Cys 30 | Ala | Ile | Phe |
| Ala | Phe 35 | Ile | Gly | Leu | Leu | Val 40 | Asp | Ala | Ile | Arg | Ile 45 | Asn | Ala | Asn | Asp |
| Leu 50 | Gly | Ile | Ala | Leu | Phe 55 | Lys | Leu | Met | Thr | Phe 60 | Gln | Ile | Phe | Pro | Thr |
| Ile 65 | Thr | Ile | Val | Met 70 | Phe | Val | Val | Ala | Phe 75 | Val | Ile | Thr | Val | Cys 80 | Ile |
| Gln | Asn | Phe | Ser 85 | Ser | Ile | Met | Leu | Ser 90 | Gly | Asp | Glu | Tyr | Lys 95 | Leu | Ile |
| Asp | Pro | Ser 100 | Thr | Gly | Phe | Lys | Leu | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:30100332 c1 17: -AA

405
Figure 332A - page 405

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 88 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HP 332

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: PERIPLASMIC DIPEPTIDE TRANSPORT PROTEIN PRECURSOR

Met Asp Met Ser His Ile Ile Lys Ser Ile Glu Ala Leu Asp Asp Tyr
1 5 10 15

Thr Ile Arg Phe Thr Leu Asn Gly Pro Glu Ala Pro Phe Leu Ala Asn
20 25 30

Leu Gly Met Asp Phe Leu Ser Ile Leu Ser Lys Asp Tyr Ala Asp Tyr
35 40 45

Leu Ala Gln Asn Asn Lys Lys Asp Glu Leu Ala Lys Asn Leu Leu Gly
50 55 60

Gln Gly Leu Ser Asn Ser Phe Cys Gly Ile Lys Asp Glu Lys Ile Ile
65 70 75 80

Leu Val Lys Asn Gln Asp Tyr Trp Glu
85

(2) INFORMATION FOR SEQ ID NO:30283516_f1_2: -AA

Figure 333A - page 406

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 187 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 333

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|
| Met | Arg | Lys | Ile | Phe | Ser | Tyr | Ile | Ser | Lys | Val | Leu | Leu | Phe | Ile | Gly | | | |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | | | | |
| Val | Val | Tyr | Ala | Glu | Pro | Asp | Ser | Lys | Val | Glu | Ala | Leu | Glu | Gly | Arg | | | |
| | | | 20 | | | | | 25 | | | | | 30 | | | | | |
| Lys | Gln | Glu | Ser | Ser | Leu | Asp | Lys | Lys | Ile | Arg | Gln | Glu | Leu | Lys | Ser | | | |
| | | | 35 | | | | 40 | | | | | 45 | | | | | | |
| Lys | Glu | Leu | Lys | Asn | Lys | Glu | Leu | Lys | Asn | Lys | Asp | Leu | Lys | Asn | Lys | | | |
| | 50 | | | | | 55 | | | | | 60 | | | | | | | |
| Glu | Glu | Lys | Lys | Glu | Thr | Lys | Ala | Lys | Arg | Lys | Pro | Arg | Ala | Glu | Val | | | |
| 65 | | | | | 70 | | | | 75 | | | | | 80 | | | | |
| His | His | Gly | Asp | Ala | Lys | Asn | Pro | Thr | Pro | Lys | Ile | Thr | Pro | Pro | Lys | | | |
| | | | | 85 | | | | | 90 | | | | | 95 | | | | |
| Ile | Lys | Gly | Ser | Ser | Lys | Gly | Val | Gln | Asn | Gln | Gly | Val | Gln | Asn | Asn | | | |
| | | | 100 | | | | | 105 | | | | | 110 | | | | | |
| Ala | Pro | Lys | Pro | Glu | Glu | Lys | Asp | Thr | Thr | Pro | Gln | Ala | Thr | Glu | Lys | | | |
| | | | 115 | | | | 120 | | | | | 125 | | | | | | |
| Asn | Lys | Glu | Thr | Ser | Pro | Ser | Ser | Gln | Phe | Asn | Ser | Ile | Phe | Gly | Asn | | | |
| | | | 130 | | | 135 | | | | | 140 | | | | | | | |
| Pro | Asn | Asn | Ala | Thr | Asn | Asn | Thr | Leu | Glu | Asp | Lys | Val | Val | Gly | Gly | | | |
| 145 | | | | | 150 | | | | | 155 | | | | 160 | | | | |
| Ile | Ser | Leu | Leu | Val | Asn | Gly | Ser | Pro | Ile | Thr | Leu | Tyr | Gln | Ile | Gln | | | |
| | | | | 165 | | | | | 170 | | | | | 175 | | | | |
| Glu | Glu | Gln | Glu | Lys | Ser | Lys | Val | Unk | Unk | Ala | Unk | | | | | | | |
| | | | 180 | | | | | 185 | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:30471091_c3_9: - AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 277 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 334

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Gly | Leu | Ser | Thr | Cys | Asp | Tyr | Asn | Leu | Leu | Ile | Leu | Ser | Ile | Ile | 1 | 5 | 10 | 15 |
| Ile | Val | Phe | Glu | Thr | Leu | Asn | Trp | Asn | Phe | Lys | Glu | His | Ser | Leu | Lys | 20 | 25 | 30 | |
| Val | Asn | Phe | Phe | Ala | Thr | Cys | Leu | Gly | Ala | Ala | Asn | Tyr | Ser | Asn | Ala | 35 | 40 | 45 | |
| Ser | Leu | Asn | Ala | Ile | Lys | Leu | Leu | Arg | Lys | Glu | Asn | Leu | Glu | Val | Val | 50 | 55 | 60 | |
| Phe | Lys | Lys | Asp | Gln | Thr | Cys | Cys | Gly | Gln | Pro | Ser | Tyr | Asn | Ser | Gly | 65 | 70 | 75 | 80 |
| Tyr | Tyr | Glu | Glu | Thr | Lys | Lys | Val | Val | Leu | Tyr | Asn | Ile | Lys | Leu | Tyr | 85 | 90 | 95 | |
| Phe | Asn | Asn | Asp | Tyr | Pro | Ile | Ile | Leu | Pro | Ser | Gly | Ser | Cys | Thr | Gly | 100 | 105 | 110 | |
| Met | Met | Arg | His | Asp | Tyr | Leu | Glu | Leu | Phe | Glu | Gly | His | Ala | Glu | Phe | 115 | 120 | 125 | |
| Asn | Met | Val | Lys | Asp | Phe | Cys | Ser | Arg | Val | Tyr | Glu | Leu | Ser | Glu | Phe | 130 | 135 | 140 | |
| Leu | Asp | Lys | Lys | Leu | Gln | Val | Lys | Tyr | Glu | Asp | Lys | Gly | Glu | Pro | Leu | 145 | 150 | 155 | 160 |
| Lys | Ile | Thr | Trp | His | Ser | Asn | Cys | His | Ala | Leu | Arg | Val | Ala | Lys | Val | 165 | 170 | 175 | |
| Ile | Asp | Ser | Ala | Lys | Asn | Leu | Ile | Arg | Gln | Leu | Lys | Asn | Val | Glu | Leu | 180 | 185 | 190 | |
| Ile | Glu | Leu | Glu | Lys | Glu | Glu | Glu | Cys | Cys | Gly | Phe | Gly | Gly | Thr | Phe | 195 | 200 | 205 | |
| Ser | Val | Lys | Glu | Pro | Glu | Ile | Ser | Ala | Val | Met | Val | Lys | Glu | Lys | Ile | 210 | 215 | 220 | |
| Lys | Asp | Ile | Glu | Ser | Arg | His | Val | Asp | Val | Ile | Val | Ser | Ala | Asp | Ala | 225 | 230 | 235 | 240 |

Asn Ile Lys Glu Leu Phe
275

(2) INFORMATION FOR SEQ ID NO:30478562_f2_3: -AA

Figure 335A - page 409

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 335

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| Val | Leu | Trp | Val | Leu | Tyr | Phe | Leu | Thr | Ser | Leu | Phe | Ile | Cys | Ser | Leu | 1 | 5 | 10 | 15 |
| Ile | Val | Leu | Trp | Ser | Lys | Lys | Ser | Met | Leu | Phe | Val | Asp | Asn | Ala | Asn | 20 | 25 | 30 | |
| Lys | Ile | Gln | Gly | Phe | His | His | Ala | Arg | Thr | Pro | Arg | Ala | Gly | Gly | Leu | 35 | 40 | 45 | |
| Gly | Ile | Phe | Leu | Ser | Phe | Ala | Leu | Ala | Cys | Tyr | Leu | Glu | Pro | Phe | Glu | 50 | 55 | 60 | |
| Met | Pro | Phe | Lys | Gly | Pro | Phe | Val | Phe | Leu | Gly | Leu | Ser | Leu | Val | Phe | 65 | 70 | 75 | 80 |
| Leu | Ser | Gly | Phe | Leu | Glu | Asp | Ile | Asn | Leu | Ser | Leu | Ser | Pro | Lys | Ile | 85 | 90 | 95 | |
| Arg | Leu | Ile | Leu | Gln | Ala | Val | Gly | Val | Val | Cys | Ile | Ile | Ser | Ser | Thr | 100 | 105 | 110 | |
| Pro | Leu | Val | Val | Ser | Asp | Phe | Ser | Pro | Leu | Phe | Ser | Leu | Pro | Tyr | Phe | 115 | 120 | 125 | |
| Ile | Ala | Phe | Leu | Phe | Ala | Ile | Phe | Tyr | Ala | Gly | Gly | Tyr | Gln | | | 130 | 135 | 140 | |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 336

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

[illegible]

(2) INFORMATION FOR SEQ ID NO:30662792_c2_6: - AA

Figure 337A - page 411

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP337

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: PREPROTEIN TRANSLOCASE SECA SUBUNIT

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| Val | Asp | Ser | Ile | Leu | Ile | Asp | Glu | Ala | Arg | Thr | Pro | Leu | Ile | Ile | Ser | 1 | 5 | 10 | 15 |
| Gly | Pro | Val | Asp | Arg | Arg | Met | Glu | Asn | Tyr | Asn | Lys | Ala | Asp | Glu | Val | 20 | 25 | 30 | |
| Ala | Lys | Ser | Met | Gln | Val | Glu | Val | Asp | Phe | Thr | Ile | Asp | Glu | Lys | Asn | 35 | 40 | 45 | |
| Arg | Ala | Ile | Leu | Ile | Thr | Glu | Glu | Gly | Ile | Lys | Lys | Ala | Glu | Asn | Leu | 50 | 55 | 60 | |
| Phe | Gly | Val | Asp | Asn | Leu | Tyr | Lys | Ile | Glu | Asn | Ala | Ala | Leu | Ser | His | 65 | 70 | 75 | 80 |
| His | Leu | Asp | Gln | Ala | Leu | Lys | Ala | Asn | Tyr | Leu | Phe | Phe | Ile | Asp | Lys | 85 | 90 | 95 | |
| Asp | Tyr | Ile | Val | Ala | Asn | Asn | Glu | Val | Val | Ile | Val | Asp | Lys | Phe | Thr | 100 | 105 | 110 | |
| Asp | Arg | Leu | Asn | Glu | Gly | Glu | Ala | Leu | | | | | | | | 115 | 120 | | |

Figure 338A - page 412

(2) INFORMATION FOR SEQ ID NO:30703183 f3 5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 58 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPD 338

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Met Thr Ile Thr Thr Leu Ser Phe Leu Phe Thr Thr Pro Glu Val Phe
1 5 10 15

Val Asn Gln Asp Phe Pro Trp Leu Ser Gly Ala Gly Arg Leu Val Val
20 25 30

Lys Asp Leu Ala Leu Phe Ala Gly Gly Leu Phe Val Ala Gly Phe Asp
35 40 45

Arg Asn Ala Ile Trp Arg Val Lys Gly Phe Ala
50 55

(2) INFORMATION FOR SEQ ID NO:30708287_f3_11: -AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 339

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Met Glu Ile Phe Gly Ser Phe Gly Ser His Cys Leu Pro Ile Ser His
1 5 10 15

Phe Met Arg Phe Phe Leu Gln Glu Ala Tyr Tyr Lys Met Asp Phe Thr
20 25 30

Glu Ser Leu Asn Ser Leu Met Pro Leu Leu Phe Phe Leu Ile Phe Leu
35 40 45

Ala Leu Gly Leu Leu Val Phe Tyr Phe Ser Phe Lys Lys Asp Lys Ala
50 55 60

Ser Ala
65

(2) INFORMATION FOR SEQ ID NO:30728393_c3_6: -AA

Figure 340A - page 414

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 340

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: POTASSIUM/COPPER-TRANSPORTING ATPASE A

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Arg | Cys | Glu | Leu | Trp | Arg | Arg | Tyr | Gly | Gln | Thr | His | Ala | Lys | Glu | 1 | 5 | 10 | 15 |
| Phe | Gly | Pro | Tyr | Arg | Tyr | Leu | Lys | Leu | Val | Gly | Ala | Ser | Gly | Val | Gly | 20 | 25 | 30 | |
| Arg | Phe | Phe | Ile | Lys | Gly | Ala | Phe | Tyr | Gly | Leu | Lys | Asn | Gly | Val | Leu | 35 | 40 | 45 | |
| Gly | Met | Asp | Leu | Ser | Val | Ser | Phe | Gly | Ala | Leu | Ser | Ala | Phe | Val | Tyr | 50 | 55 | 60 | |
| Ser | Leu | Tyr | Ala | Met | Leu | Val | Ser | Gln | Glu | Thr | Tyr | Phe | Glu | Ala | Ser | 65 | 70 | 75 | 80 |
| Ser | Thr | Ile | Leu | Thr | Leu | Val | Phe | Gly | Ser | Lys | Phe | Leu | Glu | Leu | Lys | 85 | 90 | 95 | |
| Ala | Arg | Leu | Phe | Ala | Asn | Glu | Lys | Cys | Leu | Ala | Leu | Glu | Ser | His | Glu | 100 | 105 | 110 | |
| Ile | His | Ser | Val | Ile | Val | Val | Glu | Asn | Gly | Lys | Gln | Ile | Glu | Lys | His | 115 | 120 | 125 | |
| Pro | Lys | Asp | Val | Ala | Ile | Gly | Ser | Val | Val | Trp | Val | Pro | Ser | Gly | Ala | 130 | 135 | 140 | |
| Lys | Ile | Ala | Leu | Asp | Gly | Val | Leu | Leu | Lys | Ser | Ala | Ser | Val | Asp | Ala | 145 | 150 | 155 | 160 |
| Ser | Leu | Ile | Ser | Gly | Glu | Phe | Lys | Pro | Leu | Glu | Ile | Gly | Gly | 165 | 170 | | | | |

(2) INFORMATION FOR SEQ ID NO:30730068_f1_1: -AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP341

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: similar to E.coli hypothetical nucleoside transpo

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Phe | Ser | Gly | Asn | Lys | Arg | Ala | Ile | Asn | Tyr | Arg | Thr | Ile | Val | Ser |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Ala | Phe | Val | Ile | Gln | Val | Ala | Leu | Gly | Ala | Leu | Ala | Leu | Tyr | Val | Pro |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Leu | Gly | Arg | Glu | Ile | Leu | Gln | Gly | Leu | Ala | Ser | Gly | Ile | Gln | Ser | Val |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Ile | Gly | Tyr | Gly | Tyr | Glu | Gly | Val | Arg | Phe | Leu | Phe | Gly | Asn | Leu | Ala |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Pro | Asn | Ala | Lys | Gly | Asp | Gln | Gly | Ile | Gly | Gly | Phe | Ile | Phe | Ala | Ile |
| 65 | | | | | 70 | | | | 75 | | | | | | 80 |
| Asn | Val | Leu | Ala | Ile | Ile | Ile | Phe | Phe | Ala | Ser | Leu | Ile | Ser | Leu | Leu |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| Tyr | Tyr | Leu | Lys | Ile | Met | Pro | Leu | Val | Ile | Asn | Leu | Ile | Gly | Gly | Ala |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Leu | Gln | Lys | Cys | Leu | Gly | Thr | Ser | Lys | Ala | Glu | Ser | Met | Ser | Ala | Ala |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| Ala | Asn | Unk | Unk | Val | Ala | His | Thr | Glu | Asp | Unk | Leu | Ser | His | | |
| 130 | | | | | | 135 | | | | | 140 | | | | |

(2) INFORMATION FOR SEQ ID NO:31250333_f3_7:-AA

416
Figure 342A - page 416

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

H PP 342

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: sequence predicts membrane bound protein

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Leu | Val | Gly | Ile | Ser | Asn | Ala | Ile | Asn | Ile | Ile | Asp | Gly | Phe | Asn | |
| 1 | | | | 5 | | | | 10 | | | | | | 15 | | |
| Gly | Leu | Ala | Ser | Gly | Ile | Cys | Ala | Ile | Ala | Leu | Leu | Val | Ile | His | Tyr | |
| | | | 20 | | | | | 25 | | | | | 30 | | | |
| Ile | Asp | Unk | Ser | Ser | Leu | Ser | Cys | Leu | Leu | Ala | Tyr | Met | Val | Leu | Gly | |
| | | 35 | | | | | 40 | | | | | 45 | | | | |
| Val | Tyr | Gly | Val | Lys | Unk | Pro | Phe | Arg | Lys | Asp | Phe | Leu | Gly | Arg | Ser | |
| | 50 | | | | | 55 | | | | | 60 | | | | | |
| Gly | Gly | Arg | Ile | Phe | Trp | Val | Trp | Unk | Unk | Unk | Phe | Leu | Ser | Cys | Ile | |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 | |

(2) INFORMATION FOR SEQ ID NO:31262_f3_4: -AA

417
Figure 343A - page 417

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 343

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Arg | Ser | Ser | Val | Phe | Ser | Phe | Leu | Val | Ala | Phe | Leu | Leu | Val |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Val | Gly | Cys | Ser | His | Lys | Met | Asp | Asn | Lys | Thr | Val | Ala | Gly | Asp | Val |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Ser | Thr | Lys | Ala | Val | Gln | Thr | Ala | Pro | Val | Thr | Thr | Glu | Pro | Ala | Unk |
| | | | 35 | | | | 40 | | | | | 45 | | | |
| Glu | Lys | Glu | Glu | Pro | Lys | Gln | Glu | Pro | Ala | Unk | Val | Val | Glu | Glu | Lys |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Pro | Ala | Ile | Glu | Ser | Gly | Thr | Ile | Ile | Ala | Ser | Ile | Tyr | Phe | Asp | Phe |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 |
| Asp | Lys | Unk | Unk | Unk | Lys | Asn | Pro | Ile | Lys | Arg | Leu | | | | |
| | | | | 85 | | | | | 90 | | | | | | |

(2) INFORMATION FOR SEQ ID NO:31413433_c1_8: -AA

Figure 344A - page 418

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 344

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: E.coli dGTP triphosphohydrolase and periplasmic p

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | His | Ser | Lys | Glu | Arg | Lys | Glu | Phe | Leu | Val | Ser | Glu | Phe | Lys | Ala |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Ser | Ala | Val | Glu | Met | Glu | Gly | Ala | Ser | Val | Ala | Phe | Val | Cys | Gln | Lys |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Phe | Gly | Val | Pro | Cys | Cys | Val | Leu | Arg | Ser | Ile | Ser | Asp | Asn | Ala | Asp |
| | | | 35 | | | | 40 | | | | | 45 | | | |
| Glu | Lys | Ala | Gly | Met | Ser | Phe | Asp | Glu | Phe | Leu | Glu | Lys | Ser | Ala | His |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Thr | Ser | Ala | Lys | Phe | Leu | Lys | Ser | Met | Val | Asp | Glu | Leu | | | |
| 65 | | | | | 70 | | | | | 75 | | | | | |

(2) INFORMATION FOR SEQ ID NO:3157067_c1_15:-AA

Figure 345A - page 419

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 74 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 345

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: invasion protein A

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | His | Lys | Lys | Tyr | Arg | Pro | Asn | Val | Ala | Ala | Ile | Ile | Met | Ser |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Pro | Asp | Tyr | Pro | Asn | Thr | Cys | Glu | Val | Phe | Ile | Ala | Glu | Arg | Ile | Asp |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Ile | Glu | Gly | Ala | Trp | Gln | Phe | Pro | Gln | Gly | Gly | Ile | Asp | Glu | Gly | Glu |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Thr | Pro | Leu | Glu | Ala | Leu | Tyr | Arg | Glu | Leu | Leu | Glu | Glu | Ile | Gly | Thr |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Asn | Glu | Ile | Glu | Ile | Leu | Ala | Gln | Tyr | Pro | Arg | | | | | |
| 65 | | | | | 70 | | | | | 75 | | | | | |

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 98 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 346

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Val Met Leu Met Ala Ile Phe Thr Pro Tyr Ile Leu Ile Leu Lys Met
1 5 10 15

Met Lys Lys Ser Met Ser Leu Phe Ala Asn Met Gly Leu Glu Gln Ile
20 25 30

Phe Cys Asn Arg Asp Ile Lys Asp Leu Asn Asp Phe Val Phe Gly Ile
35 40 45

Glu Val Gly Leu Asp Ser Asn Ala Arg Lys Asn Arg Ser Arg Lys Ala
50 55 60

Met Glu Asn His Leu Ile Gly Leu Phe Val Gln Ala Gln Leu Asn Phe
65 70 75 80

Lys Glu Gln Val Asp Ile Arg Glu Phe Glu Asp Leu Arg Gln Ala Phe
85 90 95

Gly Asn Asp

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 347

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

```

Met Ile Arg Leu Ala Ala Phe Phe Leu Ala Leu Ala Cys Ala Ile Thr
1           5           10           15
Pro Lys Ser Arg Leu Leu Leu Lys Asn Val Leu Leu Asn Pro Thr Arg
          20           25           30
Ile Glu Ala Phe Glu Val Leu Lys Lys Met Gly Ala His Ile Glu Tyr
          35           40           45
Val Ile Gln Ser Lys Asp Leu Glu Val Ile Gly Asp Ile Tyr Ile Glu
          50           55           60
His Ala Pro Leu Lys Ala Ile Ser Ile Asp Gln Asn Ile Ala Ser Leu
65           70           75           80
Ile Asp Glu Ile Pro Ala Leu Ser Ile Ala Met Leu Phe Ala Lys Gly
          85           90           95
Lys Ser Met Val Arg Asn Ala Lys Asp Leu Arg Ala Lys Glu Ser Asp
          100          105          110
Arg Ile Lys Ala Val Val Ser Asn Phe Lys Ala Leu Gly Ile Glu Cys
          115          120          125
Glu Glu Phe Glu Asp Gly Phe Tyr Ile Glu Gly Leu Gly Asp Ala Ser
          130          135          140
Gln Leu Lys Gln His Phe Ser Lys Ile Lys Pro Pro Ile Ile Lys Ser
          145          150          155          160
Phe Asn Asp His Arg Ile Ala Met Ser Phe Ala Val Leu Thr Leu Ala
          165          170          175
Leu Pro Leu Glu Ile Asp Asn Leu Glu Cys Ala Asn Ile Ser Phe Pro
          180          185          190
Thr Phe Gln Leu Trp Leu Asn Leu Phe Lys Lys Arg Ser Leu Asn Gly
          195          200          205

```

Asn

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 221 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 348

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: HYPOTHETICAL ABC TRANSPORTER

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Leu | Leu | Lys | Glu | Gln | Val | Leu | Lys | Pro | Leu | Lys | Gln | Val | Gln | Leu | 1 | 5 | 10 | 15 |
| Asp | Glu | Lys | Phe | Leu | Asp | Arg | Tyr | Pro | Tyr | Glu | Leu | Ser | Gly | Gly | Gln | 20 | 25 | 30 | |
| Arg | Gln | Arg | Val | Cys | Ile | Ala | Met | Gly | Ile | Ile | Asn | Ala | Pro | Lys | Leu | 35 | 40 | 45 | |
| Leu | Ile | Cys | Asp | Glu | Pro | Thr | Thr | Ala | Leu | Asp | Ala | Thr | Ile | Gln | Asn | 50 | 55 | 60 | |
| Gln | Ile | Leu | Asp | Leu | Leu | Lys | Gln | Leu | Ser | Val | Glu | Lys | Asn | Thr | Pro | 65 | 70 | 75 | 80 |
| Phe | Tyr | Unk | Phe | Unk | His | Asp | Leu | Lys | Ala | Val | Lys | Arg | Leu | Ala | Asp | 85 | 90 | 95 | |
| Arg | Unk | Tyr | Val | Leu | Lys | Lys | Gly | Glu | Ile | Val | Glu | Thr | Asn | Leu | Thr | 100 | 105 | 110 | |
| Lys | Glu | Leu | Phe | Asn | Asp | Pro | Lys | His | Glu | Tyr | Ser | Lys | Leu | Leu | Ile | 115 | 120 | 125 | |
| Gln | Ala | Ser | Asn | Leu | Pro | Ala | Lys | Asn | Leu | Lys | Ala | Leu | Asp | Glu | Thr | 130 | 135 | 140 | |
| Leu | Leu | Glu | Val | Lys | Asp | Phe | Ser | Val | Tyr | Tyr | Leu | Gln | Lys | Arg | Phe | 145 | 150 | 155 | 160 |
| Phe | Arg | Pro | Ser | Leu | Lys | Lys | Pro | Leu | Ile | Ala | Ser | Val | Asp | Phe | Ser | 165 | 170 | 175 | |
| Leu | Lys | Ala | Lys | Glu | Asn | Ile | Gly | Ile | Ile | Gly | Glu | Ser | Gly | Ser | Gly | 180 | 185 | 190 | |
| Lys | Unk | Ser | Leu | Ala | Leu | Gly | Ala | Phe | Lys | Thr | Arg | Phe | Lys | Gln | Arg | 195 | 200 | 205 | |
| Gly | Arg | Lys | Asp | Phe | Arg | Pro | Lys | Arg | Gly | Ala | Phe | Lys | Phe | 210 | 215 | 220 | | | |

(2) INFORMATION FOR SEQ ID NO:3203142_c1_5: - A A

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 74 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP349

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: PROBABLE COPPER-TRANSPORTING ATPASE

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Gly | Ser | Leu | Lys | Phe | Leu | Asn | Ala | Met | Gly | Val | Asp | Leu | Lys | Val |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Lys | Glu | Ser | Ala | Asn | Ile | Met | Val | Gly | Phe | Ala | Lys | Asn | Lys | Thr | Leu |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Cys | Ala | Leu | Phe | Ile | Leu | Glu | Glu | Arg | Leu | Lys | Ala | Asn | Ala | Lys | Glu |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Val | Ile | Gln | Ala | Leu | Gln | Asn | Gln | Gly | Leu | Glu | Leu | Glu | Ile | Leu | Ser |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Gly | Asp | Asn | Glu | Ser | Ser | Val | Lys | Glu | Cys | Ala | | | | | |
| 65 | | | | | 70 | | | | | 75 | | | | | |

(2) INFORMATION FOR SEQ ID NO:32036462_c1_12:-AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP35D

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| Met | Glu | Ala | Leu | Asn | Ala | Leu | Asn | Ala | Gln | Ser | Asp | Glu | Gln | Ile | Leu | 1 | 5 | 10 | 15 |
| Cys | Glu | Gly | Tyr | Phe | Val | Leu | Leu | Gln | Ile | Leu | Glu | Pro | Met | Ile | Pro | 20 | 25 | 30 | |
| His | Thr | Ala | Trp | Glu | Leu | Ser | Glu | Arg | Leu | Phe | Lys | Arg | Glu | Asn | Phe | 35 | 40 | 45 | |
| Lys | Pro | Ile | Glu | Val | Asp | Glu | Ser | Ala | Leu | Ile | Glu | Asp | Phe | Met | Thr | 50 | 55 | 60 | |
| Leu | Gly | Leu | Thr | Ile | Asn | Gly | Lys | Arg | Arg | Ala | Glu | Leu | Lys | Val | Asn | 65 | 70 | 75 | 80 |
| Ile | Asn | Ala | Ser | Lys | Glu | Glu | Ile | Ile | Ile | Leu | Ala | Lys | Lys | Glu | Leu | 85 | 90 | 95 | |
| Glu | Lys | Tyr | Leu | Glu | Asn | Ala | Ser | Val | Lys | Lys | Glu | Ile | Tyr | Val | Pro | 100 | 105 | 110 | |
| Asn | Lys | Leu | Val | Asn | Phe | Val | Thr | Ala | | | | | | | | 115 | 120 | | |

(2) INFORMATION FOR SEQ ID NO:32140663_f3_2:-AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 351

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Phe | Tyr | Ile | Leu | Glu | Val | Ala | Phe | Ser | Ile | Ser | Asn | Asp | Val | 1 | 5 | 10 | 15 |
| His | Leu | Val | Leu | His | His | Gln | Gln | Glu | Arg | Ile | Lys | Glu | Ala | Val | Ser | 20 | 25 | 30 | |
| Lys | Arg | Phe | Lys | Gly | Val | Ile | Phe | His | Ala | Gln | Ile | Val | Glu | Lys | Tyr | 35 | 40 | 45 | |
| Ser | Gly | Thr | Gly | Gly | Ala | Ile | Met | Gln | Glu | Asn | Lys | Thr | Pro | Ile | Pro | 50 | 55 | 60 | |
| Thr | Gln | His | Glu | Arg | Val | Leu | Ile | Leu | Asn | Ala | Asp | Met | Pro | Leu | Ile | 65 | 70 | 75 | 80 |
| Thr | Lys | Asp | Ala | Leu | Thr | Pro | Leu | Leu | Glu | Ser | His | Asn | Asn | Ala | Ile | 85 | 90 | 95 | |
| Gly | Leu | Leu | His | Leu | Ala | Asp | Pro | Lys | Gly | Tyr | Gly | Arg | Val | Ile | Leu | 100 | 105 | 110 | |
| Glu | Asn | His | Gln | Val | Lys | Lys | Ile | Val | Glu | Glu | Lys | Asp | Ala | Asn | Asp | 115 | 120 | 125 | |
| Glu | Glu | Lys | Thr | Ile | Lys | Ser | Val | Asn | Ala | Gly | Val | Tyr | Phe | Phe | Glu | 130 | 135 | 140 | |
| Arg | Lys | Phe | Leu | Glu | Arg | Tyr | Leu | Pro | Lys | Leu | His | Asp | Gln | Asn | Ala | 145 | 150 | 155 | 160 |
| Gln | Lys | Glu | Tyr | Tyr | Leu | Thr | Asp | Leu | Ile | Ala | Leu | Gly | Ile | Lys | Gly | 165 | 170 | 175 | |
| Asn | Glu | Lys | Ile | Asp | Ala | Ile | Phe | Leu | Glu | Glu | Glu | Cys | Phe | Leu | Gly | 180 | 185 | 190 | |
| Val | Asn | Ser | Gln | Thr | Glu | Arg | Arg | Lys | Leu | Lys | Lys | Ser | Cys | 195 | 200 | 205 | | | |

Val Arg Gln Pro Leu Ala
100

(2) INFORMATION FOR SEQ ID NO:32236462 c2. 4: -AA

(i) SEQUENCE CHARACTERISTICS:

(Å) LENGTH: 130 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 353

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

[illegible]

(2) INFORMATION FOR SEQ ID NO:32422343_f1_1: - AA

Figure 354A - page 428

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 440 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 354

(iii) HYPOTHETICAL: YES

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ile | Thr | Leu | Phe | Ser | Phe | Gly | Ala | Phe | Ala | Tyr | Tyr | Phe | Val | Ser | 1 | 5 | 10 | 15 |
| Ser | Gln | Ile | Ser | His | Glu | Asn | Tyr | Gln | Asn | Glu | Met | Arg | His | Tyr | Gln | 20 | 25 | 30 | |
| Phe | Val | Thr | Thr | Ile | Asn | Glu | Ile | Leu | Asn | Asn | Tyr | Ser | Asp | Tyr | Arg | 35 | 40 | 45 | |
| Ala | Ile | Glu | Asp | Tyr | Leu | Tyr | Lys | Ile | Gly | Phe | Arg | Glu | Thr | Thr | Ile | 50 | 55 | 60 | |
| Glu | Asn | Leu | Glu | Lys | Val | Leu | Ala | Lys | Arg | Arg | His | Gln | Leu | His | His | 65 | 70 | 75 | 80 |
| Arg | Asn | Ile | Trp | Tyr | Ala | Glu | Val | Phe | Lys | Phe | Ser | Asp | Met | Val | Phe | 85 | 90 | 95 | |
| Ile | Leu | Leu | Lys | Lys | Asp | Glu | His | Phe | Val | Leu | Tyr | Lys | Asp | Leu | His | 100 | 105 | 110 | |
| Ser | Val | Ser | Tyr | Arg | Asn | Tyr | Phe | Leu | Ala | Ile | Thr | Val | Gly | Leu | Leu | 115 | 120 | 125 | |
| Leu | Ile | Leu | Phe | Leu | Phe | Leu | Phe | Val | Leu | Gln | Ser | Leu | Leu | Pro | Leu | 130 | 135 | 140 | |
| Arg | Glu | Leu | Arg | Ser | Gln | Val | Lys | Arg | Phe | Ala | Gln | Gly | Asp | Lys | Ser | 145 | 150 | 155 | 160 |
| Val | Ser | Cys | Lys | Ser | Lys | Gln | Lys | Asp | Glu | Ile | Gly | Asp | Leu | Ala | Asn | 165 | 170 | 175 | |
| Glu | Phe | Asp | Asn | Cys | Ile | Gln | Lys | Ile | Asn | Ala | Met | Asn | Glu | Ser | Arg | 180 | 185 | 190 | |
| Val | Leu | Phe | Leu | Arg | Ser | Ile | Met | His | Glu | Leu | Arg | Thr | Pro | Ile | Thr | 195 | 200 | 205 | |
| Lys | Gly | Lys | Ile | Leu | Ser | Ser | Met | Leu | Lys | Glu | Glu | Leu | Ser | Cys | Lys | 210 | 215 | 220 | |
| Arg | Phe | Ser | Ser | Ile | Phe | Asp | His | Leu | Asn | Met | Leu | Ile | Glu | Gln | Phe | 225 | 230 | 235 | 240 |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Arg | Ile | Glu | Gln | Leu | Ala | Ser | Lys | Asn | Tyr | Gly | Ser | Asn | Lys | Glu |
| | | | | 245 | | | | | 250 | | | | | 255 | |
| Lys | Phe | Leu | Met | Ser | Asp | Leu | Ile | Asp | Lys | Ile | Glu | Lys | Met | Leu | Leu |
| | | | 260 | | | | | 265 | | | | | 270 | | |
| Ile | Asp | Glu | Asp | Lys | Lys | Ser | Pro | Ile | His | Val | Ser | Ser | Ser | Asn | Tyr |
| | | 275 | | | | | 280 | | | | | 285 | | | |
| Ile | Ile | Glu | Ala | Asp | Phe | Glu | Leu | Phe | Ala | Ile | Ala | Leu | Lys | Asn | Met |
| | 290 | | | | | 295 | | | | | 300 | | | | |
| Ile | Asp | Asn | Ala | Ile | Lys | Tyr | Ser | Asp | Asp | Lys | Gln | Val | Phe | Leu | Asp |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 |
| Phe | Ile | Gly | Asn | Asn | Leu | Val | Val | Ser | Asn | Lys | Ser | Lys | Pro | Leu | Lys |
| | | | | 325 | | | | | 330 | | | | | 335 | |
| Glu | Asp | Phe | Glu | Lys | Tyr | Leu | Gln | Pro | Tyr | Phe | Lys | Ser | Ser | Asn | Pro |
| | | | 340 | | | | | 345 | | | | | 350 | | |
| Ser | Gln | Ala | His | Gly | Phe | Gly | Leu | Gly | Met | Tyr | Ile | Ile | Lys | Asn | Ala |
| | | 355 | | | | | 360 | | | | | 365 | | | |
| Leu | Glu | Ala | Met | Gly | Leu | Asn | Leu | Ser | Tyr | His | Tyr | Ser | Asn | Gly | Arg |
| | 370 | | | | | 375 | | | | | 380 | | | | |
| Ile | Cys | Phe | Thr | Ile | His | Asp | Cys | Val | Phe | Asn | Ser | Phe | Tyr | Asp | Leu |
| 385 | | | | | 390 | | | | | 395 | | | | | 400 |
| Glu | Ala | Asp | Asn | Glu | Glu | Leu | Pro | Pro | Pro | Glu | Asn | Leu | Arg | Glu | Val |
| | | | | 405 | | | | | 410 | | | | | 415 | |
| Lys | Gly | Met | Lys | Gly | Thr | Glu | Lys | Ala | Asn | Cys | Gly | Val | Lys | Glu | Lys |
| | | | 420 | | | | | 425 | | | | | 430 | | |
| Gln | Lys | Glu | Arg | Thr | Cys | Ser | Asn | Asp | | | | | | | |
| | | 435 | | | | | 440 | | | | | | | | |

A. A

(A) LENGTH: 126 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

HPP 355

(A) ORGANISM: *Helicobacter pylori*

| | | | | | | | | | | | | | | | |
|-----------|-----|------------|------------|-----------|-----------|-----------|------------|------------|-----------|-----------|-----------|------------|------------|-----------|-----------|
| Val 1 | Leu | Leu | Leu | Ser 5 | Arg | Met | Gly | Ile | Ala 10 | Phe | Ala | His | Ser | Ile 15 | Phe |
| Trp | Ser | Ile | Thr 20 | Ala | Ser | Leu | Val | Ile 25 | Arg | Val | Ala | Pro | Arg 30 | Asn | Lys |
| Lys | Gln | Gln 35 | Ala | Leu | Gly | Leu | Leu 40 | Ala | Leu | Gly | Ser | Ser 45 | Leu | Ala | Met |
| Ile 50 | Leu | Gly | Leu | Pro | Leu | Gly 55 | Arg | Ile | Ile | Gly | Gln 60 | Ile | Leu | Asp | Trp |
| Arg 65 | Ser | Thr | Phe | Gly | Val 70 | Ile | Gly | Gly | Val | Ala 75 | Thr | Leu | Ile | Met | Leu 80 |
| Leu | Met | Trp | Lys | Leu 85 | Leu | Pro | His | Leu | Pro 90 | Ser | Arg | Asn | Ala | Gly 95 | Thr |
| Leu | Ala | Ser | Val 100 | Pro | Ile | Leu | Met | Lys 105 | Arg | Pro | Leu | Leu | Val 110 | Gly | Ile |
| Tyr | Leu | His 115 | Val | Asn | His | Gly | Tyr 120 | Phe | Trp | Ala | Phe | His 125 | His | Leu | |

(2) INFORMATION FOR SEQ ID NO:3242952_c2_11: - AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 356

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: similarity with eukaryotic myosins

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Thr | Leu | Ile | Glu | Lys | Trp | Phe | Gly | Phe | Ser | Gln | Ile | Arg | Glu | 1 | 5 | 10 | 15 |
| Glu | Leu | Glu | Ala | Arg | Ile | Ser | Glu | Leu | Glu | Asp | Glu | Asn | Thr | Glu | Leu | 20 | 25 | 30 | |
| Leu | Arg | Glu | Arg | Glu | Tyr | Leu | Ala | Ala | Glu | Thr | Ser | Glu | Leu | Lys | Asp | 35 | 40 | 45 | |
| Ala | Asn | Asp | Gln | Leu | Arg | Gln | Lys | Asn | Asp | Lys | Leu | Phe | Ile | Thr | Lys | 50 | 55 | 60 | |
| Asp | Lys | Leu | Thr | Lys | Glu | Asn | Thr | Glu | Leu | Phe | Ala | Glu | Asn | Glu | Ser | 65 | 70 | 75 | 80 |
| Leu | Ser | Val | Lys | Ile | Ser | Gly | Leu | Glu | His | Ser | Asn | Asp | Gln | Leu | Trp | 85 | 90 | 95 | |
| Gln | Asn | Asn | Asn | Lys | Leu | Thr | Lys | Glu | Lys | Ala | Glu | Leu | Lys | Thr | Glu | 100 | 105 | 110 | |
| Lys | Asp | Ile | Leu | Ala | Lys | Glu | Asn | Thr | Arg | Leu | Leu | Ala | Ala | Arg | Asp | 115 | 120 | 125 | |
| Arg | Leu | Thr | Glu | Glu | Lys | Arg | Glu | Leu | Thr | Thr | Glu | Lys | Glu | Arg | Leu | 130 | 135 | 140 | |
| Lys | Arg | Glu | Asn | Thr | Glu | Leu | Thr | His | Lys | Ile | Thr | Glu | Leu | Thr | Lys | 145 | 150 | 155 | 160 |
| Glu | Asn | Lys | Ala | Leu | Thr | Thr | Glu | Asn | Asp | Lys | Leu | Asn | His | Gln | Val | 165 | 170 | 175 | |
| Thr | Ala | Leu | Thr | Asn | Glu | Arg | Asp | Ser | Leu | Glu | Gln | Glu | Arg | Ala | Arg | 180 | 185 | 190 | |
| Leu | Gln | Asp | Ala | His | Gly | Phe | Leu | Glu | Lys | Arg | Cys | Thr | Asn | Leu | Glu | 195 | 200 | 205 | |
| Lys | Glu | Asn | Gln | Arg | Leu | Thr | Asp | Lys | Leu | Lys | Gln | Leu | Glu | Ser | Ala | 210 | 215 | 220 | |
| Gln | Lys | Ser | Leu | Glu | Asn | Thr | Asn | Asn | Gln | Leu | Arg | Gln | Ala | Leu | Glu | 225 | 230 | 235 | 240 |

His Arg Pro Gln Arg Glu Gly
305 310

(2) INFORMATION FOR SEQ ID NO:32431687_f2_4:-AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 357

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Leu | Arg | Lys | Leu | Leu | Gly | Lys | Asn | Cys | Ile | Glu | Thr | His | Lys | Gly |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Val | Gly | Tyr | Arg | Leu | Thr | His | Tyr | Glu | Lys | Lys | Ser | Leu | Lys | Leu | Phe |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Leu | Gly | Thr | Tyr | Leu | Gly | Ser | Ser | Phe | Val | Leu | Met | Leu | Val | Ile | Ser |
| | | 35 | | | | 40 | | | | | | 45 | | | |
| Val | Leu | Ala | Phe | Asn | Tyr | Glu | Lys | Asn | Glu | Lys | Ile | Lys | Unk | Ile | Arg |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Met | Asp | Met | Asp | Lys | Met | Ala | Ser | Lys | Ile | Ala | Ser | Glu | Ile | Ile | Gln |
| 65 | | | | | 70 | | | | 75 | | | | | 80 | |
| Leu | His | Met | Gln | Thr | His | Ala | Asp | Tyr | His | Asn | Ala | Leu | Asn | Ala | Leu |
| | | | 85 | | | | | | 90 | | | | | 95 | |
| Ile | Ser | Arg | Tyr | Lys | Asp | Val | Ser | Ile | Unk | Leu | Unk | Unk | Thr | | |
| | | | 100 | | | | | 105 | | | | | 110 | | |

(2) INFORMATION FOR SEQ ID NO:32453958_c3_15: - AA

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 93 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein HPP 358

(iii) HYPOTHETICAL: YES

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Arg | Asp | Asn | Pro | Lys | Gln | Pro | Glu | Asp | Leu | Ile | Gln | Lys | Glu | Val |
| 1 | | | | 5 | | | | 10 | | | | | | 15 | |
| Ser | Gly | Ala | Leu | Val | Ala | Phe | Tyr | Leu | Ser | Tyr | Gly | Ile | His | Gln | Leu |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Leu | Gly | Lys | Glu | Lys | Ser | His | Ser | Ser | Glu | Leu | Leu | Cys | Leu | Ala | Gly |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Val | Ala | Thr | Ile | Ala | Asp | Met | Met | Pro | Leu | Thr | Phe | Phe | Asn | Arg | Phe |
| | | 50 | | | | 55 | | | | | 60 | | | | |
| Leu | Val | Ser | Lys | Ala | Leu | Tyr | Phe | Leu | Gln | Lys | Glu | Ser | Leu | Gly | Gly |
| 65 | | | | 70 | | | | | 75 | | | | | 80 | |
| Trp | Gly | Phe | Tyr | Ala | Lys | Glu | Lys | Phe | Leu | Glu | Asn | Ala | Leu | | |
| | | | | 85 | | | | | 90 | | | | | | |

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 114 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

HPP 359

[illegible]

(A) LENGTH: 85 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Val Arg Ser Cys Lys Gln Ile Phe Asp Lys Gly Leu Lys Pro Tyr Tyr
1 5 10 15

Lys His Ser Val Cys Leu Lys Pro Phe Phe Arg Phe Cys Phe Leu Lys
20 25 30

Ile His Ala Tyr Gln Gln Arg Tyr Arg Ala Phe Ala Leu Thr Leu Phe
35 40 45

Ser Cys Lys Phe Phe Asn Ala Cys Lys Ile Phe Ile Pro Ile Ile Asp
50 55 60

Phe Lys Ile Val Phe Ile Pro Ile Leu Lys His Gln Ala Lys Leu Lys
65 70 75 80

Arg Val Ser Asn Ala Tyr
85

(2) INFORMATION FOR SEQ ID NO:32600912_c1_5: -AA

Figure 3b1A-page 437

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 361

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met Cys Gly Met Gly Phe Ile Gly Phe Lys Thr Lys Leu Thr Gln Thr
1 5 10 15

Lys Ala Phe Ile Ile Leu Ile Pro Ile Phe Gln Asp Arg Ala Val Lys
20 25 30

Ala Ala Thr Arg Ser Ala Pro Ile Gln Leu Ile Cys
35 40

(2) INFORMATION FOR SEQ ID NO:32609403_f2_3: AA

Figure 3b2 A - page 438

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 559 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 3b2

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: vacuolating cytotoxin

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Asn | Phe | Asn | Ser | Tyr | Gly | Asp | Leu | Val | Phe | Asn | Leu | Ser | His | 1 | 5 | 10 | 15 |
| Ser | Val | Ser | His | Ala | Ile | Ile | Asn | Thr | Gln | Gly | Thr | Ala | Thr | Ile | Met | 20 | 25 | 30 | |
| Ala | Asn | Asn | Asn | Pro | Leu | Ile | Gln | Phe | Asn | Ala | Ser | Ser | Lys | Glu | Val | 35 | 40 | 45 | |
| Gly | Thr | Tyr | Thr | Leu | Ile | Asp | Ser | Ala | Lys | Ala | Ile | Tyr | Tyr | Gly | Tyr | 50 | 55 | 60 | |
| Asn | Asn | Gln | Ile | Thr | Gly | Gly | Ser | Ser | Leu | Asp | Asn | Tyr | Leu | Lys | Leu | 65 | 70 | 75 | 80 |
| Tyr | Ala | Leu | Ile | Asp | Ile | Asn | Gly | Lys | His | Met | Val | Met | Thr | Asp | Asn | 85 | 90 | 95 | |
| Gly | Leu | Thr | Tyr | Asn | Gly | Gln | Ala | Val | Ser | Val | Lys | Asp | Gly | Gly | Leu | 100 | 105 | 110 | |
| Val | Val | Gly | Phe | Lys | Asp | Ser | Gln | Asn | Gln | Tyr | Ile | Tyr | Thr | Ser | Ile | 115 | 120 | 125 | |
| Leu | Tyr | Asn | Lys | Val | Lys | Ile | Ala | Val | Ser | Asn | Asp | Pro | Ile | Asn | Asn | 130 | 135 | 140 | |
| Pro | Gln | Ala | Pro | Thr | Leu | Lys | Gln | Tyr | Ile | Ala | Gln | Ile | Gln | Gly | Val | 145 | 150 | 155 | 160 |
| Gln | Ser | Val | Asp | Ser | Ile | Unk | Gln | Ala | Gly | Gly | Asn | Gln | Ala | Ile | Asn | 165 | 170 | 175 | |
| Trp | Leu | Asn | Lys | Ile | Phe | Glu | Thr | Lys | Gly | Ser | Pro | Leu | Phe | Ala | Pro | 180 | 185 | 190 | |
| Tyr | Tyr | Leu | Glu | Ser | His | Ser | Thr | Lys | Asp | Leu | Thr | Thr | Ile | Ala | Gly | 195 | 200 | 205 | |
| Asp | Ile | Ala | Asn | Thr | Leu | Glu | Val | Ile | Ala | Asn | Pro | Asn | Phe | Lys | Asn | 210 | 215 | 220 | |
| Asp | Ala | Thr | Asn | Ile | Leu | Gln | Ile | Asn | Thr | Tyr | Thr | Gln | Gln | Met | Ser | 225 | 230 | 235 | 240 |

| | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Leu | Ala | Lys | Leu | Ser | Asp | Thr | Ser | Thr | Phe | Ala | Arg | Ser | Asp | Phe | 245 | 250 | 255 |
| Leu | Glu | Arg | Leu | Glu | Ala | Leu | Lys | Asn | Lys | Arg | Phe | Ala | Asp | Ala | Ile | 260 | 265 | 270 |
| Pro | Asn | Ala | Met | Asp | Val | Ile | Leu | Lys | Tyr | Ser | Gln | Arg | Asn | Arg | Val | 275 | 280 | 285 |
| Lys | Asn | Asn | Val | Trp | Ala | Thr | Gly | Val | Gly | Gly | Ala | Ser | Phe | Ile | Ser | 290 | 295 | 300 |
| Gly | Gly | Thr | Unk | Thr | Leu | Tyr | Gly | Ile | Asn | Unk | Gly | Tyr | Asp | Arg | Phe | 305 | 310 | 315 |
| Ile | Lys | Gly | Val | Ile | Val | Gly | Gly | Tyr | Ala | Ala | Tyr | Gly | Tyr | Ser | Gly | 325 | 330 | 335 |
| Phe | His | Ala | Asn | Ile | Thr | Gln | Ser | Gly | Ser | Ser | Asn | Val | Asn | Val | Gly | 340 | 345 | 350 |
| Val | Tyr | Ser | Arg | Ala | Phe | Ile | Lys | Arg | Ser | Glu | Leu | Thr | Met | Ser | Leu | 355 | 360 | 365 |
| Asn | Glu | Thr | Trp | Gly | Tyr | Asn | Lys | Thr | Phe | Ile | Asn | Ser | Tyr | Asp | Pro | 370 | 375 | 380 |
| Leu | Leu | Ser | Ile | Ile | Asn | Gln | Ser | Tyr | Arg | Tyr | Asp | Thr | Trp | Thr | Thr | 385 | 390 | 395 |
| Asp | Ala | Lys | Ile | Asn | Tyr | Gly | Tyr | Asp | Phe | Met | Phe | Lys | Asp | Lys | Ser | 405 | 410 | 415 |
| Val | Ile | Phe | Lys | Pro | Gln | Val | Gly | Leu | Ser | Tyr | Tyr | Tyr | Ile | Gly | Leu | 420 | 425 | 430 |
| Ser | Gly | Leu | Arg | Gly | Ile | Met | Asp | Asp | Pro | Ile | Tyr | Asn | Gln | Phe | Arg | 435 | 440 | 445 |
| Ala | Asn | Ala | Asp | Pro | Asn | Lys | Lys | Ser | Val | Leu | Thr | Ile | Asn | Phe | Ala | 450 | 455 | 460 |
| Leu | Glu | Ser | Arg | His | Tyr | Phe | Asn | Lys | Asn | Ser | Tyr | Tyr | Phe | Val | Ile | 465 | 470 | 475 |
| Ala | Asp | Val | Gly | Arg | Asp | Leu | Phe | Ile | Asn | Ser | Met | Gly | Asp | Lys | Met | 485 | 490 | 495 |
| Val | Arg | Phe | Ile | Gly | Asn | Asn | Thr | Leu | Ser | Tyr | Arg | Asp | Gly | Gly | Arg | 500 | 505 | 510 |
| Tyr | Asn | Thr | Phe | Ala | Ser | Ile | Ile | Thr | Gly | Gly | Glu | Ile | Arg | Leu | Phe | 515 | 520 | 525 |
| Lys | Thr | Phe | Tyr | Val | Asn | Ala | Gly | Ile | Gly | Ala | Arg | Phe | Gly | Leu | Asp | 530 | 535 | 540 |
| Tyr | Lys | Asp | Ile | Asn | Ile | Thr | Gly | Asn | Ile | Gly | Met | Unk | Unk | Unk | Phe | 545 | 550 | 555 |

Figure 363A - page 440

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 122 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 363

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | |
|-----------|-----------|------------|------------|-----------|-----------|-----------|------------|------------|-----------|-----------|-----------|-----------|------------|-----------|-----------|
| Met 1 | Thr | Lys | Ser | Leu 5 | Lys | Leu | Ile | Gln | Lys 10 | Gly | Val | Lys | Asn | Leu 15 | Tyr |
| Glu | Thr | Leu | Lys 20 | Asn | Arg | Ala | Leu | Glu 25 | His | Gln | Asp | Thr | Leu 30 | Met | Val |
| Gly | Arg | Ser 35 | His | Gly | Val | Phe | Gly 40 | Glu | Pro | Ile | Thr | Phe 45 | Gly | Leu | Val |
| Leu | Ala 50 | Leu | Phe | Ala | Asp | Glu 55 | Ile | Lys | Arg | His | Leu 60 | Lys | Ala | Leu | Asp |
| Leu 65 | Thr | Met | Glu | Phe | Ile 70 | Unk | Val | Gly | Ala | Ile 75 | Ser | Gly | Ala | Met | Gly 80 |
| Asn | Phe | Ala | His | Ala 85 | Pro | Leu | Glu | Leu | Glu 90 | Glu | Leu | Ala | Cys | Gly 95 | Phe |
| Leu | Gly | Leu | Lys 100 | Thr | Ala | Asn | Ile | Ser 105 | Asn | Gln | Val | Ile | Gln 110 | Arg | Asp |
| Arg | Tyr | Ala 115 | Gly | Leu | His | Ala | Ile 120 | Trp | Leu | Phe | | | | | |

(2) INFORMATION FOR SEQ ID NO:32627125_c1_6: - A A

Figure 364A - page 441

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 364

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Met | Asn | Asn | Asn | Asn | Thr | Leu | Pro | Lys | Pro | Leu | Glu | Glu | Ser | Leu |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Asp | Leu | Lys | Glu | Phe | Ile | Ala | Leu | Phe | Lys | Thr | Phe | Phe | Ala | Lys | Glu |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Arg | Gly | Ser | Ile | Ala | Leu | Glu | Asn | Asp | Leu | Lys | Gln | Ala | Phe | Thr | Tyr |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Leu | Asn | Glu | Val | Asp | Ala | Ile | Gly | Leu | Pro | Ala | Pro | Lys | Ser | Val | Lys |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Glu | Ser | Asp | Leu | Ile | Val | Val | Lys | Leu | Thr | Lys | Leu | Gly | Thr | Leu | His |
| 65 | | | | 70 | | | | | | 75 | | | | 80 | |
| Leu | Asp | Glu | Ile | Tyr | Glu | Ile | Val | Lys | Arg | Leu | Arg | Tyr | Ile | Val | Val |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| Leu | Gln | Asn | Ala | Phe | Lys | Pro | Phe | Thr | His | Leu | Lys | Phe | His | Glu | Arg |
| | | | 100 | | | | | | 105 | | | | | 110 | |
| Leu | Asn | Ala | Ile | Ile | Leu | Pro | Pro | Phe | Phe | Asn | Asp | Leu | Ile | Leu | Leu |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| Leu | Asp | Asp | Glu | Gly | Gln | Ile | Lys | Gln | Gly | Ala | Asn | Ala | Thr | Leu | Asp |
| | 130 | | | | | 135 | | | | | 140 | | | | |
| Ala | Leu | Asn | Glu | Ser | Leu | Asn | Arg | Leu | Lys | Lys | Glu | Ser | Thr | Lys | Ile |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 |
| Ile | His | His | Tyr | Ala | His | Ser | Lys | Glu | Leu | Ala | Pro | Tyr | Leu | Val | Asp |
| | | | | 165 | | | | | 170 | | | | | 175 | |
| Thr | Gln | Ser | His | Leu | Lys | His | Gly | Tyr | Glu | Cys | Leu | Leu | Leu | Lys | Ser |
| | | | 180 | | | | | 185 | | | | | | 190 | |
| Gly | Phe | Ser | Ser | Ala | Ile | Lys | Gly | Val | Val | Leu | Glu | Arg | Ser | Ala | Asn |
| | | 195 | | | | | 200 | | | | | 205 | | | |
| Gly | Tyr | Phe | Tyr | Leu | Leu | Pro | Glu | Ser | Ala | Gln | Lys | Ile | Ala | Gln | Lys |
| | 210 | | | | | 215 | | | | | 220 | | | | |
| Ile | Ala | Gln | Ile | Gly | Asn | Glu | Ile | Asp | Cys | Cys | Ile | Val | Glu | Met | Cys |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Thr | Leu | Ser | Arg | Ser | Leu | Gln | Lys | His | Leu | Leu | Phe | Leu | Lys | Phe |
| | | | | 245 | | | | | 250 | | | | | 255 | |
| Leu | Phe | Lys | Glu | Phe | Asp | Phe | Leu | Asp | Ser | Leu | Gln | Ala | Arg | Leu | Asn |
| | | | 260 | | | | | 265 | | | | | 270 | | |
| Phe | Ala | Lys | Ala | Tyr | Asn | Leu | Glu | Phe | Val | Met | Pro | Ser | Phe | Thr | Gln |
| | | 275 | | | | | 280 | | | | | 285 | | | |
| Lys | Lys | Met | Ile | Leu | Glu | Asn | Phe | Ser | His | Pro | Ile | Leu | Lys | Glu | Pro |
| | 290 | | | | | 295 | | | | | 300 | | | | |
| Lys | Pro | Leu | Asn | Leu | Lys | Phe | Glu | Lys | Ser | Met | Leu | Ala | Val | Thr | Gly |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 |
| Val | Asn | Ala | Gly | Gly | Lys | Thr | His | Ala | Leu | | | | | | |
| | | | | 325 | | | | | 330 | | | | | | |

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 86 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Met Tyr Ser Gly Ser Asn Asp Ala Leu Ile Gln Trp Trp Trp Gly His
1 5 10 15

Asn Ala Val Ala Phe Val Phe Thr Ser Gly Val Ile Gly Thr Ile Tyr
20 25 30

Tyr Phe Leu Pro Lys Glu Ser Gly Gln Pro Ile Phe Ser Tyr Lys Leu
35 40 45

Thr Leu Phe Ser Phe Trp Ser Leu Met Phe Val Tyr Ile Trp Ala Gly
50 55 60

Gly His His Leu Ile Tyr Ser Thr Val Thr Asp Glu Tyr Lys Pro Phe
65 70 75 80

Leu Ala Ser Phe Gln Trp Cys
85

(2) INFORMATION FOR SEQ ID NO:32663212_c3_17: -AA

Figure 3b6A-page 444

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 366

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Val Met Met Phe Phe Ser Lys Ile Val Gly Asp Phe Ile Glu Lys His
1 5 10 15

Tyr Arg Val Lys Thr Leu Ala Phe Val Phe Leu Leu Val Val Gly Val
20 25 30

Phe Leu Phe Leu Glu Gly Leu His Leu His Ile Asn Lys Asn Tyr Leu
35 40 45

Tyr Ala Gly Ile Gly Phe Ala Leu Leu Ile Glu Cys Leu Asn Ile Phe
50 55 60

Ile Glu Lys Lys Met Lys Lys Ser
65 70

(2) INFORMATION FOR SEQ ID NO:32704686_c2_3: -AA

Figure 367A-page 445

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 367

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|
| Met | Glu | Ser | Asn | Gln | Ser | Leu | Pro | Met | Ala | Leu | Ile | Ser | Cys | Ser | Pro | | | |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | | | | |
| Asn | Ala | Lys | Gly | Ala | Asp | Ile | Lys | Gly | Tyr | Asn | Gly | Leu | Val | Gly | Glu | | | |
| | | | 20 | | | | | 25 | | | | | 30 | | | | | |
| Leu | Ile | Glu | Arg | Asn | Phe | Gln | Arg | Tyr | Gly | Val | Pro | Leu | Leu | Leu | Ser | | | |
| | | | 35 | | | | 40 | | | | | 45 | | | | | | |
| Thr | Leu | Thr | Asn | Gly | Leu | Leu | Ile | Gly | Ile | Thr | Ser | Ala | Leu | Asn | Asn | | | |
| | | | | | | 55 | | | | | 60 | | | | | | | |
| Arg | Gly | Asn | Lys | Glu | Glu | Val | Thr | Asn | Phe | Phe | Gly | Asp | Tyr | Leu | Leu | | | |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 | | | |
| Leu | Gln | Leu | Met | Arg | Gln | Ser | Gly | Met | Gly | Ile | Asn | Gln | Val | Val | Asn | | | |
| | | | | 85 | | | | 90 | | | | | | 95 | | | | |
| Gln | Ile | Leu | Arg | Asp | Lys | Ser | Lys | Ile | Ala | Pro | Ile | Val | Val | Ile | Arg | | | |
| | | | 100 | | | | | 105 | | | | | 110 | | | | | |
| Glu | Gly | Ser | Arg | Val | Phe | Ile | Ser | Pro | Asn | Thr | Asp | Ile | Phe | Phe | Pro | | | |
| | | 115 | | | | | 120 | | | | | 125 | | | | | | |
| Ile | Pro | Arg | Glu | Asn | Glu | Val | Ile | Ala | Glu | Phe | Leu | Lys | | | | | | |
| | 130 | | | | | 135 | | | | | 140 | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:32705252_f2_5: - AA

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPD 368

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xii) SEQUENCE DESCRIPTION: PHOSPHATIDYLSERINE DECARBOXYLASE

Val Asn Phe Tyr Leu Ser Pro Lys Asp Tyr His His Tyr His Ala Pro
1 5 10 15

Cys Asp Leu Glu Ile Leu Glu Ala Arg Tyr Phe Ala Gly Lys Leu Leu
20 25 30

Pro Val Asn Lys Pro Ser Leu His Lys Lys Gln Asn Leu Phe Val Gly
35 40 45

Asn Glu Arg
50

(2) INFORMATION FOR SEQ ID NO:32952_c1_11: -AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 369

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: PROBABLE ABC TRANSPORTER

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asp | Ile | Leu | Lys | Ala | Glu | His | Leu | Asn | Lys | Gln | Ile | Lys | Lys | Thr | 1 | 5 | 10 | 15 |
| Lys | Ile | Val | Ser | Asp | Val | Ser | Leu | Glu | Val | Lys | Ser | Gly | Glu | Val | Val | 20 | 25 | 30 | |
| Gly | Leu | Leu | Gly | Pro | Asn | Gly | Ala | Gly | Lys | Thr | Thr | Thr | Phe | Tyr | Met | 35 | 40 | 45 | |
| Ile | Cys | Gly | Leu | Leu | Glu | Pro | Ser | Gly | Gly | Ser | Val | Tyr | Leu | Asn | Asp | 50 | 55 | 60 | |
| Val | Asp | Leu | Ala | Lys | Tyr | Pro | Leu | His | Lys | Arg | Ser | Asn | Leu | Gly | Ile | 65 | 70 | 75 | 80 |
| Gly | Tyr | Leu | Pro | Gln | Glu | Ser | Ser | Ile | Phe | Lys | Glu | Leu | Ser | Val | Glu | 85 | 90 | 95 | |
| Glu | Asn | Leu | Ala | Leu | Ala | Gly | Glu | Ser | Thr | Phe | Lys | Asn | Ser | Lys | Glu | 100 | 105 | 110 | |
| Ser | Glu | Glu | Lys | Met | Glu | Ser | Leu | Leu | Asp | Ala | Phe | Asn | Ile | Gln | Ala | 115 | 120 | 125 | |
| Ile | Arg | Glu | Arg | Lys | Gly | Met | Ser | Leu | Ser | Gly | Gly | Glu | Arg | Arg | Arg | 130 | 135 | 140 | |
| Val | Glu | Ile | Ala | Arg | Ala | Leu | Met | Lys | Asn | Pro | Lys | Phe | Val | Leu | Leu | 145 | 150 | 155 | 160 |
| Asp | Glu | Pro | Phe | Ala | Gly | Val | Asp | Pro | Ile | Ala | Val | Ile | Asp | Ile | Gln | 165 | 170 | 175 | |
| Arg | Ile | Ile | Glu | Ser | Leu | Ile | Gly | Leu | Asn | Ile | Gly | Val | Leu | Ile | Thr | 180 | 185 | 190 | |
| Asp | His | Asn | Val | Arg | Glu | Thr | Leu | Ser | Val | Cys | His | Arg | Ala | Tyr | Val | 195 | 200 | 205 | |
| Ile | Lys | Ser | Gly | Thr | Leu | Leu | Ala | Ala | Gly | Thr | Leu | Met | Lys | Phe | Met | 210 | 215 | 220 | |
| Lys | Thr | Leu | Trp | Cys | Val | Ser | Ile | Ile | | | | | | | | 225 | 230 | | |

(2) INFORMATION FOR SEQ ID NO:3319687_f3_12: AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP371

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: molybdenum transport atp-binding protein

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| Met | Ile | Lys | Ala | Arg | Phe | Lys | Lys | Arg | Leu | Leu | Gly | Ser | Arg | Gly | Ala | 1 | 5 | 10 | 15 |
| Phe | Asp | Leu | Asn | Ile | Asp | Leu | Glu | Ile | Lys | Glu | Ala | Glu | Val | Val | Ala | 20 | 25 | 30 | |
| Leu | Leu | Gly | Glu | Ser | Gly | Ala | Gly | Lys | Ser | Thr | Ile | Leu | Arg | Ile | Leu | 35 | 40 | 45 | |
| Ala | Gly | Leu | Glu | Ala | Val | Ser | Ser | Gly | Tyr | Ile | Glu | Ala | Asn | His | Ser | 50 | 55 | 60 | |
| Val | Trp | Leu | Asp | Thr | Gln | Lys | Lys | Ile | Phe | Leu | Lys | Pro | Gln | Gln | Arg | 65 | 70 | 75 | 80 |
| Lys | Ile | Gly | Phe | Val | Phe | Gln | Asp | Tyr | Ala | Leu | Phe | Pro | His | Leu | Asn | 85 | 90 | 95 | |
| Val | Tyr | Gln | Asn | Ile | Ala | Phe | Ala | His | Pro | Lys | Asp | Lys | Asn | Lys | Thr | 100 | 105 | 110 | |
| Thr | Lys | Cys | Tyr | Ala | 115 | | | | | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:33203192_f3_3: -AA

Figure 372A-page 450

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 157 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP372

(iii) HYPOTHETICAL: YES

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: HYPOTHETICAL ABC TRANSPORTER

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| Met | Lys | Glu | Ile | Val | Thr | Ile | Glu | Asn | Val | Ser | Phe | Asn | Tyr | His | Asn | 1 | 5 | 10 | 15 |
| Arg | Ala | Ile | Phe | Lys | Asp | Phe | Asn | Leu | Ser | Ile | Gln | Glu | Gly | Asp | Phe | 20 | 25 | 30 | |
| Leu | Cys | Val | Leu | Gly | Glu | Ser | Gly | Ser | Gly | Lys | Ser | Thr | Leu | Leu | Gly | 35 | 40 | 45 | |
| Leu | Ile | Leu | Gly | Leu | Leu | Lys | Pro | Ser | Leu | Gly | Ser | Val | Lys | Ile | Phe | 50 | 55 | 60 | |
| Asn | Glu | Thr | Leu | Ser | Asn | Asn | Ala | Phe | Leu | Arg | Gln | Lys | Ile | Gly | Tyr | 65 | 70 | 75 | 80 |
| Ile | Ala | Gln | Gly | Asn | Ser | Leu | Phe | Pro | His | Leu | Asn | Ala | Leu | Gln | Asn | 85 | 90 | 95 | |
| Met | Thr | Phe | Cys | Leu | Asn | Leu | Gln | Gly | Ile | Asn | Lys | Gln | Ala | Ala | Gln | 100 | 105 | 110 | |
| Lys | Glu | Ala | Lys | Ala | Leu | Ala | Leu | Lys | Met | Gly | Leu | Asp | Glu | Ser | Leu | 115 | 120 | 125 | |
| Met | Asp | Lys | Phe | Pro | Asn | Glu | Leu | Ser | Gly | Gly | Gln | Ala | Lys | Glu | Trp | 130 | 135 | 140 | |
| Ala | Leu | Leu | Gly | Gly | Leu | Ser | Thr | Gly | Gln | Asn | Ser | Phe | Tyr | 145 | 150 | 155 | | | |

(2) INFORMATION FOR SEQ ID NO:33218912_c2_3: -AA

Figure 373A-page 451

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 190 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 373

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ile | Phe | Pro | Glu | Arg | Phe | Gln | Asn | Ala | Phe | Leu | Gly | Leu | Ser | Glu | 1 | 5 | 10 | 15 |
| Leu | Phe | Tyr | Tyr | Ala | Ser | Ser | Leu | Ser | Phe | Tyr | Thr | Ile | Leu | Ser | Leu | 20 | 25 | 30 | |
| Ser | Pro | Ile | Leu | Leu | Phe | Val | Phe | Ser | Leu | Phe | Val | Ser | His | Tyr | Leu | 35 | 40 | 45 | |
| Gln | Ala | His | Ser | Gly | Glu | Met | Glu | Ala | Leu | Ile | Phe | Pro | Asn | Ala | Pro | 50 | 55 | 60 | |
| Lys | Leu | Ile | Gly | Ala | Ile | Lys | Asp | Phe | Leu | Glu | Asn | Phe | Lys | Lys | Thr | 65 | 70 | 75 | 80 |
| Asp | Met | Thr | Leu | Gly | Thr | Leu | Glu | Glu | Val | Ser | Ile | Val | Val | Ala | Leu | 85 | 90 | 95 | |
| Val | Leu | Phe | Cys | Glu | Asn | Tyr | Arg | Ser | Ile | Ala | Ser | Lys | Ile | Phe | Asp | 100 | 105 | 110 | |
| Ala | Lys | Pro | Arg | Asp | Tyr | Ala | His | Phe | Lys | Gly | Lys | Glu | Ile | Phe | Leu | 115 | 120 | 125 | |
| Phe | Trp | Gly | Phe | Gly | Thr | Thr | Leu | Val | Phe | Leu | Phe | Ala | Leu | Pro | Leu | 130 | 135 | 140 | |
| Val | Val | Phe | Phe | Asp | Ile | Lys | Ile | Gln | Val | Phe | Phe | Glu | Asp | Lys | Asp | 145 | 150 | 155 | 160 |
| Ser | Ser | Leu | Leu | His | Val | Leu | Arg | Trp | Ile | Gly | Thr | Tyr | Ala | Phe | Phe | 165 | 170 | 175 | |
| Leu | Ile | Leu | Phe | Thr | Ile | Pro | Thr | Asn | Lys | Val | Phe | Lys | Leu | Lys | | 180 | 185 | 190 | |

(2) INFORMATION FOR SEQ ID NO:33397538_f1_4: -AA

Figure 375A - page 453

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 375

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Leu | Met | Ile | Phe | Thr | Ser | Ile | Leu | Lys | Ile | Ala | Leu | Lys | Val |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Leu | Ser | Glu | Arg | Lys | Lys | Asn | Arg | Tyr | Gly | Phe | Pro | Arg | Ile | Phe | Asp |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Val | Ala | Asp | Ile | Glu | Gln | Glu | Glu | Arg | Glu | Val | Ile | Glu | Trp | Arg | Glu |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Lys | Lys | Lys | Ala | Ser | Lys | Gln | Ser | Tyr | Lys | Gln | Asn | Leu | Gln | Ile | Asn |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Lys | Ile | Ala | Asn | Asp | Leu | Lys | Arg | Asp | Lys | Ile | Val | Asp | Lys | Arg | Thr |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 |
| Ile | Leu | Ser | Val | Ile | Asp | Ala | Asp | Ile | Glu | Arg | Gly | Phe | Ile | Pro | Pro |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| Lys | Asp | Leu | Leu | Lys | Gln | Leu | Glu | Lys | Ile | Ser | Ala | Ser | Leu | Ser | Lys |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Asp | Ile | Val | Ile | Thr | Ile | Lys | Gln | Val | Glu | Lys | Leu | Glu | Leu | Asn | Tyr |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| Ala | Leu | Ile | Asp | Asn | Ile | Gln | His | Asn | Thr | Leu | Asp | Asp | Thr | Leu | Asp |
| | | | | | | 135 | | | | | 140 | | | | |
| Phe | Thr | Phe | Ile | Val | Gly | Asp | Ser | Leu | Ser | Val | Gln | Ser | Leu | Tyr | Val |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 |
| Thr | Phe | Asn | Leu | Val | Ile | Asp | Ile | Asp | Arg | Pro | Met | Ser | Glu | Gln | Phe |
| | | | | 165 | | | | | 170 | | | | | 175 | |
| Leu | Asn | Unk | Ile | Gly | Lys | Leu | Gly | Ser | Phe | Glu | Ser | Arg | Glu | Gln | Ala |
| | | | 180 | | | | | 185 | | | | | 190 | | |
| Leu | Glu | Trp | Val | Arg | Leu | Ser | Gln | Thr | Lys | Leu | Ile | Ile | Glu | Thr | Pro |
| | | 195 | | | | | 200 | | | | | 205 | | | |
| Lys | Glu | Ala | Leu | Lys | Asn | Ala | Glu | Leu | Ser | Gln | Ile | Glu | Glu | Ile | Leu |
| | | | | | | 215 | | | | | 220 | | | | |
| Thr | Gly | Cys | Ile | Phe | Asn | Gly | Ala | Tyr | Arg | Leu | Gln | Asn | Asp | Leu | Lys |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 |

Lys Gly Arg

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 235 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 376

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: cation efflux system membrane protein czcA

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ser | Glu | Val | Ala | Ser | Val | Gly | Gly | Phe | Val | Lys | Asp | Tyr | Glu | Val | 1 | 5 | 10 | 15 |
| Thr | Leu | Gln | Asn | Asp | Ser | Leu | Ile | Arg | Tyr | Asn | Leu | Ser | Leu | Glu | Gln | 20 | 25 | 30 | |
| Val | Ala | Asn | Ala | Ile | Lys | Asn | Ser | Asn | Asn | Asp | Thr | Gly | Gly | Gly | Val | 35 | 40 | 45 | |
| Ile | Leu | Glu | Asn | Gly | Phe | Glu | Lys | Ile | Ile | Arg | Ser | His | Gly | Tyr | Ile | 50 | 55 | 60 | |
| Gln | Ser | Leu | Asn | Asp | Leu | Glu | Glu | Ile | Val | Val | Lys | Lys | Glu | Gly | Ala | 65 | 70 | 75 | 80 |
| Ile | Pro | Leu | Lys | Ile | Lys | Asp | Ile | Ala | Ser | Val | Arg | Leu | Ala | Pro | Lys | 85 | 90 | 95 | |
| Pro | Arg | Arg | Gly | Ala | Ala | Asn | Leu | Asn | Gly | Asp | Lys | Glu | Val | Val | Gly | 100 | 105 | 110 | |
| Gly | Ile | Val | Met | Val | Arg | Tyr | His | Ala | Asp | Thr | Tyr | Lys | Val | Leu | Lys | 115 | 120 | 125 | |
| Ala | Ile | Lys | Glu | Lys | Ile | Ala | Thr | Leu | Gln | Ala | Ser | Asn | Pro | Asp | Val | 130 | 135 | 140 | |
| Lys | Ile | Thr | Ser | Val | Tyr | Asp | Arg | Ser | Glu | Leu | Ile | Glu | Lys | Gly | Ile | 145 | 150 | 155 | 160 |
| Asp | Asn | Leu | Ile | His | Thr | Leu | Ile | Glu | Glu | Ser | Val | Ile | Val | Leu | Val | 165 | 170 | 175 | |
| Ile | Ile | Ala | Ile | Phe | Leu | Leu | His | Phe | Arg | Ser | Ala | Leu | Val | Val | Ile | 180 | 185 | 190 | |
| Ile | Thr | Leu | Pro | Leu | Arg | Val | Cys | Ile | Ser | Phe | Leu | Leu | Met | Ser | Tyr | 195 | 200 | 205 | |
| Phe | Asn | Ile | Glu | Ala | Ser | Ile | Met | Ser | Leu | Gly | Gly | Ile | Ala | Ile | Ala | 210 | 215 | 220 | |
| Ile | Gly | Ala | Met | Val | Asn | Ala | Ala | Ile | Val | Met | Val | | | | | 225 | 230 | 235 | |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP377

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: KERATIN- TYPE II CYTOSKELETAL-intermediate filame

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Glu | Thr | Phe | Leu | Arg | Ile | Phe | Glu | Lys | Asp | Ile | Phe | Asn | Thr | Pro | 1 | 5 | 10 | 15 |
| Tyr | Lys | Leu | Glu | Val | Ile | Asn | Ala | Thr | Glu | Gly | Gly | Ala | Arg | Ile | Lys | 20 | 25 | 30 | |
| Gly | Thr | Lys | Glu | Met | Pro | Phe | Lys | Glu | Val | Cys | Glu | Lys | Ile | Asp | Lys | 35 | 40 | 45 | |
| Ser | Lys | Pro | Lys | Pro | Pro | Ile | Asn | Leu | Ile | Tyr | Pro | Thr | Gln | Ser | Glu | 50 | 55 | 60 | |
| Gln | Ala | Lys | Asn | Leu | Lys | Ile | Ala | Lys | Lys | Lys | Cys | Glu | Glu | Ile | Ile | 65 | 70 | 75 | 80 |
| Lys | Tyr | Ala | Asn | Glu | Lys | Lys | Thr | Gln | Val | Glu | Glu | Ala | Phe | Leu | Lys | 85 | 90 | 95 | |
| Val | Ala | Glu | Phe | Leu | Glu | Lys | Val | Glu | Lys | Leu | His | Glu | Lys | Asn | Lys | 100 | 105 | 110 | |
| Leu | Glu | Glu | Leu | Asp | Phe | Glu | Glu | Leu | Glu | Asn | Leu | Ser | Ala | Glu | Ile | 115 | 120 | 125 | |
| Asp | Asn | Val | Lys | Glu | Leu | Phe | Asp | Asp | Lys | Arg | Phe | Asn | Ser | Tyr | Phe | 130 | 135 | 140 | |
| Met | Asp | Ala | Ile | Gln | Ser | Tyr | Ile | Phe | His | Gln | Glu | Leu | His | Ile | Ala | 145 | 150 | 155 | 160 |
| Glu | Ile | Val | Cys | Lys | Lys | Thr | Ser | Asn | Glu | Asp | Gly | Ile | Lys | Gly | 165 | 170 | 175 | | |

Figure 378A - page 456

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

HPP 378

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

[illegible]

(2) INFORMATION FOR SEQ ID NO:3360130_c1_11: - A A

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 379

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Met | Val | Tyr | Lys | Leu | Pro | Lys | His | Gln | Gln | Asn | Lys | Val | Met | Ile |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Leu | Gly | Leu | Gly | Leu | Ala | Met | Ile | Thr | Arg | Ile | Gly | Leu | Leu | Gly | Ser |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Leu | Phe | Phe | Ile | Ser | His | Leu | Gln | Lys | Pro | Leu | Phe | Ala | Ile | Ala | Gly |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Met | Ser | Phe | Ser | Trp | Arg | Asp | Val | Val | Leu | Leu | Leu | Gly | Gly | Ala | Phe |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Leu | Ala | Phe | Lys | Ala | Leu | Val | Glu | Leu | Lys | Arg | Ala | Asp | Leu | Ser | |
| 65 | | | | | 70 | | | | | 75 | | | | | |

(2) INFORMATION FOR SEQ ID NO:33601578_f2_4: - AA

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid

HPP 380

(A) ORGANISM: *Helicobacter pylori*

Ile Asp Ser Ile Arg Ser Pro His Ser Arg Gly Phe Gly
145 150 155

Figure 382 A - page 461

Lys Thr
210

(2) INFORMATION FOR SEQ ID NO:34089087_f3_3: - AA

Figure 383A - page 462

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 295 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP383

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Lys | Pro | Lys | Ser | Met | Lys | Glu | Lys | Leu | Arg | Gly | Ala | Met | Val | Asn | 1 | 5 | 10 | 15 |
| Ile | Leu | Arg | Ile | Lys | Met | Ile | Glu | Ile | Ser | Glu | Trp | Leu | Gln | Lys | Leu | 20 | 25 | 30 | |
| Asp | Asp | Ala | Leu | Asp | Lys | Val | Val | Ala | Lys | Lys | Glu | Pro | Glu | Ser | Phe | 35 | 40 | 45 | |
| Leu | Lys | Pro | Ile | Ile | Ser | Pro | Ile | Glu | Asp | Tyr | Gln | Lys | Ser | Val | Arg | 50 | 55 | 60 | |
| Gln | Ile | Gln | Ala | Gln | Phe | Thr | Asp | Ala | Pro | Lys | Phe | Asn | Glu | Glu | Gly | 65 | 70 | 75 | 80 |
| Ala | Tyr | Pro | Gln | Phe | Leu | Ser | Cys | Gly | Leu | Leu | Gln | Val | Arg | Gly | Lys | 85 | 90 | 95 | |
| Asn | Gly | Ala | Asn | Met | Glu | Phe | Leu | Leu | Pro | Lys | Val | Tyr | Pro | Phe | Pro | 100 | 105 | 110 | |
| Pro | Lys | Ser | Leu | Tyr | Ile | Glu | His | Glu | Lys | Asp | Gly | Gln | Phe | Leu | Arg | 115 | 120 | 125 | |
| Glu | Met | Leu | Met | Arg | Leu | Leu | Ser | Ser | Ala | Pro | Leu | Val | Gln | Leu | Glu | 130 | 135 | 140 | |
| Val | Ile | Leu | Ile | Asp | Ala | Leu | Ser | Leu | Gly | Gly | Ile | Phe | Asn | Leu | Ala | 145 | 150 | 155 | 160 |
| Arg | Arg | Leu | Leu | Asp | Lys | Asn | Asn | Asp | Phe | Ile | Tyr | Gln | Gln | Arg | Ile | 165 | 170 | 175 | |
| Leu | Thr | Glu | Ser | Lys | Glu | Ile | Glu | Glu | Ala | Leu | Lys | His | Leu | His | Glu | 180 | 185 | 190 | |
| Tyr | Leu | Lys | Val | Asn | Leu | Gln | Glu | Lys | Leu | Ala | Gly | Phe | Arg | Asp | Phe | 195 | 200 | 205 | |
| Val | His | Tyr | Asn | Glu | Asn | Ala | Lys | Asp | Ser | Leu | Pro | Leu | Lys | Ala | Leu | 210 | 215 | 220 | |
| Phe | Leu | Ser | Gly | Val | Asp | Ala | Leu | Ser | Lys | Asp | Ala | Leu | Tyr | Tyr | Leu | 225 | 230 | 235 | 240 |

(2) INFORMATION FOR SEQ ID NO:34097707_c2_18: - AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 384

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Leu | Ile | Ser | Val | Met | Ile | Gly | Gln | Asn | Gln | Val | Leu | Gly | Phe | Ile |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Gly | Thr | Asn | Phe | Lys | Gln | Glu | Leu | Val | Val | Asp | Phe | Ile | Val | Pro | Ser |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Ala | Glu | Ile | Asn | Ile | Gly | Asn | Gln | Val | Ile | Thr | Ser | Gly | Leu | Asp | Gly |
| | | | 35 | | | | 40 | | | | | 45 | | | |
| Ile | Phe | Gly | Ala | Gly | Val | Phe | Val | Gly | Glu | Val | Ser | Ser | Val | Glu | Asp |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| His | Tyr | Thr | Tyr | Lys | Ser | Ala | Val | Leu | Lys | Asn | Ala | Phe | Leu | Ser | Glu |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 |
| Ala | Lys | Leu | Leu | Arg | His | Val | Phe | Leu | Ser | Gly | Val | Lys | Asn | | |
| | | | | 85 | | | | | 90 | | | | | | |

(2) INFORMATION FOR SEQ ID NO:34099062_c1_8: -AA

Figure 385A - page 465

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 82 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP: 385

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Met Glu Ala Gln Leu Arg Phe Thr Gly Val Gly Gly Gln Gly Val Leu
1 5 10 15

Leu Ala Gly Glu Ile Leu Ala Glu Ala Lys Ile Val Ser Gly Gly Tyr
20 25 30

Gly Thr Lys Thr Ser Thr Tyr Thr Ser Gln Val Arg Gly Gly Pro Thr
35 40 45

Lys Val Asp Ile Leu Leu Asp Lys Asp Glu Ile Ile Phe Pro Tyr Ala
50 55 60

Lys Glu Gly Glu Ile Asp Phe Met Leu Ser Val Ala Gln Ile Ser Tyr
65 70 75 80

Asn Gln Phe

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 202 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP386

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gln | Ala | Trp | Val | Asp | Lys | Pro | Val | Leu | Glu | Pro | Asp | Ser | Asn | 1 | 5 | 10 | 15 | |
| Ala | Gln | Tyr | Ala | Ala | Val | Ile | Glu | Ile | Asp | Val | Ala | Glu | Ile | Thr | Glu | 20 | 25 | 30 | |
| Pro | Ile | Leu | Ala | Cys | Pro | Asn | Asp | Pro | Asp | Asp | Val | Ala | Thr | Leu | Ser | 35 | 40 | 45 | |
| Glu | Val | Leu | Ala | Asp | Thr | Thr | Gly | Lys | Arg | Pro | His | Ala | Ile | Asp | Glu | 50 | 55 | 60 | |
| Val | Phe | Ile | Gly | Ser | Cys | Met | Thr | Asn | Ile | Gly | His | Phe | Arg | Ala | Phe | 65 | 70 | 75 | 80 |
| Gly | Glu | Ile | Val | Lys | Asn | Ala | Pro | Pro | Ser | Gln | Ala | Arg | Leu | Trp | Val | 85 | 90 | 95 | |
| Val | Pro | Pro | Ser | Lys | Met | Asp | Glu | Gln | Glu | Leu | Ile | Asn | Glu | Gly | Tyr | 100 | 105 | 110 | |
| Tyr | Ala | Ile | Phe | Gly | Ala | Ala | Gly | Ala | Arg | Thr | Glu | Val | Pro | Gly | Cys | 115 | 120 | 125 | |
| Ser | Leu | Cys | Met | Gly | Asn | Gln | Ala | Arg | Val | Arg | Asp | Asn | Ala | Val | Val | 130 | 135 | 140 | |
| Phe | Ser | Thr | Ser | Thr | Arg | Asn | Phe | Asp | Asn | Arg | Met | Gly | Arg | Gly | Ala | 145 | 150 | 155 | 160 |
| Lys | Val | Tyr | Leu | Gly | Ser | Ala | Glu | Leu | Gly | Ala | Ala | Cys | Ala | Leu | Leu | 165 | 170 | 175 | |
| Gly | Arg | Ile | Pro | Thr | Lys | Glu | Glu | Tyr | Met | Asn | Leu | Val | Ser | Glu | Lys | 180 | 185 | 190 | |
| Leu | Glu | Ser | Gln | Lys | Asp | Lys | Ile | Tyr | Arg | Ser | | | | | | 195 | 200 | | |

(2) INFORMATION FOR SEQ ID NO:34161500_c2_8: - AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP387

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Gly | Asn | Ala | Gly | Val | Ala | Leu | Ala | Gly | Leu | Met | Ser | Asp | Glu | Ile | 1 | 5 | 10 | 15 |
| Tyr | Leu | Cys | Ala | Leu | Asp | Cys | Ala | Tyr | Ile | Lys | Gly | Phe | Lys | Lys | His | 20 | 25 | 30 | |
| Ala | Gln | Asn | Ser | Tyr | Tyr | Gly | Asp | Glu | Lys | Glu | Ile | Asp | Thr | Ser | Ser | 35 | 40 | 45 | |
| Leu | Ile | Ser | Val | Glu | Gly | Asn | Val | Glu | Gly | Tyr | Glu | Thr | Phe | Ser | Asp | 50 | 55 | 60 | |
| Ser | Leu | Phe | Leu | Leu | Ser | Lys | Glu | Arg | Ile | Glu | Glu | Ala | Leu | His | Tyr | 65 | 70 | 75 | 80 |
| Tyr | Gln | Pro | Lys | Lys | Val | Tyr | Asn | Leu | Ser | Tyr | Gly | Ala | Lys | Ile | Lys | 85 | 90 | 95 | |
| His | Ala | Val | Ser | Leu | Asn | His | Ser | Gln | Val | Lys | Leu | Lys | Gln | Ile | Asn | 100 | 105 | 110 | |
| Lys | Gln | Asp | Ala | Ile | Val | Arg | Ile | Lys | Ser | Met | Phe | Ser | Pro | Arg | Ser | 115 | 120 | 125 | |
| Asn | His | Ala | Lys | Asp | Leu | Lys | Asn | Leu | Gln | Lys | Asn | Leu | Ile | Arg | Phe | 130 | 135 | 140 | |
| Lys | Glu | Asp | Phe | Phe | Thr | His | Leu | Asn | Thr | Pro | Cys | Lys | Thr | Lys | Gln | 145 | 150 | 155 | 160 |
| Glu | Ala | Phe | Glu | Trp | Val | Asp | Ser | Leu | Ser | Gly | Phe | Cys | Gln | Thr | Ala | 165 | 170 | 175 | |
| Ser | Ala | Lys | Thr | Pro | Thr | Ile | Gly | Ile | Leu | Phe | Glu | Gly | Ser | Val | Ala | 180 | 185 | 190 | |
| His | Ile | Leu | Gln | Ser | Val | Leu | Ile | Val | Ser | Leu | His | Leu | Lys | Glu | Asn | 195 | 200 | 205 | |
| Glu | Leu | Thr | Leu | Leu | Ser | Asn | Ser | Leu | Lys | Thr | Pro | 210 | 215 | 220 | | | | | |

(2) INFORMATION FOR SEQ ID NO:34172639_c1_5: -AA

Figure 388A-page 468

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 79 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 388

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Met | Asn | Phe | Phe | Val | Gly | Gly | Leu | Ser | Ile | Val | Cys | Asn | Val | Val |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Val | Ile | Thr | Tyr | Ser | Ala | Leu | His | Pro | Thr | Ala | Pro | Val | Glu | Gly | Ala |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Glu | Asp | Ile | Val | Gln | Val | Ser | His | His | Leu | Thr | Ser | Phe | Tyr | Gly | Pro |
| | | | 35 | | | | | 40 | | | | 45 | | | |
| Ala | Thr | Gly | Leu | Leu | Phe | Gly | Leu | Pro | Thr | Cys | Met | Pro | Leu | Ser | Thr |
| | | | 50 | | | 55 | | | | | 60 | | | | |
| Thr | Leu | Leu | Val | Trp | Ile | Gly | Asp | Pro | Ile | Leu | Gly | Ile | Ala | Tyr | Ser |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 |

(2) INFORMATION FOR SEQ ID NO:34179577_f2_5: - AA

Figure 389A - page 469

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 247 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP389

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gln | Lys | Ser | Ile | Phe | Lys | Ile | Thr | Leu | Leu | Val | Phe | Leu | Phe | 1 | 5 | 10 | 15 | |
| Leu | Arg | Asn | Ala | Val | Gly | Leu | Asp | Asp | Lys | Lys | Ala | Ala | Pro | Lys | Ser | 20 | 25 | 30 | |
| Val | Gln | Asn | Thr | Pro | Lys | Asn | Leu | Pro | Pro | Ile | Gln | Leu | Arg | Leu | Asp | 35 | 40 | 45 | |
| Gln | Ala | Tyr | Glu | Asp | Leu | Ile | Lys | Met | Leu | Asp | Asn | Met | Gly | Lys | Ser | 50 | 55 | 60 | |
| Thr | Gln | Tyr | Glu | Phe | Pro | Lys | Ile | Lys | Glu | Ile | Leu | Glu | Gln | Ser | Glu | 65 | 70 | 75 | 80 |
| Glu | Glu | Trp | Leu | Gly | Val | Ala | His | Glu | Glu | Cys | Val | Ala | Leu | Val | Met | 85 | 90 | 95 | |
| Leu | Ile | Ser | Pro | Lys | Ala | Ser | Ile | Glu | Asn | Ser | Pro | Ile | Tyr | Lys | Asn | 100 | 105 | 110 | |
| Cys | Tyr | Glu | Ala | Tyr | Val | Lys | Gln | Arg | Ile | His | Asp | Leu | Tyr | Asp | Phe | 115 | 120 | 125 | |
| Tyr | Ile | Glu | Gly | Lys | Lys | Val | Lys | Arg | Lys | Ile | Lys | Lys | Ala | His | Glu | 130 | 135 | 140 | |
| His | Glu | Met | Ala | Leu | Asn | Lys | Ser | Gln | Pro | Leu | Lys | Lys | Glu | Pro | Pro | 145 | 150 | 155 | 160 |
| Lys | Ser | Glu | Asn | Lys | Lys | Gly | Leu | Thr | Lys | Pro | Ser | Leu | Lys | Asp | Ala | 165 | 170 | 175 | |
| Lys | Ile | Pro | Lys | Gly | Tyr | Tyr | Leu | Gln | Ile | Gly | Ala | Phe | Leu | Asn | Ser | 180 | 185 | 190 | |
| Pro | Ser | Lys | Asp | Phe | Leu | Gln | Thr | Leu | Lys | Thr | Phe | Pro | His | Gln | Met | 195 | 200 | 205 | |
| Glu | Glu | Lys | Asp | Ser | Leu | Thr | His | Tyr | Leu | Ile | Gly | Pro | Tyr | Lys | Thr | 210 | 215 | 220 | |
| Lys | Glu | Glu | Ala | Leu | Lys | Gln | Leu | Glu | Asn | Ala | Ala | Lys | Ser | Phe | Lys | 225 | 230 | 235 | 240 |

Asn Lys Pro Ala Leu Val Glu Lys
245

Figure 389A - page 470

(2) INFORMATION FOR SEQ ID NO:34189716_c3_7:- AA

Figure 390A -page 471

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 149 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein HPP 390

(iii) HYPOTHETICAL: YES

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| Met | Gln | Glu | Ile | Leu | Ile | Pro | Leu | Lys | Glu | Lys | Ser | Tyr | Lys | Val | Phe | 1 | 5 | 10 | 15 |
| Leu | Gly | Glu | Leu | Pro | Glu | Ile | Lys | Leu | Lys | Gln | Lys | Ala | Leu | Ile | Ile | 20 | 25 | 30 | |
| Ser | Asp | Ser | Ile | Val | Ala | Gly | Leu | His | Leu | Pro | Tyr | Leu | Leu | Glu | Arg | 35 | 40 | 45 | |
| Leu | Asn | Ala | Leu | Glu | Val | Arg | Val | Cys | Val | Ile | Glu | Ser | Gly | Glu | Lys | 50 | 55 | 60 | |
| Tyr | Lys | Asn | Phe | His | Ser | Leu | Glu | Arg | Ile | Leu | Asn | Asn | Ala | Phe | Glu | 65 | 70 | 75 | 80 |
| Met | Gln | Leu | Asn | Arg | His | Ser | Leu | Met | Ile | Ala | Leu | Gly | Gly | Gly | Val | 85 | 90 | 95 | |
| Ile | Ser | Asp | Met | Val | Gly | Phe | Ala | Ser | Ser | Ile | Tyr | Phe | Arg | Gly | Ile | 100 | 105 | 110 | |
| Asp | Phe | Ile | Asn | Ile | Pro | Tyr | Asp | Phe | Thr | Arg | Ser | Ser | Gly | Cys | Glu | 115 | 120 | 125 | |
| Arg | Gly | Gly | Glu | Asn | Arg | Asp | Gln | His | Ala | Leu | Trp | Gln | Glu | Pro | Asn | 130 | 135 | 140 | |
| Arg | Ile | Val | Pro | Pro | Ala | | | | | | | | | | | 145 | 150 | | |

(2) INFORMATION FOR SEQ ID NO:34194093_f1_3: AA

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 228 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 391

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

[illegible]

(2) INFORMATION FOR SEQ ID NO:34253912_f2_2: - A A

- ```
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 101 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

ii) MOLECULE TYPE: protein

iii) HYPOTHETICAL: YES

vi) ORIGINAL SOURCE:
 (A) ORGANISM: Helicobacter pylori

xi) SEQUENCE DESCRIPTION:
```

HPP 392

[illegible]

(2) INFORMATION FOR SEQ ID NO:34265691\_f3\_8: - AA

Figure 393A - page 474

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 393

(iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

## (xi) SEQUENCE DESCRIPTION: UDP-N-ACETYLMURAMYL-TRIPETIDE SYNTHETASE

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Arg | Ile | Leu | His | Tyr | Gly | Gly | Glu | Leu | Pro | Cys | Asp | Cys | Pro | Lys | 1   | 5   | 10  | 15  |
| Arg | Ile | Ala | Gly | Leu | Asp | Phe | Ala | Leu | Lys | Ile | Leu | Thr | Asn | Ile | Thr | 20  | 25  | 30  |     |
| Ser | Asp | His | Leu | Asp | Phe | His | Gln | Asn | Ile | Glu | Asn | Tyr | Arg | Asp | Ala | 35  | 40  | 45  |     |
| Lys | Asn | Ser | Phe | Phe | Lys | Asp | Glu | Gly | Leu | Lys | Val | Ile | Asn | Arg | Asp | 50  | 55  | 60  |     |
| Glu | Thr | Asn | Ala | Leu | Phe | Asn | Pro | Ile | Asn | Ala | Arg | Thr | Tyr | Ala | Leu | 65  | 70  | 75  | 80  |
| Asp | Lys | Lys | Ala | His | Leu | Asn | Val | Gln | Ala | Phe | Ser | Leu | Asn | Pro | Ser | 85  | 90  | 95  |     |
| Ile | Ser | Ala | Ser | Leu | Cys | Tyr | Gln | His | Asp | Leu | Arg | Asp | Pro | Asn | Leu | 100 | 105 | 110 |     |
| Lys | Glu | Thr | Ala | Leu | Ile | His | Ser | Pro | Leu | Leu | Gly | Arg | Tyr | Asn | Leu | 115 | 120 | 125 |     |
| Tyr | Asn | Ile | Leu | Ala | Gly | Val | Leu | Gly | Val | Lys | Leu | Leu | Thr | Gln | Leu | 130 | 135 | 140 |     |
| Pro | Leu | Glu | Thr | Ile | Ala | Pro | Leu | Leu | Glu | Asn | Phe | Tyr | Gly | Val | Lys | 145 | 150 | 155 | 160 |
| Gly | Arg | Leu | Glu | Ile | Val | His | Ser | Lys | Pro | Leu | Val | Val | Val | Asp | Phe | 165 | 170 | 175 |     |
| Ala | His | Thr | Thr | Asp | Gly | Met | Gln | Gln | Val | Phe |     |     |     |     |     | 180 | 185 |     |     |



Ser Gln Phe Tyr Leu Ser  
195

(2) INFORMATION FOR SEQ ID NO:34489543\_f2\_2: -AA

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HDP 395

(iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: putative chemoreceptor

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Val | Ala | Asp | Glu | Val | Arg | Lys | Leu | Ala | Glu | Lys | Thr | Gln | Lys | Ala | 1   | 5   | 10  | 15  |
| Thr | Lys | Glu | Ile | Ala | Val | Val | Val | Lys | Ser | Met | Gln | Gln | Glu | Ala | Asn | 20  | 25  | 30  |     |
| Asp | Ile | Gln | Thr | Asn | Thr | His | Asp | Ile | Asn | Ser | Ile | Val | Gly | Ser | Ile | 35  | 40  | 45  |     |
| Lys | Gly | Asp | Val | Glu | Glu | Leu | Lys | Ser | Thr | Val | Lys | Asn | Asn | Met | Ile | 50  | 55  | 60  |     |
| Val | Ala | Gln | Ala | Ala | Lys | Tyr | Thr | Ile | Tyr | Asn | Ile | Asn | Asn | Arg | Val | 65  | 70  | 75  | 80  |
| Phe | Cys | Gly | Unk | Ala | Lys | Leu | Asp | His | Val | Val | Phe | Lys | Asn | Asn | Leu | 85  | 90  | 95  |     |
| Tyr | Gly | Met | Val | Unk | Leu | Val | Ser | Ile | Pro | Leu | Thr | Leu | Pro | Ala | His | 100 | 105 | 110 |     |
| Lys | Ser | Unk | Arg | Leu | Gly | Lys | Trp | Tyr | Tyr | Glu | Gly | Ala | Gly | Lys | Glu | 115 | 120 | 125 |     |
| Asn | Phe | Ala | Asn | Thr | Ser | Gly | Tyr | Arg | Ala | Leu | Glu | Ser | His | His | Ala | 130 | 135 | 140 |     |
| Ser | Val | His | Ala | Glu | Ala | Asn | Asp | Leu | Val | Lys | Ala | Val | Gln | Glu | Asp | 145 | 150 | 155 | 160 |
| His | Val | Thr | Asp | Ser | Lys | Tyr | Leu | Glu | His | Lys | Val | His | Leu | Met | Glu | 165 | 170 | 175 |     |
| Asp | Ser | Ala | Lys | His | Val | Lys | Glu | Asn | Ile | Asp | Lys | Met | Phe | Tyr | Glu | 180 | 185 | 190 |     |
| Lys | Gln | Asp | Glu | Leu | Asn | Lys | Ile | Ile | Glu | Lys | Ile | Gln | Lys | Gly | Glu | 195 | 200 | 205 |     |

(2) INFORMATION FOR SEQ ID NO:34489549\_f2\_2:- AA

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 61 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 396

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: aspartate chemoreceptor

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Val | Ala | Asp | Glu | Val | Arg | Lys | Leu | Ala | Glu | Arg | Thr | Gln | Lys | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Ser | Glu | Ile | Glu | Ala | Asn | Ile | Asn | Ile | Leu | Val | Gln | Ser | Ile | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asp | Asn | Ala | Glu | Ser | Ile | Lys | Met | Gln | Asn | Lys | Gly | Val | Glu | Asn | Ile |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| His | Asn | Ser | Ile | Asn | Ala | Phe | Asn | Lys | Met | Cys | Arg | Ile | Ile |     |     |
| 50  |     |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |

$\therefore A-A$ 

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 135 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 397

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Met Ser Val Val Ala Ala Met Val Ile Val Gly Cys Ser His Ala Pro  
1 5 10 15

Lys Ser Gly Ile Ser Lys Ser Asn Lys Ala Tyr Lys Glu Ala Thr Lys  
20 25 30

Gly Ala Pro Asp Trp Val Val Gly Asp Leu Glu Lys Val Ala Lys Tyr  
35 40 45

Glu Lys Tyr Ser Gly Val Phe Leu Gly Arg Ala Glu Asp Leu Ile Thr  
50 55 60

Asn Asn Asp Val Asp Tyr Ser Thr Asn Gln Ala Thr Ala Lys Ala Arg  
65 70 75 80

Ala Asn Leu Ala Ala Asn Leu Lys Unk Thr Leu Gln Lys Asp Leu Glu  
85 90 95

Asn Glu Lys Thr Arg Thr Val Asp Ala Ser Gly Lys Arg Ser Ile Ser  
100 105 110

Gly Thr Asp Thr Glu Lys Ile Ser Gln Leu Val Asp Lys Glu Leu Ile  
115 120 125

Ala Ser Lys Met Leu Ala Arg Tyr  
130 135

Figure 398A - page 479

(2) INFORMATION FOR SEQ ID NO:34573431 c3 28: - AA

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 200 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 398

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

|            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Met<br>1   | Asn        | Thr        | Ser        | Lys<br>5   | Lys        | Leu        | Gly        | Asn        | Pro<br>10  | Leu        | Leu        | Phe        | Leu        | His<br>15  | Asp        |
| Asn        | Lys        | Ile        | Leu<br>20  | Leu        | Phe        | Val        | Val        | Gly<br>25  | Val        | Ser        | Met        | Gly        | Gly<br>30  | Trp        | Ala        |
| Thr        | Ser        | Lys<br>35  | Ile        | Tyr        | Gln        | Phe        | Glu<br>40  | Ser        | Ala        | Leu        | Glu        | Pro<br>45  | Ile        | His        | Phe        |
| Lys        | Phe<br>50  | Ala        | Arg        | Lys        | Leu        | Ser<br>55  | Leu        | Ser        | Pro        | Phe        | Leu<br>60  | Asn        | Leu        | Ser        | His        |
| Leu<br>65  | Val        | Arg        | Asn        | Lys        | Pro<br>70  | Leu        | Asn        | Thr        | Thr        | Asp<br>75  | Gly        | Gly        | Phe        | Met        | Leu<br>80  |
| Pro        | Leu        | Tyr        | His        | Glu<br>85  | Leu        | Ala        | Thr        | Gln        | Tyr<br>90  | Pro        | Leu        | Leu        | Leu        | Lys<br>95  | Phe        |
| Asp        | Gln        | Gln        | Asn<br>100 | Asn        | Pro        | Arg        | Glu        | Leu<br>105 | Leu        | Arg        | Pro        | Asn        | Thr<br>110 | Leu        | Asn        |
| His        | Gln        | Leu<br>115 | Gln        | Pro        | Ser        | Leu        | Thr<br>120 | Pro        | Phe        | Lys        | Asp        | Cys<br>125 | Ala        | Val        | Met        |
| Ala        | Phe<br>130 | Arg        | Asn        | His        | Ser        | Phe<br>135 | Lys        | Asp        | Ser        | Leu        | Met<br>140 | Leu        | Glu        | Thr        | Cys        |
| Lys<br>145 | Thr        | Pro        | Thr        | Asp        | Trp<br>150 | Gln        | Lys        | Pro        | Ile        | Ser<br>155 | Thr        | Asn        | Leu        | Lys        | Asn<br>160 |
| Leu        | Asp        | Asp        | Ser        | Leu<br>165 | Asn        | Leu        | Leu        | Asn        | Leu<br>170 | Asn        | Gly        | Ile        | Leu        | Tyr<br>175 | Leu        |
| Ile        | His        | Asn        | Pro<br>180 | Ser        | Asp        | Leu        | Ser        | Leu<br>185 | Arg        | Arg        | Lys        | Glu        | Leu<br>190 | Trp        | Leu        |
| Ser        | Lys        | Leu<br>195 | Glu        | Asn        | Gln        | Gln        | Leu<br>200 | Ile        |            |            |            |            |            |            |            |

(2) INFORMATION FOR SEQ ID NO:34574062\_c1\_4:- AA

Figure 399- page 480

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 126 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 399

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

## (xi) SEQUENCE DESCRIPTION:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| Met | Ser | Ile | Gln | His | Phe | Arg | Val | Ala | Leu | Ile | Pro | Phe | Phe | Ala | Ala | 1   | 5   | 10  | 15 |
| Phe | Cys | Leu | Pro | Val | Phe | Ala | His | Pro | Glu | Thr | Leu | Val | Lys | Val | Lys | 20  | 25  | 30  |    |
| Asp | Ala | Glu | Asp | Gln | Leu | Gly | Ala | Arg | Val | Gly | Tyr | Ile | Glu | Leu | Asp | 35  | 40  | 45  |    |
| Leu | Asn | Ser | Gly | Lys | Ile | Leu | Glu | Ser | Phe | Arg | Pro | Glu | Glu | Arg | Phe | 50  | 55  | 60  |    |
| Pro | Met | Met | Ser | Thr | Phe | Lys | Val | Leu | Leu | Cys | Gly | Ala | Val | Leu | Ser | 65  | 70  | 75  | 80 |
| Arg | Ile | Asp | Ala | Gly | Gln | Glu | Gln | Leu | Gly | Arg | Arg | Ile | His | Tyr | Ser | 85  | 90  | 95  |    |
| Gln | Asn | Asp | Leu | Val | Glu | Tyr | Ser | Pro | Val | Thr | Glu | Lys | His | Leu | Thr | 100 | 105 | 110 |    |
| Asp | Gly | Met | Thr | Val | Arg | Glu | Leu | Ser | Arg | Trp | Cys | His | Asn | His | 115 | 120 | 125 |     |    |

(2) INFORMATION FOR SEQ ID NO:34658285\_c2\_3:- A A

Figure 400A - page 481

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 400

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: L-LACTATE PERMEASE

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Gly | Leu | Ala | Gly | Lys | Glu | Ser | Asp | Leu | Phe | Lys | Phe | Thr | Val | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Tyr | Ser | Leu | Ile | Phe | Val | Ala | Ile | Met | Gly | Val | Val | Ile | Ser | Ala | Ile |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Tyr | Trp | Ile | Pro | Glu | Val | Val | Pro | Ala | Ile | Lys |     |     |     |     |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:34666680\_c1\_4: - A A

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 401

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: Cu<sup>++</sup>-transporting P-type ATPase

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Asn | Val | Gly | Val | Pro | Phe | Ser | Tyr | Gln | Val | Ser | Ala | Thr | Phe | Gln |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asn | Ser | Arg | Leu | Ser | Ser | Leu | Leu | Glu | Thr | Leu | Lys | Lys | Ser | Phe | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Lys | Pro | Leu | Ile | Glu | Ser | Ser | Ala | Asn | Lys | Ile | Ala | Asp | Ile | Phe |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Lys | Ala | Val | Leu | Phe | Leu | Ala | Phe | Val | Ser | Phe | Leu | Leu | Trp | Gln |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Phe | Gly | Leu | Gly | Gly | Asn | Phe | Glu | Lys | Ser | Phe | Asn | Gly | Val | Tyr |     |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     |



(2) INFORMATION FOR SEQ ID NO:35156938\_c2\_14: - AA

Figure 402A - page 483

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 402

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: antigen [Entamoeba histolytica]

Met Leu Met Val Asn Gly Tyr Gln Ile Thr Met His Lys Gly Tyr Lys  
1 5 10 15

Val Gly Phe Phe Thr Ser Gly Tyr Asn Pro Asp Phe Ala Gln Thr Ile  
20 25 30

Gln Asn Arg Ser Tyr Leu Met Ser Ser Tyr Glu Leu Ser Phe Leu Arg  
35 40 45

Asn

(2) INFORMATION FOR SEQ ID NO:35163962\_f3\_6 - AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 411 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP403

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Gln | Phe | Gln | Asn | Thr | Leu | Ile | Lys | Phe | His | Ala | Leu | Ser | Phe | 1   | 5   | 10  | 15  |
| Lys | Asn | Ala | Asn | Leu | Ile | Tyr | Asn | Ala | Lys | Leu | Asn | Lys | Thr | Cys | Tyr | 20  | 25  | 30  |     |
| Lys | Glu | Asn | Ser | Asn | Thr | Ile | Ile | Leu | Arg | Ile | Lys | Met | Leu | Thr | Gln | 35  | 40  | 45  |     |
| Glu | Asp | Val | Leu | Asn | Ala | Leu | Lys | Thr | Ile | Ile | Tyr | Pro | Asn | Phe | Glu | 50  | 55  | 60  |     |
| Lys | Asp | Ile | Val | Ser | Phe | Gly | Phe | Val | Lys | Asn | Ile | Thr | Leu | His | Asp | 65  | 70  | 75  | 80  |
| Asn | Gln | Leu | Gly | Leu | Leu | Ile | Glu | Ile | Pro | Ser | Ser | Ser | Glu | Glu | Thr | 85  | 90  | 95  |     |
| Ser | Ala | Ile | Leu | Arg | Glu | Asn | Ile | Ser | Lys | Ala | Met | Gln | Glu | Lys | Gly | 100 | 105 | 110 |     |
| Val | Lys | Ala | Leu | Asn | Leu | Asp | Ile | Lys | Thr | Pro | Pro | Lys | Pro | Gln | Ala | 115 | 120 | 125 |     |
| Pro | Lys | Pro | Thr | Thr | Lys | Asn | Leu | Ala | Lys | Asn | Ile | Lys | His | Val | Val | 130 | 135 | 140 |     |
| Met | Ile | Ser | Ser | Gly | Lys | Gly | Gly | Val | Gly | Lys | Ser | Thr | Thr | Ser | Val | 145 | 150 | 155 | 160 |
| Asn | Leu | Ser | Ile | Ala | Leu | Ala | Asn | Leu | Asn | Gln | Lys | Val | Gly | Leu | Leu | 165 | 170 | 175 |     |
| Asp | Ala | Asp | Val | Tyr | Gly | Pro | Asn | Ile | Pro | Arg | Met | Met | Gly | Leu | Gln | 180 | 185 | 190 |     |
| Asn | Ala | Asp | Val | Ile | Met | Asp | Pro | Ser | Gly | Lys | Lys | Leu | Ile | Pro | Leu | 195 | 200 | 205 |     |
| Lys | Ala | Phe | Gly | Val | Ser | Val | Met | Ser | Met | Gly | Leu | Leu | Tyr | Asp | Glu | 210 | 215 | 220 |     |
| Gly | Gln | Ser | Leu | Ile | Trp | Arg | Gly | Pro | Met | Leu | Met | Arg | Ala | Ile | Glu | 225 | 230 | 235 | 240 |

|            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |  |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|--|
| Gln        | Met        | Leu        | Ser        | Asp<br>245 | Ile        | Ile        | Trp        | Gly        | Asp<br>250 | Leu        | Asp        | Val        | Leu        | Val<br>255 | Val        |  |
| Asp        | Met        | Pro        | Pro<br>260 | Arg        | Asn        | Arg        | Arg        | Cys<br>265 | Ala        | Ala        | His        | Ala        | Ala<br>270 | Gln        | Ala        |  |
| Val        | Pro        | Leu<br>275 | Ser        | Ala        | Gly        | Ile        | Thr<br>280 | Val        | Thr        | Thr        | Pro        | Gln<br>285 | Ile        | Val        | Ser        |  |
| Leu        | Asp<br>290 | Asp        | Ala        | Lys        | Arg        | Ser<br>295 | Leu        | Asp        | Met        | Phe        | Lys<br>300 | Lys        | Leu        | His        | Ile        |  |
| Pro<br>305 | Ile        | Ala        | Gly        | Ile        | Val<br>310 | Glu        | Asn        | Met        | Gly        | Ser<br>315 | Phe        | Val        | Cys        | Glu        | His<br>320 |  |
| Cys        | Lys        | Lys        | Glu        | Ser<br>325 | Glu        | Ile        | Phe        | Gly        | Ser<br>330 | Asn        | Ser        | Met        | Ser        | Gly<br>335 | Leu        |  |
| Leu        | Glu        | Ala        | Tyr<br>340 | Asn        | Thr        | Gln        | Ile        | Leu<br>345 | Ala        | Lys        | Leu        | Pro        | Leu<br>350 | Glu        | Pro        |  |
| Lys        | Val        | Arg<br>355 | Leu        | Gly        | Gly        | Asp        | Lys<br>360 | Gly        | Glu        | Pro        | Ile        | Val<br>365 | Ile        | Ser        | His        |  |
| Pro        | Thr<br>370 | Ser        | Val        | Ser        | Ala        | Lys<br>375 | Ile        | Phe        | Glu        | Lys        | Met<br>380 | Ala        | Lys        | Asp        | Leu        |  |
| Ser<br>385 | Ala        | Phe        | Leu        | Asp        | Lys<br>390 | Val        | Glu        | Arg        | Glu        | Lys<br>395 | Leu        | Ala        | Asp        | Asn        | Lys<br>400 |  |
| Asp        | Ile        | Gln        | Pro        | Thr<br>405 | Gln        | Thr        | His        | Ala        | Tyr<br>410 | Ser        | His        |            |            |            |            |  |

(2) INFORMATION FOR SEQ ID NO:35269000\_c3\_11:-AA

Figure 404A-page 486

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 404

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |    |    |    |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|----|----|----|
| Met | Gly | Val | Val | Ile | Gly | Glu | Thr | Thr | Glu | Ile | Gly | Asp | Asp | Val | Thr | 1  | 5  | 10 | 15 |
| Ile | Tyr | His | Gly | Val | Thr | Leu | Gly | Gly | Thr | Gly | Lys | Phe | Lys | Gly | Lys | 20 | 25 | 30 |    |
| Arg | His | Pro | Thr | Leu | Gly | Asn | Arg | Val | Val | Val | Gly | Ala | Gly | Ala | Lys | 35 | 40 | 45 |    |
| Val | Leu | Gly | Ala | Ile | Cys | Val | Gly | Asp | Asp | Val | Arg | Ile | Gly | Ala | Asn | 50 | 55 | 60 |    |
| Ala | Val | Val | Leu | Ser | Asp | Leu | Pro | Thr | Gly | Ser | Thr | Ala | Val | Gly | Ala | 65 | 70 | 75 | 80 |
| Lys | Ala | Lys | Thr | Ile | Thr | Lys | Asp | Arg | 85  |     |     |     |     |     |     |    |    |    |    |

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 191 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 405

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Met Leu Ser Phe Ile Ser Ala Phe Asp Lys Arg Gly Val Ser Ile Arg  
1 5 10 15

Leu Leu Thr Ala Leu Leu Leu Leu Phe Ser Leu Gly Leu Ala Lys Asp  
20 25 30

Leu Glu Ile Gln Thr Phe Val Ala Lys Tyr Leu Ser Lys Asn Gln Lys  
35 40 45

Ile Gln Ala Leu Gln Glu Gln Ile Asp Ala Leu Asp Ser Gln Glu Lys  
50 55 60

Val Val Ser Lys Trp Asp Asn Pro Ile Leu Tyr Leu Gly Tyr Asn Asn  
65 70 75 80

Ala Asn Val Ser Asp Phe Phe Arg Leu Asp Ser Thr Leu Met Gln Asn  
85 90 95

Met Ser Leu Gly Leu Ser Gln Lys Val Asp Leu Asn Gly Lys Lys Leu  
100 105 110

Thr Gln Ser Lys Met Ile Asn Leu Glu Lys Gln Lys Lys Ile Leu Glu  
115 120 125

Leu Lys Lys Thr Lys Gln Gln Leu Val Ile Asn Leu Met Ile Asn Gly  
130 135 140

Ile Glu Asn Tyr Lys Asn Gln Gln Glu Ile Glu Leu Leu Asn Thr Ala  
145 150 155 160

Ile Lys Asn Leu Glu Asn Thr Leu Tyr Gln Ala Asn His Ser Ser Ser  
165 170 175

Pro Asp Leu Ile Glu Ile Asp Lys Leu Glu Asn Leu Lys Ile Ala Asn  
180 185 190

Figure 406A - page 488

(2) INFORMATION FOR SEQ ID NO:35345228 f2 8:-AA

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 107 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 406

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: norepinephrine transporter

|           |           |           |            |           |           |           |           |            |           |           |           |           |           |           |           |
|-----------|-----------|-----------|------------|-----------|-----------|-----------|-----------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| Val<br>1  | Unk       | Leu       | Tyr        | Leu<br>5  | Ala       | Leu       | Thr       | Leu        | Ser<br>10 | Leu       | Gly       | Ile       | Ala       | Met<br>15 | Leu       |
| Leu       | Val       | Glu       | Met<br>20  | Leu       | Ile       | Gly       | Asn       | Leu<br>25  | Gly       | Lys       | Lys       | Asp       | Val<br>30 | Val       | Ser       |
| Asn       | Tyr       | Gln<br>35 | Ile        | Leu       | Asp       | Pro       | Lys<br>40 | Arg        | Lys       | Lys       | Tyr       | Tyr<br>45 | Pro       | Phe       | Thr       |
| Ser       | Phe<br>50 | Phe       | Ile        | Leu       | Gly       | Gly<br>55 | Pro       | Leu        | Ile       | Leu       | Ser<br>60 | Phe       | Tyr       | Ala       | Val       |
| Val<br>65 | Leu       | Gly       | Trp        | Val       | Leu<br>70 | Tyr       | Tyr       | Leu        | Phe       | Val<br>75 | Val       | Thr       | Phe       | Asp       | Leu<br>80 |
| Pro       | Lys       | Asp       | Leu        | Gly<br>85 | Arg       | Leu       | Lys       | Cys        | Unk<br>90 | Ser       | Met       | Leu       | Gln       | Asn<br>95 | Gly       |
| Ser       | Leu       | Ile       | Trp<br>100 | Pro       | Val       | Ile       | Asp       | Phe<br>105 | Ser       | Ala       | Cys       |           |           |           |           |

(2) INFORMATION FOR SEQ ID NO:35360843\_f1\_1: -AA

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 115 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 407

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

[illegible]

(2) INFORMATION FOR SEQ ID NO:35397265\_f1\_1:-AA

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 11 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES HPP 408

- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

|     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Arg | Val | Arg | Unk | His | Glu | Lys | Unk | Lys | Phe | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |



491

[illegible]

(2) INFORMATION FOR SEQ ID NO:35428912\_f3\_6: - AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 410

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: HAEMOLYSIN SECRETION ATP-BINDING PROTEIN

Met Asp Glu Ile Tyr Gln Ile Ala Lys Asn Lys Thr Leu Ile Val Ile  
1 5 10 15

Ala His Arg Leu Ser Thr Ile Glu Arg Cys Glu Val Ile Ile Asp Met  
20 25 30

Ser Gln His Lys Asp Asn Leu Gly  
35 40

(2) INFORMATION FOR SEQ ID NO:35442513\_f1\_1:- AA

Figure 411A - page 493

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 44 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein HPP 411

(iii) HYPOTHETICAL: YES

- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ala | Gly | Ser | Phe | Ile | Ile | Ala | Leu | Phe | Ser | Val | Leu | Ala | Asp | Gln |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Phe | Val | Ser | Val | Phe | Gln | His | Glu | Asn | Ala | Leu | Gln | Arg | Leu | Phe | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gln | Asn | Ala | Thr | Gln | Lys | Gln | Lys | Lys | Lys | Ser | Leu | Cys |     |     |     |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |

(i) SEOUENCE CHARACTERISTICS:

(A) LENGTH: 117 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 412

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Met Val Ala Leu Ser Asn Ala Leu Ser Arg Val Phe Gly Ser Val Ala  
1 5 10 15

Gly Tyr Lys Phe Pro Ser Phe Ile Gln Lys Ser Ile Asn Ala Leu Tyr  
20 25 30

Val Lys Ile Phe Lys Ile Asp Leu Ser Glu Phe Glu Pro Leu Glu Asn  
35 40 45

Tyr Lys Ser Leu Asn Ala Leu Phe Met Arg Ser Leu Lys Lys Glu Arg  
50 55 60

Pro Phe Asp Lys Ala Pro Ile Phe Ala Leu Arg Leu Ala Met Ala Leu  
65 70 75 80

Ile Thr Glu Cys Ala Phe Leu Asp Asn Asp Ser Ala Leu Gln Ile Lys  
85 90 95

Gly Met Pro Tyr Lys Ala His Glu Leu Val Gly Glu Ile Asn Pro Leu  
100 105 110

Ser Pro Leu Phe Ser Met  
115



(2) INFORMATION FOR SEQ ID NO:35837767\_c2\_13: - AA

Figure 4/4A-page 496

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP414

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Gly | Gly | Phe | Thr | Ser | Ile | Trp | His | Trp | Val | Ile | Val | Leu | Leu | Val |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Ile | Val | Leu | Leu | Phe | Gly | Ala | Lys | Lys | Ile | Pro | Glu | Leu | Ala | Lys | Gly |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Leu | Gly | Ser | Gly | Ile | Lys | Asn | Phe | Lys | Lys | Ala | Val | Lys | Asp | Asp | Glu |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Glu | Glu | Ala | Lys | Asn | Glu | Leu | Lys | Thr | Leu | Asp | Ala | Gln | Ala | Thr | Gln |  |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Thr | Lys | Val | His | Glu | Thr | Ser | Glu | Ile | Lys | Ser | Lys | Gln | Glu | Ser |     |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     |  |

497  
Figure 415A-page 497

HPP 415

Ala Pro  
130

(2) INFORMATION FOR SEQ ID NO:35949212\_f1\_1: - A A

Figure 416A -page 498

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 219 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP416

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|
| Val | Leu | Leu | Pro | Lys | His | Ala | Ile | Leu | Phe | Ser | Ser | Arg | Ala | Pro | Ile |  |  |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |  |  |
| Gly | Tyr | Val | Ala | Ile | Ala | Glu | Lys | Arg | Leu | Cys | Thr | Asn | Gln | Gly | Phe |  |  |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |  |  |
| Lys | Ser | Ile | Ile | Pro | Asn | Lys | Lys | Ile | Tyr | Phe | Glu | Phe | Leu | Tyr | Tyr |  |  |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |  |  |
| Leu | Leu | Lys | Tyr | Tyr | Lys | Asp | Asn | Ile | Ser | Asn | Ile | Gly | Gly | Gly | Thr |  |  |  |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |  |  |
| Thr | Phe | Lys | Glu | Val | Ser | Gly | Ala | Thr | Leu | Gly | Leu | Phe | Gln | Val | Lys |  |  |  |
|     |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |  |  |
| Ile | Pro | Pro | Thr | Tyr | Tyr | Glu | Gln | Gln | Lys | Ile | Ala | His | Thr | Leu | Ser |  |  |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |  |  |
| Ile | Leu | Asp | Gln | Lys | Ile | Glu | Asn | Asn | His | Lys | Ile | Asn | Glu | Leu | Leu |  |  |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |  |  |
| His | Lys | Ile | Leu | Glu | Leu | Leu | Tyr | Glu | Gln | Tyr | Phe | Val | Arg | Phe | Asp |  |  |  |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |  |  |
| Phe | Leu | Asp | Glu | Asn | Asn | Lys | Pro | Tyr | Gln | Thr | Ser | Gly | Gly | Lys | Met |  |  |  |
|     |     |     | 130 |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |  |  |
| Lys | Phe | Ser | Lys | Glu | Leu | Asn | Arg | Leu | Ile | Pro | Asn | Asp | Phe | Lys | Val |  |  |  |
|     |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |  |  |
| Lys | Thr | Leu | Gly | Glu | Leu | Ile | Thr | Trp | Ile | Ser | Gly | Unk | Gln | Pro | Pro |  |  |  |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |  |  |  |
| Lys | Val | Val | Thr | Tyr | Thr | Ser | Ile | Lys | Arg | Val | Thr | Phe | Val | Ser | Tyr |  |  |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |  |  |
| Lys | Thr | Glu | Ile | Ile | Ala | Leu | Ile | Ile | Met | Leu | His | Ile | Phe | Leu | Tyr |  |  |  |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |  |  |
| Gln | Lys | Ile | Thr | Arg | Phe | Val | Ile | Asn | Met | Ile | Leu |     |     |     |     |  |  |  |
|     |     |     | 210 |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |  |  |





(2) INFORMATION FOR SEQ ID NO:36131282\_f3\_10: - AA

Figure 418A - page 500

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 97 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

HPP 418

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

[illegible]

(2) INFORMATION FOR SEQ ID NO:36134661\_c1\_7: AA

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 196 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 419

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

[illegible]

(2) INFORMATION FOR SEQ ID NO:36203402\_f3\_1: - AA

Figure 42DA - page 502

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP420

(iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: integral membrane protein

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Phe | Tyr | Gly | Leu | Pro | Ala | Leu | Gly | Val | Tyr | Met | Asp | Pro | Ile | Pro |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Ala | Gly | Ile | Ile | Ala | Phe | Ser | Phe | Asn | Val | Gly | Ala | Tyr | Ala | Ser | Glu |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Thr | Leu | Arg | Ala | Ser | Phe | Leu | Ser | Val | Pro | Lys | Asp | Gln | Trp | Asp | Ser |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Leu | Ser | Leu | Gly | Leu | Asn | Tyr | Leu | Gln | Thr | Phe | Trp | His | Val | Ile |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Phe | Phe | Gln | Ala | Leu | Lys | Val | Ala | Thr | Pro | Ser | Leu | Ser | Asn | Thr | Phe |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| Ile | Ser | Leu | Phe | Lys | Glu | Thr | Ser | Leu | Ala | Ser | Val | Val | Thr | Ile | Ala |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Glu | Val | Leu | Glu | Ser | His | Ser | Lys | Lys | Unk | Thr | Ser | Ala | Met | Thr | Unk |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Unk | Leu | Phe | Ile | Trp | Lys | Arg | Phe | Asp | Leu | Leu | Ala | Phe | Leu | Leu | Gly |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Phe | Arg | Ser | Asp | Ser | Lys | Ala | Arg | Gly | Lys | Asn | Leu | Lys | Leu | Ser | Trp |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Leu | Asn | Leu | Ile | Pro | Leu | Ile | Phe | Asp | Tyr | Asn | Thr | Ala |     |     |     |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     |     |

(ii) MOLECULE TYPE: protein

HPP 421

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

[illegible]

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP422

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: methyl-accepting chemotaxis protein

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Val | Ala | Asp | Glu | Val | Arg | Asn | Leu | Ala | Gly | Arg | Thr | Gln | Lys | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Ala | Glu | Ile | Asn | Ser | Thr | Ile | Met | Val | Ile | Val | Gln | Glu | Ile | Asn |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asp | Val | Ser | Ser | Gln | Met | Asn | Leu | Asn | Ser | Gln | Lys | Met | Glu | Arg | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Asp | Met | Ser | Lys | Ser | Val | Gln | Glu | Thr | Tyr | Glu | Lys | Met | Ser | Ser |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Asn | Leu | Ser | Ser | Val | Val | Leu | Asp | Ser | Asn | Gln | Ser | Met | Asp | Asp | Tyr |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     |     | 80  |
| Ala | Lys | Ser | Gly | His | Gln | Ile | Glu | Ala | Met | Val | Ser | Asp | Phe | Ala | Glu |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Val | Glu | Lys | Val | Ala | Ser | Lys | Thr | Leu | Ala | Asp | Ser | Ser | Asp | Ile | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Asn | Ile | Ala | Thr | His | Val | Ser | Gly | Thr | Thr | Met | Asn | Leu | Thr | Asn | Lys |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |

(2) INFORMATION FOR SEQ ID NO:36523442\_c3\_14: - AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 423

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |    |    |    |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|----|----|----|
| Val | Leu | Lys | Thr | Leu | Ser | Ile | Arg | Leu | Val | Ile | Leu | Leu | Asn | Cys | Ser | 1  | 5  | 10 | 15 |
| Leu | Ala | Thr | Asn | Ala | Cys | Ser | Gly | Val | Gln | Lys | Leu | Arg | Asp | Glu | Ser | 20 | 25 | 30 |    |
| His | Arg | Tyr | Ala | Ile | Asn | Phe | His | Arg | Ser | Thr | Lys | Leu | Lys | Asn | Met | 35 | 40 | 45 |    |
| Lys | Gln | Ile | Ala | Leu | Leu | Lys | Glu | Lys | Gly | Ile | Gly | Glu | Ala | Ser | Val | 50 | 55 | 60 |    |
| Lys | Lys | Leu | Leu | Asp | Tyr | Phe | Gly | Ser | Phe | Glu | Ala | Ile | Glu | Lys | Ala | 65 | 70 | 75 | 80 |
| Ser | Asp | Gln | Glu | Lys | Asn | Ala | Val | Leu | Lys | Lys | Arg | Lys | 85  | 90  |     |    |    |    |    |

Figure 424A - page 50b

(A) LENGTH: 72 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 424

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: SULFATE TRANSPORT ATP-BINDING

Val Gly Ile Ile Arg Gly Ile Ile His Arg Pro Glu Leu Ile Leu Leu  
1 5 10 15

Asp Glu Pro Phe Ser Ala Leu Asp Ser Leu Asn Arg Lys Asn Leu Gln  
20 25 30

Asp Leu Ile Lys Glu Ile His Gln Asn Ser Cys Ala Thr Phe Ile Met  
35 40 45

Val Thr His Asp Glu Asn Glu Ala Gln Lys Leu Ala Thr Lys Thr Leu  
50 55 60

Glu Ile Lys Ala Leu Lys Gln Glu Gln  
65 70



(2) INFORMATION FOR SEQ ID NO:36594167\_f2\_2: AA

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

Figure 425A-page 587

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 425

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

## (xi) SEQUENCE DESCRIPTION:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ile | Phe | Ile | Ala | Thr | Ala | Asn | Asn | Ile | Asp | Arg | Ile | Pro | Ala | Pro | 1   | 5   | 10  | 15  |
| Leu | Arg | Asp | Arg | Met | Glu | Phe | Ile | Ser | Val | Ser | Ser | Tyr | Thr | Pro | Ser | 20  | 25  | 30  |     |
| Glu | Lys | Glu | Glu | Ile | Ala | Lys | Asn | Tyr | Leu | Ile | Pro | Gln | Glu | Leu | Glu | 35  | 40  | 45  |     |
| Lys | His | Ala | Leu | Lys | Pro | Ser | Glu | Val | Asp | Ile | Ser | His | Glu | Cys | Leu | 50  | 55  | 60  |     |
| Lys | Leu | Ile | Ile | Glu | Lys | Tyr | Thr | Arg | Glu | Ala | Gly | Val | Arg | Asp | Leu | 65  | 70  | 75  | 80  |
| Arg | Arg | Gln | Ile | Ala | Thr | Ile | Met | Arg | Lys | Ala | Ala | Leu | Lys | Tyr | Leu | 85  | 90  | 95  |     |
| Glu | Asp | Asn | Pro | His | Lys | Lys | Gly | Arg | Thr | Lys | Lys | Ser | Glu | Asp | Lys | 100 | 105 | 110 |     |
| Asp | Lys | Lys | Gly | Gly | Asn | Glu | Glu | Asn | Glu | Lys | Arg | Gly | Glu | Ser | Lys | 115 | 120 | 125 |     |
| Asp | Phe | Cys | Val | Ser | Ile | Thr | Pro | Asp | Asn | Leu | Lys | Glu | Tyr | Leu | Glu | 130 | 135 | 140 |     |
| Arg | Met | Val | Phe | Glu | Ile | Unk | Pro | Ile | Asp | Glu | Glu | Asn | Lys | Ile | Gly | 145 | 150 | 155 | 160 |
| Ile | Val | Asn | Gly | Leu | Ala | Trp | Thr | Pro | Val | Gly | Gly | Asp | Val | Leu | Lys | 165 | 170 | 175 |     |
| Ile | Glu | Ala | Val | Lys | Ile | Arg | Gly | Lys | Gly | Glu | Leu | Lys | Leu | Thr | Gly | 180 | 185 | 190 |     |
| Ser | Leu | Gly | Asp | Val | Met | Lys | Glu | Ser | Ala | Ile | Ile | Ala | Phe | Ser | Val | 195 | 200 | 205 |     |
| Val | Lys | Val | Leu | Leu | Asp | Asn | Glu | Thr | Leu | Lys | Val | Pro | Lys | Ile | Pro | 210 | 215 | 220 |     |
| Ser | Glu | Thr | Asp | Ala | Glu | Asn | Unk | Lys | Lys | Lys | Lys | Val | Leu | Lys | Val | 225 | 230 | 235 | 240 |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Unk | Asn | Ala | Tyr | Asp | Leu | His | Leu | His | Val | Pro | Lys | Gly | Leu | Arg | Leu |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Lys | Thr | Ala | Arg | Ala | Leu | Gly | Ser | Leu | Trp | Arg | Ala |     |     |     |     |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:38080063\_c2\_9: -AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: major outer membrane protein

HPP 426 7611

Met Glu Ile Ile Lys Lys Phe Val Ala Leu Gly Leu Leu Ser Ala Val  
1 5 10 15  
Leu Ser Ser Ser Leu Leu Ala Glu Gly Asp Gly Val Tyr Ile Gly Thr  
20 25 30  
Asn Tyr Gln Leu Gly Gln Ala Arg Leu Asn Ser Asn Ile Tyr Asn Thr  
35 40 45  
Gly Asp Cys Thr Gly Ser Val Val Gly Cys Pro Pro Gly Leu Thr Ala  
50 55 60  
Asn Lys His Asn Pro Gly Gly Thr Asn Ile Asn Trp His Ser Lys Tyr  
65 70 75 80  
Ala Asn Gly Ala Leu Asn Gly Phe Gly Leu Asn Val Gly Tyr Lys Lys  
85 90 95  
Phe Phe Gln Phe Lys Ser Leu Asp Met Thr Ser Lys Trp Phe Gly Phe  
100 105 110  
Arg Val Tyr Gly Leu Phe Asp Tyr Gly His Ala Asp Leu Gly Lys Gln  
115 120 125  
Val Tyr Ala Pro Asn Lys Ile Gln Leu Asp Met Val Ser Trp Gly Val  
130 135 140  
Gly Ser Ile Cys  
145

08/437,032

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 97 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: *Helicobacter pylori*

[illegible]

(2) INFORMATION FOR SEQ ID NO:3906937\_f2\_3: -AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 428

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Pro | Pro | Thr | Unk | Pro | Gln | Ala | Ser | Ile | Leu | Arg | Leu | Thr | Leu | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asn | Pro | Leu | Ala | Ala | Ile | Ser | Leu | Phe | Ala | Leu | Ser | Val | Glu | Lys | Asn |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Leu | Ala | Asn | Asn | Ile | Lys | Gln | Arg | Thr | Lys | Ser | Met | Leu | Asp | Cys |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gly | Leu | Ile | Glu | Glu | Ile | Lys | Ala | Leu | Tyr | Ile | Lys | Tyr | Pro | Lys | Asp |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ser | Gln | Pro | Phe | Lys | Ala | Ile | Gly | Val | Lys | Glu | Ser | Val | Leu | Tyr | Leu |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Glu | Lys | Arg | Leu | Thr | Leu | Lys | Glu | Leu | Glu | Glu | Ala | Ile | Ile | Ser | Asn |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Thr | Met | Lys | Leu | Ala | Lys | Arg | Gln | Asn | Thr | Phe | Asn | Lys | Pro | Asn | Ser |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ile | Thr | Phe | Ile | Trp | Gly | Ala | Leu | Glu | Arg | Leu | Gly | Met | Arg | Phe |     |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 146 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 429

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Met Gly Cys Ser Phe Ile Phe Lys Lys Val Arg Val Tyr Ser Lys Met  
1 5 10 15

Leu Val Ala Leu Gly Leu Ser Ser Val Leu Ile Gly Cys Ala Met Asn  
20 25 30

Pro Ser Ala Glu Thr Lys Lys Pro Asn Asp Ala Lys Asn Gln Gln Pro  
35 40 45

Val Gln Thr His Glu Arg Met Thr Thr Ser Ser Glu His Val Thr Pro  
50 55 60

Leu Asp Phe Asn Tyr Pro Val His Ile Val Gln Ala Pro Gln Asn His  
65 70 75 80

His Val Val Gly Ile Leu Met Pro Arg Ile Gln Val Ser Asp Asn Leu  
85 90 95

Lys Pro Tyr Ile Asp Lys Phe Gln Asp Ala Leu Ile Asn Gln Ile Gln  
100 105 110

Thr Ile Phe Glu Lys Arg Gly Tyr Gln Val Leu Arg Phe Gln Asp Glu  
115 120 125

Lys Ala Leu Asn Val Gln Asp Lys Lys Lys Ile Phe Ser Val Leu Asp  
130 135 140

Leu Lys Gly  
145

(2) INFORMATION FOR SEQ ID NO:3907042\_c1\_3: -AA

Figure 43DA page 513

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP430

(iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- Helicobacter pylori*

## (xi) SEQUENCE DESCRIPTION:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asp | Arg | Lys | Leu | Leu | Arg | Leu | Tyr | Gln | Pro | Leu | Asn | Ala | Tyr | Ser |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Tyr | Asn | Ser | Asp | Ser | Leu | Phe | Leu | Tyr | Asp | Phe | Ser | Arg | Pro | Phe | Ile |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Lys | Asn | Ser | Gly | Ala | Ile | Leu | Asp | Ile | Gly | Ser | Gly | Cys | Gly | Val | Leu |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gly | Leu | Leu | Cys | Ala | Arg | Asp | Asn | Pro | Leu | Ala | Ser | Val | His | Leu | Val |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Glu | Lys | Asp | Ser | Lys | Met | Ala | Phe | Cys | Ser | Gln | Lys | Asn | Ala | Leu | Lys |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Phe | Pro | Asn | Ala | Gln | Val | Phe | Glu | Ser | Asp | Phe | Leu | Asp | Phe | Asn | Pro |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Pro | Ile | Leu | Tyr | Asp | Ala | Ile | Val | Cys | Asn | Pro | Pro | Phe | Tyr | Ala | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gly | Ser | Ile | Lys | Ser | Gln | Ile | Lys | Gly | His | Ala | Arg | His | Gln | Ser | Glu |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Leu | Asp | Phe | Ala | Ser | Leu | Val | Ala | Lys | Val | Lys | Lys | Cys | Leu | Lys | Pro |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:391313\_f2\_5: - AA

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 46 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

HPP 431

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Ser | Ala | Leu | Val | Met | Leu | Pro | Phe | Met | Glu | Val | Phe | Tyr | Tyr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Phe | Asn | Phe | Pro | Leu | Trp | Leu | Asn | Leu | Phe | Leu | Gly | Gln | Thr | Ile | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Val | Ile | Phe | Phe | Lys | Leu | Asp | Lys | Leu | Ile | Phe | Ser | Lys | Lys |     |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |



(2) INFORMATION FOR SEQ ID NO:392900\_f2\_3: -AA

Figure 432A-page 515

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 432

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: 190kD surface antigen

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| Val | Gly | Val | Gly | Ala | Asn | Cys | Ser | Thr | Ser | Gly | Pro | Ser | Tyr | Ser | Phe | 1   | 5   | 10  | 15 |
| Lys | Gly | Thr | Thr | Asn | Ala | Thr | Asn | Thr | Thr | Phe | Ser | Unk | Ser | Ser | Gly | 20  | 25  | 30  |    |
| Ser | Phe | Thr | Phe | Glu | Unk | Asn | Ala | Thr | Phe | Ser | Gly | Ala | Lys | Leu | Asn | 35  | 40  | 45  |    |
| Gly | Gly | Ala | Phe | Thr | Phe | Asn | Lys | Lys | Phe | Asn | Ala | Thr | Asn | Asn | Thr | 50  | 55  | 60  |    |
| Ala | Phe | Asn | Ser | Gly | Ser | Phe | Thr | Phe | Lys | Gly | Thr | Ser | Ser | Phe | Asn | 65  | 70  | 75  | 80 |
| Gly | Ala | Asn | Phe | Ser | Asn | Ala | Ser | Tyr | Thr | Phe | Asn | Asn | Gln | Ala | Thr | 85  | 90  | 95  |    |
| Phe | Gln | Asn | Ser | Ser | Phe | Asn | Gly | Gly | Thr | Phe | Thr | Phe | Asn |     |     | 100 | 105 | 110 |    |

Figure 433A - page 516

(A) LENGTH: 128 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 433

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Met Asn Thr Ile Ile Arg Tyr Ala Ser Leu Trp Gly Leu Cys Ile Thr  
1 5 10 15

Leu Thr Leu Ala Gln Thr Pro Ser Lys Thr Pro Asp Glu Ile Lys Gln  
20 25 30

Ile Leu Asn Asn Tyr Ser His Lys Asn Leu Lys Leu Ile Asp Unk Pro  
35 40 45

Thr Ser Ser Leu Unk Ala Thr Pro Gly Phe Unk Pro Ser Pro Lys Glu  
50 55 60

Thr Ala Thr Thr Ile Asn Gln Glu Ile Ala Lys Tyr His Glu Lys Ser  
65 70 75 80

Asp Lys Ala Ala Leu Gly Leu Tyr Glu Leu Leu Lys Gly Ala Thr Thr  
85 90 95

Asn Leu Ser Leu Gln Ala Gln Glu Leu Ser Val Lys Gln Ala Met Glu  
100 105 110

Glu Pro His His Arg Gln Ser Asp Val Phe Ala Tyr Phe Glu Arg Glu  
115 120 125

Leu

(2) INFORMATION FOR SEQ ID NO:3933437\_c3\_2: - AA

Figure 434A - page 517

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP434

(iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

## (xi) SEQUENCE DESCRIPTION:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Leu | Phe | Leu | Ser | Ile | Phe | Lys | Lys | Ser | Phe | Asn | Asp | Phe | Leu | 1   | 5   | 10  | 15  |
| Ser | Ala | Arg | Met | Leu | Leu | Ile | Asn | Leu | Gly | Pro | Ile | Leu | Leu | Ser | Leu | 20  | 25  | 30  |     |
| Ala | Phe | Phe | Gly | Ala | Ile | Phe | Tyr | Tyr | Asn | Gly | Gly | Ser | Ile | Val | Asn | 35  | 40  | 45  |     |
| Tyr | Cys | Gln | Thr | Leu | Leu | Pro | Gln | Ser | Leu | Asn | Asp | Tyr | Ala | His | Ser | 50  | 55  | 60  |     |
| Gln | Gly | Phe | Phe | Ala | Gly | Val | Phe | Ala | Trp | Val | Phe | Lys | Ala | Leu | Val | 65  | 70  | 75  | 80  |
| Tyr | Phe | Leu | Ile | Phe | Trp | Ile | Val | Ile | Leu | Leu | Ser | Leu | Val | Ile | Asn | 85  | 90  | 95  |     |
| Ile | Phe | Ala | Ser | Ile | Phe | Tyr | Thr | Pro | Leu | Val | Val | Ser | Tyr | Leu | His | 100 | 105 | 110 |     |
| Gln | Lys | Tyr | Tyr | Pro | His | Val | Val | Leu | Glu | Glu | Phe | Gly | Ser | Ile | Leu | 115 | 120 | 125 |     |
| Phe | Ser | Ile | Lys | Tyr | Phe | Leu | Lys | Ser | Leu | Thr | Phe | Met | Leu | Leu | Phe | 130 | 135 | 140 |     |
| Leu | Ala | Val | Leu | Thr | Pro | Leu | Tyr | Phe | Ile | Pro | Phe | Ile | Gly | Val | Phe | 145 | 150 | 155 | 160 |
| Gly | Val | Phe | Phe | Ser | Ile | Val | Pro | His | Phe | His | Phe | Phe | Lys | Asn | Thr | 165 | 170 | 175 |     |
| Met | Ser | Leu | Asp | Ile | Ala | Ser | Met | Ile | Phe | Asn | His | Gln | Ser | Tyr | Gln | 180 | 185 | 190 |     |
| Asn | Leu | Leu | Lys | Gln | His | Arg | Leu | Lys | His | Tyr | Arg | Phe | Ser | Phe | Phe | 195 | 200 | 205 |     |
| Cys | Tyr | Leu | Phe | Ser | Leu | Ile | Pro | Phe | Phe | Asn | Phe | Phe | Ala | Thr | Leu | 210 | 215 | 220 |     |
| Leu | Gln | Thr | Leu | Lys | Leu | Thr | His | Tyr | Ile | Phe | Ile | Phe | Lys | Glu | Lys | 225 | 230 | 235 | 240 |

Glu Cys

518  
Figure 434 A - page 518

579  
Figure 435A - page 519

(A) LENGTH: 96 amino acids

(D) TOPOLOGY: linear

H PP 435

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: flagellar protein fljS

Glu

(2) INFORMATION FOR SEQ ID NO:3953143\_f2\_1: - AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 436

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Met | Phe | Asp | Asn | Thr | Leu | Ile | Asn | Leu | Phe | Glu | Thr | Ala | Pro | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Thr | Ser | Leu | Leu | Ala | Gly | Ile | Leu | Thr | Phe | Leu | Ser | Pro | Cys | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Pro | Leu | Ile | Pro | Ala | Tyr | Met | Ser | Tyr | Ile | Ser | Gln | Ile | Ser | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Glu | Asp | Ile | Lys | Asp | Gly | Lys | Ala | Lys | Arg | Val | Ser | Val | Phe | Leu | Lys |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ser | Leu | Met | Phe | Val | Val | Gly | Phe | Ser | Leu | Val | Phe | Leu | Gly | Val | Gly |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |     |
| Met | Ser | Met | Ala | Lys | Leu | Ile | His | Ser | Phe | Ser | Phe | Ser | Trp | Val | Asn |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Tyr | Ile | Ala | Gly | Gly | Ile | Val | Ile | Leu | Phe | Gly | Leu | His | Phe | Leu | Gly |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Val | Phe | Arg | Phe | Ala | Phe | Leu | Tyr | Lys | Thr | Gln | Ser | Val | Gly | Leu | Ala |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ser | Lys | Ser | Asn | Ser | Met | Gln | Arg | Phe | Thr | Pro | Phe | Phe | Leu | Ala |     |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 216 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 437

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

|            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Met<br>1   | Pro        | Val        | Ile        | Arg<br>5   | Val        | Leu        | Val        | Met        | Leu<br>10  | Ala        | Thr        | Met        | Met        | Met<br>15  | Lys        |
| Leu        | Val        | Lys        | Thr<br>20  | Ala        | Lys        | Glu        | Lys        | Lys<br>25  | Val        | Phe        | Lys        | Asn        | Val<br>30  | Gly        | Ile        |
| Ser        | Ile        | Met<br>35  | Gly        | Ile        | Ala        | Phe        | Trp<br>40  | Glu        | Ala        | Ile        | Lys        | Asp<br>45  | Ser        | Ile        | Lys        |
| Lys        | Gln<br>50  | Ile        | Lys        | Lys        | Ser        | Asp<br>55  | Trp        | Ile        | Cys        | Gly        | Asn<br>60  | Val        | Lys        | Thr        | Ala        |
| Asp<br>65  | Asp        | Tyr        | Leu        | Lys        | Thr<br>70  | His        | Pro        | Asn        | Ser        | Trp<br>75  | Phe        | Asn        | Ser        | Ala        | Ile<br>80  |
| Gly        | Val        | Thr        | Ala        | Ile<br>85  | Thr        | Ala        | Met        | Leu        | Met<br>90  | Asn        | Val        | Cys        | Phe        | Ala<br>95  | Asp        |
| Asp        | Gln        | Ser        | Lys<br>100 | Lys        | Glu        | Val        | Ala        | Gln<br>105 | Ala        | Gln        | Lys        | Glu        | Ala<br>110 | Glu        | Asn        |
| Ala        | Arg        | Asp<br>115 | Arg        | Ala        | Asn        | Lys        | Ser<br>120 | Gly        | Ile        | Glu        | Leu        | Glu<br>125 | Gln        | Glu        | Glu        |
| Gln        | Lys<br>130 | Thr        | Glu        | Gln        | Glu        | Lys<br>135 | Gln        | Lys        | Thr        | Glu        | Gln<br>140 | Glu        | Lys        | Gln        | Lys        |
| Thr<br>145 | Glu        | Gln        | Glu        | Lys        | Gln<br>150 | Lys        | Thr        | Glu        | Gln        | Glu<br>155 | Lys        | Gln        | Lys        | Thr        | Glu<br>160 |
| Gln        | Glu        | Lys        | Gln        | Lys<br>165 | Thr        | Ser        | Asn        | Ile        | Glu<br>170 | Thr        | Asn        | Asn        | Gln        | Ile<br>175 | Unk        |
| Val        | Glu        | Thr        | Arg<br>180 | Thr        | Thr        | Lys        | Ser<br>185 | Arg        | Thr        | Gly        | Lys        | Gln        | Lys<br>190 | Thr        | Asn        |
| Unk        | Thr        | Gln<br>195 | Lys        | Asp        | Leu        | Val        | Asn<br>200 | Lys        | Ala        | Glu        | Gln        | Asn<br>205 | Cys        | Gln        | Glu        |
| Asn        | His<br>210 | Asn        | Gln        | Phe        | Phe        | Ile<br>215 | Lys        | Unk        |            |            |            |            |            |            |            |

HPP 438

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: *Helicobacter pylori*

Val Leu Val Val Gly Lys Pro Asn Glu Ser Tyr Ala Asp Thr His Ala  
1 5 10 15

Arg Ile Glu His Phe Ile Lys Leu Val Asp Phe Lys Gly Glu Ile Val  
20 25 30

Phe Ile Asn Glu Asp Asn Ser Ser Val Glu Ala Tyr Glu Asn Leu Glu  
35 40 45

His Leu Gly Lys Lys Asn Lys Arg Ile Ala Thr Lys Asp Gly Arg Leu  
50 55 60

Asp Ser Leu Ser Ala Cys Arg Ile Leu Glu Arg Tyr Cys Gln Gln Val  
65 70 75 80

Leu Lys Lys Gly



(2) INFORMATION FOR SEQ ID NO:3962777\_c1\_10: -AA

Figure 439A - page 523

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 74 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

HPP 439

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: similiar to CHLORAMPHENICOL RESISTANCE PROTEIN

Met Val Ile Ser Gly His Phe Thr Thr Tyr Ser Tyr Ile Glu Pro Phe  
1 5 10 15

Ile Ile Gln Ile Ser Gln Phe Ser Pro Asp Ile Thr Thr Leu Met Leu  
20 25 30

Phe Val Phe Gly Leu Ala Gly Val Val Gly Ser Phe Leu Phe Gly Arg  
35 40 45

Leu Tyr Ala Lys Asn Ser Arg Lys Phe Ile Ala Phe Ala Met Val Leu  
50 55 60

Val Ile Cys Pro Gln Pro Leu Ala Phe Cys Val  
65 70 75

(2) INFORMATION FOR SEQ ID NO:3964593\_f2\_5: -AA

Figure 440A - page 524

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 4.40

(iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (xi) SEQUENCE DESCRIPTION:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| Met | Arg | Ile | Leu | Ile | Leu | Lys | Asn | Lys | Pro | Thr | Leu | Arg | Ser | Lys | 1   | 5   | 10  | 15  |    |
| Ala | Leu | Thr | Arg | Ser | Trp | Gly | Ile | Asn | Phe | Ser | Leu | Lys | Asn | Thr | Leu | 20  | 25  | 30  |    |
| Ala | Tyr | Ala | Phe | Met | Gly | Phe | Phe | Asp | Tyr | Ala | His | Ala | Asn | Ser | Ile | 35  | 40  | 45  |    |
| Lys | Leu | Lys | Asn | Pro | Asn | Tyr | Asn | Ser | Glu | Ala | Ala | Gln | Val | Ala | Ser | 50  | 55  | 60  |    |
| Gln | Ile | Leu | Gly | Lys | Gln | Glu | Ile | Asn | Arg | Leu | Thr | Asn | Ile | Ala | Asp | 65  | 70  | 75  | 80 |
| Pro | Arg | Thr | Phe | Glu | Pro | Asn | Met | Leu | Thr | Tyr | Gly | Gly | Ala | Met | Asp | 85  | 90  | 95  |    |
| Val | Met | Val | Asn | Val | Ile | Asn | Asn | Gly | Ile | Met | Ser | Leu | Gly | Ala | Phe | 100 | 105 | 110 |    |
| Gly | Gly | Ile | Gln | Leu | Ala | Gly | Asn | Ser | Trp | Leu | Met | Ala | Unk | Pro | Ser | 115 | 120 | 125 |    |
| Phe | Glu | Gly | Ile | Leu | Gly | Glu | Gln | Ala | Leu | Val | Ser | Arg | Lys | Pro | Leu | 130 | 135 | 140 |    |
| Leu | Ser | Asn | Phe | Tyr | Ser | Met | Trp | Gly | Leu | Ala |     |     |     |     |     | 145 | 150 | 155 |    |

(2) INFORMATION FOR SEQ ID NO:3987580\_c3\_10:-44

Figure 441A - page 525

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP441

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| Met | Lys | Ser | Thr | Arg | Ile | Gly | Ser | Lys | Ile | Val | Met | Met | Val | Cys | Ala | 1   | 5   | 10  | 15 |
| Val | Val | Ile | Val | Ile | Ser | Ala | Val | Met | Gly | Val | Ile | Ile | Ser | Tyr | Lys | 20  | 25  | 30  |    |
| Val | Glu | Ser | Val | Leu | Gln | Ser | Gln | Ala | Thr | Glu | Leu | Leu | Gln | Lys | Lys | 35  | 40  | 45  |    |
| Ala | Gln | Leu | Val | Ser | Phe | Lys | Ile | Gln | Gly | Ile | Met | Lys | Arg | Ile | Phe | 50  | 55  | 60  |    |
| Met | Gly | Ala | Asn | Thr | Leu | Glu | Arg | Phe | Leu | Ser | Asp | Glu | Asn | Gly | Ala | 65  | 70  | 75  | 80 |
| Ile | Asn | Asp | Thr | Leu | Lys | Arg | Arg | Met | Leu | Ser | Glu | Phe | Leu | Leu | Ala | 85  | 90  | 95  |    |
| Asn | Pro | His | Val | Leu | Leu | Val | Ser | Ala | Ile | Tyr | Thr | Asn | Asn | Asn | Glu | 100 | 105 | 110 |    |
| Arg | Met | Ile | Thr | Ala | Met | Asn | Met | Asp | Ser | Lys | Ile | Ala | Tyr | Pro | Asn | 115 | 120 | 125 |    |
| Thr | Ala | Leu | Asn | Glu | Asn | Met | Thr | Thr | Gln | Ser | Ile | Arg | Ser | Lys | Val | 130 | 135 | 140 |    |

(2) INFORMATION FOR SEQ ID NO:3991067\_c3\_21: - AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 442

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asn | Val | Lys | Lys | Lys | Glu | Lys | Pro | Gln | Ser | Gly | Lys | Ile | Asp | Arg | 1   | 5   | 10  | 15  |
| Val | Asp | Cys | Leu | Glu | Lys | Leu | Gly | Lys | Glu | Asn | Thr | Thr | Phe | Leu | Ser | 20  | 25  | 30  |     |
| Ser | Ile | Ala | Met | Gly | Ser | Ile | Gly | Gln | Leu | Ala | Ile | Pro | Ile | Pro | Gly | 35  | 40  | 45  |     |
| Val | Gly | Val | Leu | Ile | Gly | Gly | Phe | Val | Gly | Gly | Val | Met | Ser | Lys | Thr | 50  | 55  | 60  |     |
| Phe | Tyr | Asp | Val | Ser | Leu | Thr | Ile | Phe | Lys | Glu | Ala | Lys | Leu | Ala | Arg | 65  | 70  | 75  | 80  |
| Gln | Arg | Arg | Ile | Glu | Ile | Glu | Lys | Glu | Cys | Arg | Glu | Ser | Ile | Arg | Gln | 85  | 90  | 95  |     |
| Leu | Glu | Met | Tyr | Gln | Asn | Gln | Phe | Asn | Glu | Val | Phe | Glu | Arg | Tyr | Phe | 100 | 105 | 110 |     |
| His | Gly | Thr | Ile | Lys | Phe | Phe | Asn | Glu | Ser | Phe | Asp | Glu | Leu | Glu | Arg | 115 | 120 | 125 |     |
| Ala | Leu | Cys | Ala | Gly | Asp | Ala | Asp | Leu | Ala | Ile | Ala | Val | Asn | Asn | Lys | 130 | 135 | 140 |     |
| Ile | Gln | Glu | Gly | Met | Gly | Gln | Glu | Leu | Leu | Phe | Asp | Asn | Lys | Gln | Glu | 145 | 150 | 155 | 160 |
| Cys | Trp | Glu | Phe | Ile | Thr | Ser | Arg | Lys | Glu | Gly | 165 | 170 |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:40339452\_f3\_2:- AA

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 140 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein HPP443

(iii) HYPOTHETICAL: YES

- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Trp | Pro | Unk | Lys | Leu | Phe | Leu | Lys | Pro | Leu | Lys | Glu | Thr | Ser | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Leu | Val | Gly | Val | Ala | Lys | Asn | Ile | Lys | Ile | Val | Ala | Leu | Lys | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | Leu | Lys | Arg | Ala | Tyr | Leu | Pro | Asn | Arg | Ser | Leu | Ile | Phe | Phe | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ile | Lys | Arg | Tyr | Leu | Arg | Phe | Asp | Lys | Ser | Gln | Pro | Phe | Ile | Ser | Ile |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Thr | Ala | Leu | Leu | Ala | Phe | Phe | Gly | Val | Ala | Val | Gly | Val | Met | Val | Leu |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     |     | 80  |
| Ile | Val | Ala | Met | Ala | Ile | Met | Asn | Gly | Met | Ser | Lys | Glu | Phe | Glu | Lys |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Lys | Leu | Phe | Val | Met | Asn | Tyr | Pro | Leu | Thr | Leu | Tyr | Thr | Thr | Ser | Pro |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Tyr | Gly | Ile | Ser | Glu | Glu | Val | Val | Gln | Ala | Leu | Glu | Lys | Lys | Phe | Pro |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Asn | Leu | Pro | Phe | Ser | Unk | Pro | Ile | Cys | Lys | Pro | Lys | Ala |     |     |     |
| 130 |     |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:4035262\_c2\_16:-AA

Figure 444A - page 528

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 444

(iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

## (xi) SEQUENCE DESCRIPTION:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |    |    |    |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|----|----|----|
| Met | Val | Ser | Leu | Leu | Gly | Ala | Leu | Lys | Arg | Thr | Pro | Cys | Thr | Asn | Arg | 1  | 5  | 10 | 15 |
| Phe | Tyr | Leu | Lys | Ala | Leu | Leu | Phe | Ala | Ile | Phe | Tyr | His | Ala | Val | Asn | 20 | 25 | 30 |    |
| Asn | Phe | Leu | Thr | Gln | Cys | Pro | Pro | His | Gln | Val | Arg | Glu | Phe | Phe | Ser | 35 | 40 | 45 |    |
| Ser | Arg | His | Ala | Gln | Gly | Trp | Lys | Arg | Glu | Thr | Leu | Pro | Cys | Ala | Leu | 50 | 55 | 60 |    |
| Ser | Phe | Gln | Asn | Ala | Leu |     |     |     |     |     |     |     |     |     |     | 65 | 70 |    |    |

AA

(A) LENGTH: 152 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

HPP 445

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION:

|            |            |            |            |           |            |            |            |            |           |           |            |            |            |           |           |
|------------|------------|------------|------------|-----------|------------|------------|------------|------------|-----------|-----------|------------|------------|------------|-----------|-----------|
| Val<br>1   | His        | His        | Leu        | Unk<br>5  | Arg        | Leu        | Leu        | Asp        | Ser<br>10 | Gly       | Ser        | Glu        | Arg        | Cys<br>15 | Ile       |
| Gly        | Cys        | Gly        | Leu<br>20  | Cys       | Glu        | Lys        | Ile        | Cys<br>25  | Thr       | Ser       | Asn        | Cys        | Ile<br>30  | Arg       | Ile       |
| Ile        | Thr        | His<br>35  | Lys        | Gly       | Glu        | Asp        | Asn<br>40  | Arg        | Lys       | Lys       | Ile        | Asp<br>45  | Ser        | Tyr       | Thr       |
| Ile        | Asn<br>50  | Leu        | Gly        | Arg       | Cys        | Ile<br>55  | Tyr        | Cys        | Gly       | Leu       | Cys<br>60  | Ala        | Glu        | Val       | Cys       |
| Pro<br>65  | Glu        | Leu        | Ala        | Ile       | Val<br>70  | Met        | Gly        | Asn        | Arg       | Phe<br>75 | Glu        | Asn        | Ala        | Ser       | Thr<br>80 |
| Gln        | Arg        | Ser        | Gln        | Tyr<br>85 | Gly        | Ser        | Lys        | Ser        | Glu<br>90 | Phe       | Leu        | Thr        | Ser        | Glu<br>95 | Gln       |
| Asp        | Ala        | Lys        | Asn<br>100 | Cys       | Ser        | His        | Ala        | Glu<br>105 | Phe       | Leu       | Gly        | Phe        | Gly<br>110 | Ala       | Val       |
| Ser        | Pro        | Asn<br>115 | Tyr        | Asn       | Glu        | Arg        | Met<br>120 | Gln        | Ala       | Thr       | Pro        | Leu<br>125 | Asp        | Tyr       | Val       |
| Gln        | Glu<br>130 | Pro        | Ser        | Lys       | Glu        | Glu<br>135 | Ser        | Lys        | Glu       | Glu       | Phe<br>140 | Unk        | Thr        | Ser       | Pro       |
| Glu<br>145 | Ser        | His        | Lys        | Gly       | Asp<br>150 | Glu        | Asn        | Val        |           |           |            |            |            |           |           |

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 182 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 446

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Met Ala Ile Trp Gly Trp Cys Phe Leu Phe Leu Ser Ser Leu Met Trp  
1 5 10 15

Gly Ser Ser Met His Glu Leu Val Leu Arg Ser Gln Ala Leu Gly Phe  
20 25 30

Glu Thr Arg Leu Val Gln Cys Asp Leu Ser Phe Ser Tyr Glu Arg Phe  
35 40 45

Ile Ser Lys Thr Lys Arg Ser Leu Ala Val Leu Glu Glu Phe Asp Trp  
50 55 60

Leu Asn Ser Gly Phe Asp Phe Ser Arg Leu Asn Val Glu Asn Asp Thr  
65 70 75 80

Leu Glu Leu Leu Lys Ala Leu Tyr Phe Lys Leu Glu Lys Leu Glu Ser  
85 90 95

Leu Leu Leu Lys Glu Asn Leu Leu Glu Leu Glu Gln Lys Asp Arg Ile  
100 105 110

Ile Ala Leu Gly His Gly Leu Val Cys Leu Lys Lys Gln Ser Leu Ile  
115 120 125

Ala Pro Gln Thr Tyr Tyr Gly Arg Cys Val Leu Glu Gly Lys Ile Leu  
130 135 140

Ala Phe Phe Gly Val Ala Arg Asp Lys Asp Phe Leu Glu Ile Thr Arg  
145 150 155 160

Met His Ala Leu Asp Ile Lys Arg Tyr Asp Ser Phe Ile Val Asp Ser  
165 170 175

Glu Arg Lys Gly Leu Lys Leu  
180



(A) LENGTH: 66 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 447

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Met Pro Glu Asn Ser Lys Leu Gln Pro Ala Lys Leu Gly Lys Asn Phe  
1 5 10 15

Asp Pro Val Asp His Ser Asn Arg Asn Phe Phe Phe Ser Leu Ile Leu  
20 25 30

Ser Val Leu Leu His Trp Leu Ile Tyr Phe Leu Phe Glu His Arg Glu  
35 40 45

Asp Phe Phe Pro Ser Lys Pro Lys Leu Val Lys Leu Asn Pro Glu Asn  
50 55 60

Leu Leu Val  
65

(2) INFORMATION FOR SEQ ID NO:4095342\_f1\_2: - AA

Figure 448A - page 532

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 448

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

## (xi) SEQUENCE DESCRIPTION:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asn | Glu | Glu | Leu | Thr | Ser | Leu | Thr | Glu | Tyr | Gln | Arg | Tyr | Gly | His | 1   | 5   | 10  | 15  |
| Asp | Tyr | Ala | Lys | Tyr | Pro | Arg | Arg | Ile | Ala | Glu | Glu | Leu | Gln | Arg | Tyr | 20  | 25  | 30  |     |
| Gly | Gly | Asn | Ser | Phe | Ala | Asn | Phe | Phe | Arg | Asp | Glu | Gly | Val | Leu | Tyr | 35  | 40  | 45  |     |
| Lys | Glu | Ile | Leu | Cys | Asp | Ala | Cys | Asp | His | Leu | Asp | Ile | Asn | Tyr | Asn | 50  | 55  | 60  |     |
| Glu | Arg | Ser | Ala | Thr | Ser | Leu | Ile | Glu | Gln | Asn | Met | Leu | Ser | Lys | Leu | 65  | 70  | 75  | 80  |
| Leu | Lys | Asp | Ser | Leu | Glu | Lys | Met | Ser | Gly | Arg | Glu | Ile | Lys | Glu | Leu | 85  | 90  | 95  |     |
| Cys | Asp | Gly | Leu | Gly | Met | Pro | Asn | Ile | Asp | Lys | Val | Ile | Gly | Glu | Asn | 100 | 105 | 110 |     |
| Lys | Gln | Val | Leu | Ile | Ala | Ser | Val | Leu | Thr | Leu | Phe | Lys | Ala | Gly | Gly | 115 | 120 | 125 |     |
| Ser | His | Ser | Tyr | Ala | Leu | Ala | Val | Ala | Val | Ala | Asp | Ala | Met | Val | Arg | 130 | 135 | 140 |     |
| Gln | Thr | Leu | Gly | His | Gly | Leu | Ser | Ser | Val | Val | Gly | Lys | Val | Ala | Leu | 145 | 150 | 155 | 160 |
| Lys | Lys | Thr | Leu | Asp | Ile | Leu | Ala | Gly | Pro | Ile | Gly | Trp | Val | Ile | Thr | 165 | 170 | 175 |     |
| Gly | Ala | Leu | Val | Ser | Ile | Asn | Leu | Ala | Gly | Pro | Ala | Tyr | Arg | Val | Thr | 180 | 185 | 190 |     |
| Val | Pro | Ala | Cys | Val | Leu | Val | Ala | Thr | Leu | Arg | Lys | Lys | Leu | Lys | Ala | 195 | 200 | 205 |     |
| Glu |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:41552656\_c1\_12: - A A

Figure 449A - page 533

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 297 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP449

(iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

## (xi) SEQUENCE DESCRIPTION:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Leu | Leu | Gln | Ser | Leu | Ser | Ser | Asn | Tyr | Tyr | Ala | Ile | Phe | Ala | Leu | 1   | 5   | 10  | 15  |
| Ile | Ala | Val | Phe | Leu | Thr | Ile | Leu | Trp | Gln | Ile | Asn | Leu | Pro | Ser | Met | 20  | 25  | 30  |     |
| Arg | Lys | Tyr | Gln | Asn | Ile | Gly | Val | Lys | Asp | Phe | Tyr | Ser | Glu | Gln | Glu | 35  | 40  | 45  |     |
| Glu | Asp | Ser | Ser | Lys | Leu | Ala | Pro | Leu | Ser | Leu | Leu | Pro | Leu | Ser | Ile | 50  | 55  | 60  |     |
| Leu | Leu | Leu | Ile | Val | Ser | Ile | Ser | Ser | Leu | Ile | Phe | Tyr | Thr | Gly | Val | 65  | 70  | 75  | 80  |
| Ile | Leu | Lys | Asn | Thr | Asp | Ala | Ser | Phe | Ser | Leu | Phe | Tyr | Gly | Gly | Leu | 85  | 90  | 95  |     |
| Phe | Ser | Leu | Ile | Val | Thr | Tyr | Leu | Leu | Ala | Tyr | Pro | Phe | Leu | Glu | Lys | 100 | 105 | 110 |     |
| Gly | Ser | Phe | Leu | Lys | Leu | Ile | Ile | Glu | Gly | Phe | Lys | Ser | Val | Gly | Pro | 115 | 120 | 125 |     |
| Ala | Ile | Leu | Val | Leu | Thr | Leu | Ala | Trp | Ala | Ile | Gly | Pro | Val | Ile | Arg | 130 | 135 | 140 |     |
| Asp | Asp | Ala | Gln | Thr | Gly | Leu | Tyr | Leu | Ala | Gln | Val | Ser | Lys | Gly | Phe | 145 | 150 | 155 | 160 |
| Leu | Asn | Ser | Gly | Gly | Gly | Val | Tyr | Met | Pro | Leu | Ile | Phe | Phe | Leu | Ile | 165 | 170 | 175 |     |
| Ser | Gly | Phe | Ile | Ala | Phe | Ser | Thr | Gly | Thr | Ser | Trp | Gly | Ala | Phe | Ala | 180 | 185 | 190 |     |
| Ile | Met | Leu | Pro | Ile | Gly | Ala | Gly | Met | Ala | Asn | Glu | Ser | Asp | Ile | Ile | 195 | 200 | 205 |     |
| Leu | Ile | Ile | Ser | Ala | Ile | Leu | Ser | Gly | Ala | Val | Tyr | Gly | Asp | His | Thr | 210 | 215 | 220 |     |
| Ser | Pro | Ile | Ser | Asp | Thr | Thr | Ile | Leu | Ser | Ala | Thr | Gly | Ala | Gly | Cys | 225 | 230 | 235 | 240 |



(2) INFORMATION FOR SEQ ID NO:4177212\_c2\_9: -AA

Figure 4SDA -page 535

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP4SD

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

## (xi) SEQUENCE DESCRIPTION:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Phe | Leu | Val | Gln | Ser | Trp | Ala | Leu | Ser | Leu | Lys | Ile | Asp | Ser | Leu | 1   | 5   | 10  | 15  |
| Phe | Ser | Leu | Phe | Ser | Val | Gly | Lys | Ile | Pro | Ser | Gly | Ser | Lys | Asp | Pro | 20  | 25  | 30  |     |
| Phe | Ala | Leu | Arg | Arg | Leu | Ser | Phe | Gly | Leu | Leu | Lys | Ile | Ile | Ala | His | 35  | 40  | 45  |     |
| Tyr | Gly | Leu | Glu | Phe | Asp | Leu | Lys | Ala | Asp | Leu | Lys | Asn | Leu | Phe | Glu | 50  | 55  | 60  |     |
| Lys | Val | Gly | Val | Tyr | Gln | Ser | Phe | Asp | Leu | Glu | Val | Leu | Glu | Lys | Phe | 65  | 70  | 75  | 80  |
| Leu | Leu | Glu | Arg | Phe | His | Asn | Leu | Ile | Asp | Cys | Asn | Leu | Ser | Ile | Ile | 85  | 90  | 95  |     |
| Arg | Ser | Val | Leu | Asn | Thr | Asn | Glu | Arg | Asp | Ile | Val | Lys | Ile | Ile | Gln | 100 | 105 | 110 |     |
| Lys | Val | Lys | Ala | Leu | Lys | Arg | Phe | Leu | Asp | Asn | Pro | Lys | Asn | Ala | Gln | 115 | 120 | 125 |     |
| Lys | Lys | Glu | Leu | Leu | Phe | Ser | Ala | Phe | Lys | Arg | Leu | Ala | Asn | Ile | Asn | 130 | 135 | 140 |     |
| Lys | Asp | Arg | Asn | Pro | Asn | Glu | Ser | Ser | Gly | Phe | Ser | Thr | Ser | Leu | Phe | 145 | 150 | 155 | 160 |
| Lys | Glu | Leu | Gln | Glu | His | Ala | Leu | Phe | Glu | Ala | Phe | Asn | 165 | 170 |     |     |     |     |     |

(i) SEQUENCE CHARACTERISTICS:

(Å) LENGTH: 258 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 451

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

|            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Met<br>1   | Ser        | Leu        | Ala        | Pro<br>5   | Ser        | Val        | Met        | Ala        | Gly<br>10  | Phe        | Leu        | Phe        | Cys        | Ala<br>15  | Gly        |
| Ser        | Cys        | Ser        | Leu<br>20  | Arg        | Phe        | Pro        | Asn        | Tyr<br>25  | Ser        | Lys        | Ile        | Ile        | Ser<br>30  | Ile        | Asp        |
| Val        | Asp        | Thr<br>35  | Val        | Phe        | Leu        | Gly        | Asp<br>40  | Val        | Ala        | Ser        | Ala        | Tyr<br>45  | Phe        | Ala        | Leu        |
| Asp        | Asn<br>50  | Glu        | Pro        | Thr        | Lys        | Leu<br>55  | Leu        | Gly        | Met        | Val        | Arg<br>60  | Asp        | Thr        | Phe        | Ser        |
| His<br>65  | Leu        | Pro        | Phe        | Glu        | Ala<br>70  | Phe        | Cys        | Asp        | Phe        | Cys<br>75  | Glu        | Arg        | Thr        | Cys        | Lys<br>80  |
| Asn        | Phe        | Lys        | Ile        | Asp<br>85  | Leu        | Leu        | Arg        | Phe        | Ser<br>90  | Gln        | Asn        | Glu        | Leu        | Lys<br>95  | Arg        |
| Ile        | His        | Gln        | Gly<br>100 | Phe        | Asn        | Met        | Gly        | Phe<br>105 | Leu        | Val        | Ala        | Asn        | Leu<br>110 | Asp        | Leu        |
| Trp        | Arg        | Glu<br>115 | Asn        | Gly        | Phe        | Glu        | Lys<br>120 | Ile        | Ala        | Leu        | Glu        | Phe<br>125 | Leu        | Lys        | Thr        |
| Arg        | Gly<br>130 | Lys        | Asp        | Leu        | Phe        | Tyr<br>135 | Pro        | Glu        | Gln        | Cys        | Leu<br>140 | Ile        | Asn        | Met        | Val        |
| Phe<br>145 | Leu        | Glu        | Arg        | Ile        | Leu<br>150 | Glu        | Leu        | Pro        | Ile        | His<br>155 | Tyr        | Asn        | Cys        | Tyr        | Ser<br>160 |
| Asp        | Phe        | Phe        | Lys        | Glu<br>165 | His        | Tyr        | Pro        | Lys        | Ser<br>170 | Ile        | Ile        | Met        | Leu        | His<br>175 | Phe        |
| Ile        | Lys        | Tyr        | Lys<br>180 | Pro        | Trp        | Arg        | Ser        | Val<br>185 | Ser        | Ser        | Leu        | Asn        | Gly<br>190 | Arg        | Leu        |
| Ile        | Cys        | Tyr<br>195 | Glu        | Ala        | Glu        | Ala        | Ser<br>200 | Phe        | Trp        | Leu        | Ala        | Asn<br>205 | Leu        | Phe        | Cys        |
| Thr        | Pro<br>210 | Phe        | Lys        | Asn        | Asp        | Phe<br>215 | Phe        | Lys        | Glu        | Arg        | Leu<br>220 | Glu        | Met        | Ala        | Lys        |
| Asp<br>225 | Gln        | Gln        | Met        | Gln        | Ser<br>230 | Phe        | Lys        | Thr        | His        | Ile<br>235 | Arg        | Ser        | Lys        | Thr        | Ile<br>240 |

Arg Asp Tyr Phe Tyr Phe Arg Ile Lys Asn Ile Leu Lys Lys Val Phe  
245 250 255

Glu Leu Ser

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 87 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 452

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ile | Thr | Ser | Leu | Val | Lys | Asn | Thr | Ile | Pro | Asn | Ile | Trp | Leu | Thr |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

Lys Ile Leu Tyr Met Ala Ile Leu Leu Cys Ala Ile Ala His Ser Val  
20 25 30

Gly Unk Ile Leu Arg Trp Tyr Val Ser Gly His Ser Pro Trp Ser Asn  
35 40 45

Ala Tyr Glu Ser Met Phe Tyr Ile Ala Trp Ala Ser Val Ile Ala Gly  
50 55 60

Phe Val Leu Arg Leu Asn Ser Arg Tyr Arg Leu Leu Ala Phe Trp Pro  
65 70 75 80

Val Ser Arg Ser Leu Trp Leu Ile  
85



(2) INFORMATION FOR SEQ ID NO:42683\_c2\_6: - A A

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 193 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

HPP 453

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: GLUTATHIONE-REGULATED POTASSIUM-EFFLUX SYSTEM PRO

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ile | Val | Cys | Ser | Ala | Ala | Gly | Leu | Ser | His | Phe | Phe | Gly | Phe | Ser | 1   | 5   | 10  | 15  |
| Met | Ser | Leu | Gly | Ala | Phe | Ile | Val | Gly | Met | Ala | Ile | Ser | Lys | Ser | Arg | 20  | 25  | 30  |     |
| Tyr | Lys | Ile | Asn | Val | Gln | Glu | Glu | Phe | Ala | Gln | Leu | Lys | Asn | Leu | Phe | 35  | 40  | 45  |     |
| Leu | Ala | Leu | Phe | Phe | Ile | Thr | Ile | Gly | Met | Gln | Ile | Asn | Val | Ser | Phe | 50  | 55  | 60  |     |
| Phe | Met | Glu | Lys | Phe | Phe | Val | Val | Ile | Phe | Leu | Leu | Ile | Leu | Val | Met | 65  | 70  | 75  | 80  |
| Ser | Phe | Lys | Thr | Phe | Ile | Ile | Tyr | Ala | Leu | Leu | Arg | Phe | Phe | Arg | Asp | 85  | 90  | 95  |     |
| Ala | Lys | Thr | Ala | Ile | Lys | Thr | Ala | Leu | Ser | Leu | Ala | Gln | Ile | Gly | Glu | 100 | 105 | 110 |     |
| Phe | Ser | Phe | Val | Ile | Phe | Leu | Asn | Ser | Gly | Ser | His | Gln | Leu | Phe | Asn | 115 | 120 | 125 |     |
| Leu | Gln | Glu | Lys | Lys | Gly | Ile | Leu | Gly | Phe | Leu | His | Gln | Lys | Asn | Ile | 130 | 135 | 140 |     |
| Leu | Asn | Ile | Ala | Gln | Asn | Asp | Ile | His | Gln | Leu | Leu | Ile | Leu | Met | Val | 145 | 150 | 155 | 160 |
| Val | Phe | Ser | Met | Leu | Ala | Thr | Pro | Phe | Ile | Leu | Lys | Tyr | Leu | Glu | Ser | 165 | 170 | 175 |     |
| Ile | Ala | Gln | Phe | Ile | Leu | His | Gln | Lys | Ser | Gln | Glu | Asn | Glu | Pro | Ala | 180 | 185 | 190 |     |
| Lys | Lys |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(A) ORGANISM: *Helicobacter pylori*

Met Phe Tyr Leu Ile Asn Thr Gly Val Pro His Leu Val Gly Phe Val  
1 5 10 15

Lys Asn Lys Gly Leu Leu Asn Ser Leu Asn Thr Leu Glu Leu Arg Ala  
20 25 30

Leu Arg His Glu Phe Asn Ala Asn Ile Asn Ile Ala Phe Ile Glu Asn  
35 40 45

Lys Glu Thr Ile Phe Leu Gln Thr Tyr Glu Arg Gly Val Glu Asp Phe  
50 55 60

Thr Leu Ala Cys Gly Thr Gly Met Ala Ala Val Phe Ile Ala Ala Arg  
65 70 75 80

Leu Phe His Asn Thr Pro Lys Lys Ala Thr Leu Ile Pro Lys Ser Asn  
85 90 95

Glu Phe Leu Glu Leu Ser Leu Lys Asn Asp Gly Ile Phe Tyr Lys Gly  
100 105 110

Val Ala Arg Tyr Ile Gly Met Ser Val Leu Gly Met Gly Val Phe Lys  
115 120 125

Asn Gly Cys Phe  
130

(2) INFORMATION FOR SEQ ID NO:4338438\_c3\_16:- AA

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 212 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein HPP 455

(iii) HYPOTHETICAL: YES

- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: hypothetical abc transporter n tesA region

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|
| Met | Ile | Lys | Ala | Ile | Asp | Ile | Ser | His | Asp | Phe | Glu | Lys | Pro | Leu | Tyr |  |  |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |  |  |
| Asn | Gly | Val | Asn | Leu | Arg | Ile | Lys | Pro | Lys | Glu | Ser | Met | Glu | Ile | Leu |  |  |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |  |  |
| Gly | Val | Ser | Gly | Ser | Gly | Lys | Ser | Thr | Leu | Ile | Ser | His | Leu | Ala | Thr |  |  |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |  |  |
| Met | Leu | Lys | Pro | Asp | Ser | Gly | Thr | Val | Ser | Leu | Leu | Glu | His | Gln | Asp |  |  |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |  |  |
| Ile | Tyr | Ala | Leu | Asn | Ser | Lys | Lys | Leu | Leu | Glu | Leu | Arg | Arg | Leu | Lys |  |  |  |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     | 80  |     |  |  |  |
| Val | Gly | Ile | Val | Phe | Gln | Ser | His | Tyr | Leu | Phe | Lys | Gly | Phe | Ser | Ala |  |  |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |  |  |
| Leu | Glu | Asn | Leu | Gln | Val | Ala | Ser | Ile | Leu | Ala | Lys | Gln | Glu | Ile | Asn |  |  |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |  |  |
| His | Ser | Leu | Leu | Glu | Gln | Leu | Gly | Ile | Ala | His | Thr | Leu | Lys | Gln | Gly |  |  |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |  |  |
| Val | Gly | Glu | Leu | Ser | Gly | Gly | Gln | Gln | Gln | Arg | Leu | Ser | Ile | Ala | Arg |  |  |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |  |  |
| Val | Leu | Ser | Lys | Lys | Pro | Gln | Ile | Ile | Ile | Ala | Asp | Glu | Pro | Thr | Gly |  |  |  |
| 145 |     |     |     | 150 |     |     |     |     |     | 155 |     |     |     |     | 160 |  |  |  |
| Asn | Leu | Asp | Thr | Thr | Ser | Ala | Asn | Gln | Val | Ile | Ser | Met | Leu | Gln | Asn |  |  |  |
|     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     | 175 |     |  |  |  |
| Tyr | Ile | Thr | Glu | Asn | Glu | Gly | Ala | Leu | Val | Leu | Ala | Thr | His | Asp | Glu |  |  |  |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |  |  |
| His | Leu | Ala | Phe | Thr | Cys | Ser | Gln | Val | Tyr | Arg | Leu | Glu | Lys | Glu | Ser |  |  |  |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |  |  |
| Leu | Ile | Lys | Glu | Lys |     |     |     |     |     |     |     |     |     |     |     |  |  |  |
| 210 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |  |

(2) INFORMATION FOR SEQ ID NO:4339708\_f3\_3: -AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 456

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met Leu Asp Lys Arg Ile Lys Thr Leu Leu Leu Phe Phe Gly Leu Asn  
1 5 10 15

Met Val Cys Leu Ser Val Ser Phe Thr Asn Lys Pro His Leu Cys Phe  
20 25 30

Trp Phe Leu Val Leu Gly Cys Tyr Leu Val Tyr Glu Trp Gln Lys  
35 40 45

(2) INFORMATION FOR SEQ ID NO:43490713\_f2\_5:-AA

Figure 457A - page 543

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP: 457

(iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: glycerolphosphate auxotrophy in plsB background

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| Val | Glu | Met | Ile | His | Thr | Gln | Asp | Tyr | Ile | Lys | Met | Glu | Glu | Ala | Ala | 1   | 5   | 10  | 15 |
| Thr | Glu | Ala | Ile | Lys | Arg | Lys | Glu | Ser | Ser | Ile | Tyr | Leu | Gly | Met | Asp | 20  | 25  | 30  |    |
| Ile | Leu | Lys | Asn | Gly | Ala | Asp | Ala | Leu | Ile | Ser | Ala | Gly | His | Ser | Gly | 35  | 40  | 45  |    |
| Ala | Thr | Met | Gly | Leu | Ala | Thr | Leu | Arg | Leu | Gly | Arg | Ile | Lys | Gly | Val | 50  | 55  | 60  |    |
| Glu | Arg | Pro | Ala | Ile | Cys | Thr | Leu | Met | Pro | Ser | Val | Gly | Lys | Arg | Pro | 65  | 70  | 75  | 80 |
| Ser | Val | Leu | Leu | Asp | Ala | Gly | Ala | Asn | Thr | Asp | Cys | Lys | Pro | Glu | Tyr | 85  | 90  | 95  |    |
| Leu | Ile | Asp | Phe | Ala | Leu | Met | Gly | Tyr | Glu | Tyr | Ala | Lys | Ser | Val | Leu | 100 | 105 | 110 |    |
| His | Tyr | Asp | Ser | Pro | Lys | Val | Gly | Leu | Leu | Ser | Asn | Gly | Glu | Glu | Asp | 115 | 120 | 125 |    |
| Ile | Lys | Gly | Gly | Ile | Arg | Ser | Leu | Lys | Lys | Arg | Ile | Lys | Cys | 130 | 135 | 140 |     |     |    |

(2) INFORMATION FOR SEQ ID NO:4414000\_c2\_5: -AA

(A) LENGTH: 68 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 458

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Met Lys Thr Ile Lys Asn Gly Ile Met Ile Gly Thr Leu Gly Ala Leu  
1 5 10 15

Leu Leu Ser Gly Cys Ser Ser Phe Asp Ala Gln Arg Phe Ala Cys Leu  
20 25 30

Pro Lys Asp His Ser Ser Lys Asp Ala Ser Thr Lys Lys Glu Ala Gln  
35 40 45

Tyr Ile Pro Lys Gly Phe Phe Asp Pro Tyr Ser Ser Asn Leu Asn His  
50 55 60

Trp Asp Ser Thr Phe  
65

(2) INFORMATION FOR SEQ ID NO:4455467\_f3\_5: - AA

Figure 459A - page 545

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

HPP459

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: D-xylose transport atp-binding protein xylg

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Glu | Ile | Lys | Asn | Leu | Asn | Cys | Val | Leu | Asn | Ser | His | Phe | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Gln | Asn | Ile | Asn | Ile | Ser | Leu | Ser | Tyr | Ser | Glu | Arg | Val | Ala | Ile |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Gly | Glu | Ser | Gly | Ser | Gly | Lys | Ser | Ser | Ile | Ala | Asn | Leu | Val | Met |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Arg | Leu | Asn | Pro | Arg | Phe | Lys | Ser | His | Asn | Gly | Glu | Ile | Leu | Phe | Glu |
|     |     |     | 50  |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Thr | Thr | Asn | Leu | Leu | Lys | Glu | Ser | Glu | Ala | Unk | Cys | Ser | Ile |     |     |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:4486092\_f1\_1: -AA

Figure 460A -page 546

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 189 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein HPP 460

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: E.coli mreD gene Rod shape-determining protein

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Leu | Ile | Leu | Gly | Ser | Gln | Ser | Ser | Ala | Arg | Ala | Asn | Leu | Leu | 1   | 5   | 10  | 15  |
| Lys | Glu | His | Gly | Ile | Lys | Phe | Glu | Gln | Lys | Ala | Leu | Tyr | Phe | Asp | Glu | 20  | 25  | 30  |     |
| Glu | Ser | Leu | Lys | Thr | Thr | Asp | Pro | Arg | Glu | Phe | Val | Tyr | Leu | Ala | Cys | 35  | 40  | 45  |     |
| Lys | Gly | Lys | Leu | Glu | Lys | Ala | Lys | Glu | Leu | Leu | Ala | Asn | Asn | Cys | Ala | 50  | 55  | 60  |     |
| Ile | Val | Val | Ala | Asp | Ser | Val | Val | Ser | Val | Gly | Asn | Arg | Met | Gln | Arg | 65  | 70  | 75  | 80  |
| Lys | Ala | Lys | Asn | Lys | Arg | Glu | Ala | Leu | Glu | Phe | Leu | Lys | Arg | Gln | Asn | 85  | 90  | 95  |     |
| Gly | Asn | Glu | Ile | Glu | Val | Leu | Thr | Cys | Ser | Ala | Leu | Ile | Ser | Pro | Val | 100 | 105 | 110 |     |
| Leu | Glu | Trp | Leu | Asp | Leu | Ser | Val | Phe | Arg | Ala | Arg | Leu | Lys | Ala | Phe | 115 | 120 | 125 |     |
| Asp | Cys | Ser | Glu | Ile | Glu | Lys | Tyr | Leu | Glu | Ser | Gly | Leu | Trp | Gln | Gly | 130 | 135 | 140 |     |
| Ser | Ala | Gly | Cys | Val | Arg | Leu | Glu | Asp | Phe | His | Lys | Pro | Tyr | Ile | Lys | 145 | 150 | 155 | 160 |
| Ser | Ser | Ser | Lys | Asn | Leu | Ser | Val | Gly | Leu | Gly | Leu | Asn | Val | Glu | Gly | 165 | 170 | 175 |     |
| Leu | Leu | Gly | Ala | Leu | Lys | Leu | Gly | Val | Lys | Leu | Ser | Leu | Leu | 180 | 185 | 190 |     |     |     |



(2) INFORMATION FOR SEQ ID NO:4490717\_f1\_1: - AA

Figure 461A-page 547

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 461

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asn | Tyr | Lys | Val | Ala | Ser | Ala | Arg | Asn | Ile | Ala | Thr | Leu | Leu | Phe |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Phe | Phe | Ser | Gln | Ser | Glu | Ala | Phe | Asp | Leu | Gly | Lys | Ile | Ala | Lys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ile | Lys | Ala | Gly | Ala | Glu | Ser | Phe | Ser | Lys | Val | Gly | Phe | Asn | Asn | Lys |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Pro | Ile | Asn | Ile | Ile | Lys | Gly | Phe | Thr | Leu | Pro | Lys | Pro | Leu |     |     |
| 50  |     |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:4491093\_c1\_9:-AA

Figure 462A-page 548

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP462

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| Met | Leu | Ile | Leu | Gly | His | Pro | Leu | Ile | Pro | Ser | Ala | Arg | Phe | Val | Phe | 1   | 5   | 10  | 15 |
| Ile | Lys | Asn | Thr | Asp | Ala | Ile | His | Ser | Ser | Ala | Asn | Asn | Asp | Ile | Val | 20  | 25  | 30  |    |
| Cys | Phe | Glu | Ala | Asn | Pro | Lys | Asn | Leu | Glu | Leu | Ala | Gln | Tyr | Cys | Cys | 35  | 40  | 45  |    |
| Glu | Asn | Gly | Val | His | Phe | Ser | Val | Ile | Phe | Leu | Ser | His | Lys | Ile | Glu | 50  | 55  | 60  |    |
| Thr | Asp | Thr | Phe | Phe | Leu | Phe | Asn | Ala | Phe | Lys | Pro | Leu | Tyr | Cys | Ile | 65  | 70  | 75  | 80 |
| Phe | Lys | Asp | Ile | Lys | Gln | Ala | Ile | Leu | Ala | Gln | Gln | His | Ala | Thr | Asn | 85  | 90  | 95  |    |
| Tyr | Leu | Leu | Asp | Ser | Lys | Ile | Leu | Phe | Ser | Met | Asp | Phe | Asn | Asp | Thr | 100 | 105 | 110 |    |
| Glu | Ser | Trp | Glu | Ile | Cys | Ala | Lys | Asn | Gln | Ile | Asp | Gly | Val | Ile | Ser | 115 | 120 | 125 |    |
| Lys | Asp | Ser | Leu | Leu | Leu | Lys |     |     |     |     |     |     |     |     |     | 130 | 135 |     |    |

(2) INFORMATION FOR SEQ ID NO:4492217\_c3\_15: - AA

Figure 463A - page 549

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 463

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (xi) SEQUENCE DESCRIPTION:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Lys | Arg | Leu | Asn | Ile | Gly | Leu | Val | Gly | Leu | Gly | Cys | Val | Gly | 1   | 5   | 10  | 15  |
| Ser | Thr | Val | Ala | Lys | Ile | Leu | Gln | Glu | Asn | Gln | Glu | Ile | Ile | Lys | Asp | 20  | 25  | 30  |     |
| Arg | Ala | Gly | Val | Glu | Ile | Lys | Ile | Lys | Lys | Ala | Val | Val | Arg | Asp | Val | 35  | 40  | 45  |     |
| Lys | Lys | His | Lys | Gly | Tyr | Ala | Phe | Glu | Ile | Ser | Asp | Asp | Leu | Glu | Ser | 50  | 55  | 60  |     |
| Val | Ile | Glu | Asp | Lys | Gly | Ile | Asp | Ile | Val | Val | Glu | Leu | Met | Gly | Gly | 65  | 70  | 75  | 80  |
| Val | Glu | Ala | Pro | Tyr | Leu | Leu | Ala | Lys | Lys | Thr | Leu | Ala | Lys | Gln | Lys | 85  | 90  | 95  |     |
| Ala | Phe | Val | Thr | Ala | Asn | Lys | Ala | Met | Leu | Ala | Tyr | His | Arg | Tyr | Glu | 100 | 105 | 110 |     |
| Leu | Glu | Gln | Ile | Ala | Lys | Asn | Thr | Pro | Ile | Gly | Phe | Glu | Ala | Ser | Val | 115 | 120 | 125 |     |
| Cys | Gly | Gly | Ile | Pro | Ile | Ile | Lys | Ala | Leu | Lys | Asp | Gly | Leu | Ser | Ala | 130 | 135 | 140 |     |
| Asn | His | Ile | Leu | Ser | Phe | Lys | Gly | Ile | Leu | Asn | Gly | Thr | Ser | Asn | Tyr | 145 | 150 | 155 | 160 |
| Ile | Leu | Ser | Gln | Met | Phe | Lys | Asn | Gln | Ala | Ser | Phe | Lys | Asp | Ala | Leu | 165 | 170 | 175 |     |
| Lys | Asp | Ala | Gln | His | Leu | Gly | Tyr | Ala | Glu | Leu | Asn | Pro | Glu | Phe | Asp | 180 | 185 | 190 |     |
| Ile | Lys | Gly | Ile | Asp | Ala | Ala | His | Lys | Leu | Leu | Ile | Leu | Ala | Ser | Leu | 195 | 200 | 205 |     |
| Ala | Tyr | Gly | Ile | Asp | Ala | Lys | Leu | Glu | Glu | Ile | Leu | Ile | Glu | Gly | Ile | 210 | 215 | 220 |     |
| Glu | Lys | Ile | Glu | Pro | Asp | Asp | Met | Glu | Phe | Ala | Lys | Glu | Phe | Gly | Tyr | 225 | 230 | 235 | 240 |

Ser Ile Lys Leu Leu Gly Ile Ala Lys Lys His Gln Gly Leu His  
245 250 255

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 242 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 464

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

## (xi) SEQUENCE DESCRIPTION:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| Met | Gln | Glu | Lys | Arg | Leu | Lys | Ala | Ile | Gln | Asn | Lys | Ile | Ala | Ser | Trp | 1   | 5   | 10  | 15 |
| Ile | Lys | Glu | Ile | Glu | Ser | Gly | Phe | Ile | Asp | Ala | Leu | Phe | Ser | Lys | Ile | 20  | 25  | 30  |    |
| Gly | Pro | Ser | Lys | Met | Leu | Arg | Ser | Lys | Leu | Met | Leu | Ala | Leu | Leu | Asp | 35  | 40  | 45  |    |
| Glu | Lys | Thr | Asp | Ala | Ile | Leu | Leu | Asp | Lys | Ala | Leu | Asn | Leu | Cys | Ala | 50  | 55  | 60  |    |
| Ile | Val | Glu | Met | Ile | Gln | Thr | Ala | Ser | Leu | Leu | His | Asp | Asp | Val | Ile | 65  | 70  | 75  |    |
| Asp | Lys | Ala | Thr | Met | Arg | Arg | Lys | Leu | Pro | Ser | Ile | Asn | Ala | Leu | Phe | 85  | 90  | 95  |    |
| Gly | Asn | Phe | Asn | Ala | Val | Met | Leu | Gly | Asp | Val | Phe | Tyr | Ser | Lys | Ala | 100 | 105 | 110 |    |
| Phe | Phe | Glu | Leu | Ser | Lys | Met | Gly | Glu | Ser | Ile | Ala | Gln | Ala | Leu | Ser | 115 | 120 | 125 |    |
| Asn | Ala | Val | Leu | Arg | Leu | Ser | Arg | Gly | Glu | Ile | Glu | Asp | Val | Phe | Val | 130 | 135 | 140 |    |
| Gly | Glu | Cys | Phe | Asn | Ser | Asp | Lys | Gln | Lys | Tyr | Trp | Arg | Ile | Leu | Glu | 145 | 150 | 155 |    |
| Asp | Lys | Thr | Ala | His | Phe | Ile | Glu | Ala | Ser | Leu | Lys | Ser | Met | Ala | Ile | 165 | 170 | 175 |    |
| Leu | Leu | Asn | Lys | Asp | Ala | Lys | Met | Tyr | Ala | Asp | Phe | Gly | Leu | His | Phe | 180 | 185 | 190 |    |
| Gly | Met | Ala | Phe | Gln | Ile | Ile | Asp | Asp | Leu | Leu | Asp | Ile | Thr | Gln | Asp | 195 | 200 | 205 |    |
| Ala | Asn | Thr | Leu | Gly | Lys | Pro | Asn | Phe | Ser | Asp | Phe | Lys | Glu | Gly | Lys | 210 | 215 | 220 |    |
| Thr | Thr | Leu | Pro | Tyr | Leu | Leu | Leu | Tyr | Glu | Lys | Leu | Asn | Gln | His | Glu | 225 | 230 | 235 |    |

Gln Gly Phe

(2) INFORMATION FOR SEQ ID NO:4548792\_c1\_27: -AA

Figure 465A-page 553

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 465

(iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM:
- Helicobacter pylori*

## (xi) SEQUENCE DESCRIPTION:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Gly | Lys | Lys | Asn | Glu | Glu | Val | Leu | Ile | Asp | Glu | Asn | Leu | Val | 1   | 5   | 10  | 15  |
| Gly | Gly | Val | Ile | Ala | Leu | Asp | Arg | Leu | Ala | Lys | Leu | Asn | Lys | Ala | Asn | 20  | 25  | 30  |     |
| Arg | Thr | Phe | Lys | Arg | Ala | Phe | Tyr | Leu | Ser | Met | Val | Leu | Asn | Val | Ala | 35  | 40  | 45  |     |
| Ala | Val | Thr | Ser | Ile | Val | Met | Met | Pro | Leu | Lys | Lys | Thr | Asp | Ile | 50  | 55  | 60  |     |     |
| Phe | Val | Tyr | Gly | Ile | Asp | Arg | Tyr | Thr | Gly | Glu | Phe | Lys | Ile | Val | Lys | 65  | 70  | 75  | 80  |
| Arg | Ser | Asp | Ala | Arg | Gln | Ile | Val | Asn | Ser | Glu | Ala | Val | Val | Asp | Ser | 85  | 90  | 95  |     |
| Ala | Thr | Ser | Lys | Phe | Val | Ser | Leu | Leu | Phe | Gly | Tyr | Ser | Lys | Asn | Ser | 100 | 105 | 110 |     |
| Leu | Arg | Asp | Arg | Lys | Asp | Gln | Leu | Met | Gln | Tyr | Cys | Asp | Val | Ser | Phe | 115 | 120 | 125 |     |
| Gln | Thr | Gln | Ala | Met | Arg | Met | Phe | Asn | Glu | Asn | Ile | Arg | Gln | Phe | Val | 130 | 135 | 140 |     |
| Asp | Lys | Val | Arg | Ala | Glu | Ala | Ile | Ile | Ser | Ser | Asn | Ile | Gln | Arg | Glu | 145 | 150 | 155 | 160 |
| Lys | Val | Lys | Asn | Ser | Pro | Leu | Thr | Arg | Leu | Thr | Phe | Phe | Ile | Thr | Ile | 165 | 170 | 175 |     |
| Lys | Ile | Thr | Pro | Asp | Thr | Met | Glu | Asn | Tyr | Glu | Tyr | Ile | Thr | Lys | Lys | 180 | 185 | 190 |     |
| Gln | Val | Thr | Ile | Tyr | Tyr | Asp | Phe | Ala | Arg | Gly | Asn | Ser | Ser | Gln | Glu | 195 | 200 | 205 |     |
| Asn | Leu | Ile | Ile | Asn | Pro | Phe | Gly | Phe | Lys | Val | Phe | Asp | Ile | Gln | Ile | 210 | 215 | 220 |     |
| Thr | Asp | Leu | Gln | Asn | Glu | Gln | Thr | Val | Ser | Glu | Ile | Leu | Arg | Lys | Ile | 225 | 230 | 235 | 240 |

Lys Glu Val Glu Ser Lys Asn Lys Ala Leu Asn Lys  
245 250

Figure 465A-page 554



(2) INFORMATION FOR SEQ ID NO:4551291\_f2\_2: - AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 466

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ile | Val | Gly | Val | Gly | Lys | Ser | Ala | Leu | Val | Ala | Gln | Lys | Ile | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Ser | Met | Leu | Ser | Thr | Gly | Asn | Arg | Ser | Ala | Phe | Leu | His | Pro | Thr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Ala | Met | His | Gly | Asp | Leu | Gly | Met | Gly | Lys | Lys | Thr | Met |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |

Figure 467A-page 556

(Å) LENGTH: 164 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 467

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Met Arg Ala Ile Ala Ile Val Leu Ala Arg Ser Ser Ser Lys Arg Ile  
1 5 10 15

Lys Asn Lys Asn Met Ile Asp Phe Phe Asn Lys Pro Met Leu Ala Tyr  
20 25 30

Pro Ile Glu Thr Ala Leu Asn Ser Lys Leu Phe Glu Lys Val Phe Ile  
35 40 45

Ser Ser Asp Ser Met Glu Tyr Val Asn Leu Ala Lys Asn Tyr Gly Ala  
50 55 60

Ser Phe Leu Asn Leu Arg Pro Lys Asn Leu Ala Asp Asp Arg Ala Thr  
65 70 75 80

Thr Leu Glu Val Met Ala Tyr His Met Lys Glu Leu Glu Leu Lys Asp  
85 90 95

Glu Asp Ile Ala Cys Cys Leu Tyr Gly Val Ser Val Phe Leu Gln Glu  
100 105 110

Lys His Leu Gln Asn Ala Phe Glu Thr Leu Lys Gln Asn Gln Asn Thr  
115 120 125

Asp Tyr Val Phe Thr Cys Ser Pro Phe Ser Ala Ser Pro Ile Val Leu  
130 135 140

Leu Ala Leu Lys Thr Ala Phe Lys Trp Leu Leu Lys Ser Ile Gln Thr  
145 150 155 160

Arg Ala Arg Lys Ile  
165

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 170 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

HPD 468

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: *Helicobacter pylori*

|            |            |            |            |            |           |            |            |            |            |            |            |            |            |           |            |
|------------|------------|------------|------------|------------|-----------|------------|------------|------------|------------|------------|------------|------------|------------|-----------|------------|
| Met<br>1   | Ser        | Asn        | Gln        | Ala<br>5   | Ser       | His        | Leu        | Asp        | Asn<br>10  | Phe        | Met        | Asn        | Ala        | Lys<br>15 | Asn        |
| Pro        | Lys        | Ser        | Phe<br>20  | Phe        | Asp       | Asn        | Lys        | Gly<br>25  | Asn        | Thr        | Lys        | Phe        | Ile<br>30  | Ala       | Ile        |
| Thr        | Ser        | Gly<br>35  | Lys        | Gly        | Gly       | Val        | Gly<br>40  | Lys        | Ser        | Asn        | Ile        | Ser<br>45  | Ala        | Asn       | Leu        |
| Ala        | Tyr<br>50  | Ser        | Leu        | Tyr        | Lys       | Lys<br>55  | Gly        | Tyr        | Lys        | Val        | Gly<br>60  | Val        | Phe        | Asp       | Ala        |
| Asn<br>65  | Ile        | Gly        | Leu        | Ala        | Asn<br>70 | Leu        | Asp        | Val        | Ile        | Phe<br>75  | Gly        | Val        | Lys        | Thr       | Gln<br>80  |
| Lys        | Asn        | Ile        | Leu        | His<br>85  | Asp       | Leu        | Lys        | Gly        | Glu<br>90  | Asp        | Lys        | Leu        | Lys        | Glu<br>95 | Ile        |
| Ile        | Cys        | Glu        | Ile<br>100 | Glu        | Pro       | Gly        | Leu        | Cys<br>105 | Leu        | Ile        | Pro        | Gly        | Asp<br>110 | Ser       | Gly        |
| Glu        | Glu        | Ile<br>115 | Leu        | Lys        | Tyr       | Ile        | Ser<br>120 | Glu        | Ala        | Glu        | Asp        | Phe<br>125 | Asp        | Ser       | Phe        |
| Leu        | Asp<br>130 | Glu        | Glu        | Gly        | Val       | Leu<br>135 | Ser        | Ala        | Leu        | Ile        | Tyr<br>140 | Ile        | Leu        | Ile       | Asn        |
| Thr<br>145 | Phe        | Ser        | Lys        | Asn<br>150 | Leu       | Gly        | Pro        | Leu        | Ser        | Gln<br>155 | Thr        | Phe        | Leu        | Asn       | Phe<br>160 |
| Gln        | Ser        | Phe        | Leu        | Phe<br>165 | Ile       | Phe        | Ile        | Gln        | Ser<br>170 | Pro        |            |            |            |           |            |

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 61 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein H PP469

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gln | His | Leu | Val | Leu | Ile | Gly | Phe | Met | Gly | Ser | Gly | Lys | Ser | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Ala | Gln | Glu | Leu | Gly | Leu | Ala | Leu | Lys | Leu | Glu | Val | Leu | Asp | Thr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |
| Asp | Met | Ile | Ile | Ser | Glu | Arg | Val | Gly | Leu | Ser | Val | Arg | Gly | Ile | Phe |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Glu | Glu | Leu | Gly | Glu | Asp | Asn | Phe | Arg | Met | Phe | Glu | Lys | Ile |     |     |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |

559

Figure 470A - page 559

(D) TOPOLOGY: linear

HPP 470

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Tyr Gly Met Leu Glu Asp Ile  
195



561

Figure 472A-page 561

## HPP 472

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Arg Lys Asn Gly Val  
100

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 473

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Lys | Phe | Phe | Ser | Gln | Ser | Leu | Leu | Ala | Leu | Ile | Ile | Ser | Met |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asn | Ala | Val | Ser | Gly | Met | Asp | Gly | Asn | Gly | Val | Phe | Leu | Gly | Ala | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Tyr | Leu | Gln | Gly | Gln | Ala | Gln | Met | His | Ala | Asp | Ile | Asn | Ser | Gln | Lys |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gln | Ala | Thr | Asn | Ala | Thr | Ile | Lys | Gly | Phe | Asp | Ala | Leu | Leu | Gly | Tyr |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Gln | Phe | Phe | Phe | Glu | Lys | His | Phe | Gly | Leu | Arg | Leu | Tyr | Gly | Val | Phe |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |



## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 446 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 474

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: penicillin binding protein

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Lys | Lys | Ile | Phe | Tyr | Gly | Phe | Ile | Val | Leu | Phe | Leu | Ile | Ile | 1   | 5   | 10  | 15  |
| Val | Gly | Leu | Leu | Ala | Val | Leu | Val | Ala | Gln | Val | Trp | Val | Thr | Thr | Asp | 20  | 25  | 30  |     |
| Lys | Asp | Ile | Ala | Lys | Ile | Lys | Asp | Tyr | Arg | Pro | Ser | Val | Ala | Ser | Gln | 35  | 40  | 45  |     |
| Ile | Leu | Asp | Arg | Lys | Gly | Arg | Leu | Ile | Ala | Asn | Ile | Tyr | Asp | Lys | Glu | 50  | 55  | 60  |     |
| Phe | Arg | Phe | Tyr | Ala | Arg | Phe | Glu | Glu | Ile | Pro | Pro | Arg | Phe | Val | Glu | 65  | 70  | 75  | 80  |
| Ser | Leu | Leu | Ala | Val | Glu | Asp | Thr | Leu | Phe | Phe | Glu | His | Gly | Gly | Ile | 85  | 90  | 95  |     |
| Asn | Leu | Asp | Ala | Val | Met | Arg | Ala | Met | Ile | Lys | Asn | Ala | Lys | Ser | Gly | 100 | 105 | 110 |     |
| Arg | Tyr | Thr | Glu | Gly | Gly | Ser | Thr | Leu | Thr | Gln | Gln | Leu | Val | Lys | Asn | 115 | 120 | 125 |     |
| Met | Val | Leu | Thr | Arg | Glu | Lys | Thr | Leu | Thr | Arg | Lys | Leu | Lys | Glu | Ala | 130 | 135 | 140 |     |
| Ile | Ile | Ser | Ile | Arg | Ile | Glu | Lys | Val | Leu | Ser | Lys | Glu | Glu | Ile | Leu | 145 | 150 | 155 | 160 |
| Glu | Arg | Tyr | Leu | Asn | Gln | Thr | Phe | Phe | Gly | His | Gly | Tyr | Tyr | Gly | Val | 165 | 170 | 175 |     |
| Lys | Thr | Ala | Ser | Leu | Gly | Tyr | Phe | Lys | Lys | Pro | Leu | Asp | Lys | Leu | Thr | 180 | 185 | 190 |     |
| Leu | Lys | Glu | Ile | Thr | Met | Leu | Val | Ala | Leu | Pro | Arg | Ala | Pro | Ser | Phe | 195 | 200 | 205 |     |
| Tyr | Asp | Pro | Thr | Lys | Asn | Leu | Glu | Phe | Ser | Leu | Ser | Arg | Ala | Asn | Asp | 210 | 215 | 220 |     |
| Ile | Leu | Arg | Arg | Leu | Tyr | Ser | Leu | Gly | Unk | Ile | Ser | Ser | Asn | Glu | Leu | 225 | 230 | 235 | 240 |

|            |     |            |            |            |            |            |            |            |            |            |            |            |            |            |            |
|------------|-----|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Lys        | Ser | Ala        | Leu        | Asn<br>245 | Glu        | Val        | Pro        | Ile        | Val<br>250 | Tyr        | Asn        | Gln        | Thr        | Ser<br>255 | Thr        |
| Gln        | Asn | Ile        | Ala<br>260 | Pro        | Tyr        | Val        | Val        | Asp<br>265 | Glu        | Val        | Leu        | Lys        | Gln<br>270 | Leu        | Asp        |
| Gln        | Leu | Asp<br>275 | Gly        | Leu        | Lys        | Thr        | Gln<br>280 | Gly        | Tyr        | Thr        | Ile        | Lys<br>285 | Leu        | Thr        | Ile        |
| Asp<br>290 | Leu | Asp        | Tyr        | Gln        | Arg        | Leu<br>295 | Ala        | Leu        | Glu        | Ser        | Leu<br>300 | Arg        | Phe        | Gly        | His        |
| Gln<br>305 | Lys | Ile        | Leu        | Glu        | Lys<br>310 | Ile        | Ala        | Lys        | Glu        | Lys<br>315 | Pro        | Lys        | Thr        | Asn        | Ala<br>320 |
| Ser        | Asn | Asp        | Lys        | Asp<br>325 | Glu        | Asp        | Asn        | Leu        | Asn<br>330 | Ala        | Ser        | Met        | Ile        | Val<br>335 | Thr        |
| Glu        | Thr | Ser        | Thr<br>340 | Gly        | Lys        | Ile        | Leu        | Ala<br>345 | Leu        | Val        | Gly        | Gly        | Ile<br>350 | Asp        | Tyr        |
| Lys        | Lys | Ser<br>355 | Ala        | Phe        | Asn        | Arg        | Ala<br>360 | Thr        | Gln        | Ala        | Lys        | Arg<br>365 | Gln        | Phe        | Gly        |
| Ser<br>370 | Ala | Ile        | Lys        | Pro        | Phe        | Val<br>375 | Tyr        | Gln        | Ile        | Ala        | Phe<br>380 | Asp        | Asn        | Gly        | Tyr        |
| Ser<br>385 | Thr | Thr        | Ser        | Lys        | Ile<br>390 | Pro        | Asp        | Thr        | Ala        | Arg<br>395 | Asn        | Phe        | Glu        | Asn        | Gly<br>400 |
| Asn        | Tyr | Ser        | Lys        | Asn<br>405 | Ser        | Val        | Gln        | Asn        | His<br>410 | Ala        | Trp        | His        | Pro        | Ser        | Asn<br>415 |
| Tyr        | Unk | Arg        | Lys<br>420 | Phe        | Leu        | Gly        | Leu        | Val<br>425 | Thr        | Leu        | Gln        | Glu        | Ala<br>430 | Leu        | Ser        |
| His        | Ser | Leu<br>435 | Asn        | Leu        | Ala        | Thr        | Ile<br>440 | Asn        | Leu        | Ala        | Ile        | Ala<br>445 | Trp        | Leu        |            |

$$-AA$$

565

Phe Ala Ser Lys Lys Gln Gly Gly Ala Glu  
210 215

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 476

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Met | Asp | Lys | Val | Gly | Phe | Lys | Ser | Gln | Gly | Ile | Phe | Val | Met | Asp |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Ala | Ser | Lys | Arg | Asp | Gly | Arg | Leu | Asn | Ala | Tyr | Phe | Gly | Gly | Leu | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Lys | Asn | Lys | Arg | Val | Val | Leu | Phe | Asp | Thr | Leu | Ile | Ser | Lys | Val | Gly |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Thr | Glu | Unk | Leu | Leu | Ala | Ile | Leu | Gly | His | Glu | Leu | Gly | His | Phe | Lys |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Asn | Lys | Asp | Leu | Leu | Lys | Asn | Leu | Gly | Ile | Met | Gly | Gly | Leu | Leu | Ala |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |
| Leu | Val | Phe | Ala | Leu | Ile | Ala | His | Leu | Pro | Pro | Leu | Val | Phe | Glu | Gly |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Phe | Asn | Val | Ser | Gln | Thr | Pro | Ala | Ser | Leu | Ile | Thr | Ile | Leu | Leu | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Phe | Leu | Pro | Val | Phe | Ser | Phe | Tyr | Ala | Met | Pro | Leu | Ile | Gly | Phe | Phe |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ser | Arg | Lys | Asn | Glu | Tyr | Asn | Ala | Asp | Lys | Phe | Gly | Ala | Ser | Leu | Ser |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ser | Lys | Glu | Thr | Leu | Ala | Lys | Ala | Leu | Val | Ser | Ile | Val | Asn | Glu | Asn |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Lys | Ala | Phe | Pro | Tyr | Ser | His | Pro | Phe | Tyr | Val | Phe | Leu | His | Phe | Thr |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| His | Pro | Pro | Leu | Leu | Glu | Arg | Leu | Lys | Ala | Leu | Asp | Tyr | Glu | Ile | Glu |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP477

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: O-SYALOGLYCOPROTEIN ENDOPEPTIDASE-lacks signal se

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ile | Leu | Ser | Ile | Glu | Ser | Ser | Cys | Asp | Asp | Ser | Ser | Leu | Ala | Leu | 1   | 5   | 10  | 15  |
| Thr | Arg | Ile | Glu | Asp | Ala | Lys | Leu | Ile | Ala | His | Phe | Lys | Ile | Ser | Gln | 20  | 25  | 30  |     |
| Glu | Lys | His | His | Ser | Ser | Tyr | Gly | Gly | Val | Val | Pro | Glu | Ile | Ala | Ser | 35  | 40  | 45  |     |
| Arg | Leu | His | Ala | Glu | Asn | Leu | Pro | Leu | Leu | Leu | Glu | Arg | Val | Lys | Ile | 50  | 55  | 60  |     |
| Ser | Leu | Asn | Lys | Asp | Phe | Ser | Lys | Ile | Lys | Ala | Ile | Ala | Ile | Thr | Asn | 65  | 70  | 75  | 80  |
| Gln | Pro | Gly | Leu | Ser | Val | Thr | Leu | Ile | Glu | Gly | Leu | Met | Met | Ala | Lys | 85  | 90  | 95  |     |
| Ala | Leu | Ser | Leu | Ser | Leu | Asn | Leu | Pro | Leu | Ile | Leu | Glu | Asp | His | Leu | 100 | 105 | 110 |     |
| Arg | Gly | His | Val | Tyr | Ser | Leu | Phe | Ile | Asn | Glu | Lys | Gln | Thr | Arg | Met | 115 | 120 | 125 |     |
| Pro | Leu | Ser | Val | Leu | Leu | Val | Ser | Gly | Gly | His | Ser | Leu | Ile | Leu | Glu | 130 | 135 | 140 |     |
| Ala | Arg | Asp | Tyr | Glu | Asp | Ile | Lys | Ile | Val | Ala | Thr | Ser | Leu | Asp | Asp | 145 | 150 | 155 | 160 |
| Ser | Phe | Gly | Glu | Ser | Phe | Asp | Lys | Val | Ser | Lys | Met | Leu | Asp | Leu | Gly | 165 | 170 | 175 |     |
| Tyr | Pro | Gly | Gly | Pro | Ile | Val | Glu | Lys | Leu | Ala | Leu | Asp | Tyr | Ala | His | 180 | 185 | 190 |     |
| Pro | Asn | Glu | Pro | Leu | Met | Phe | Pro | Ile | Pro | Leu | Lys | Asn | Ser | Pro | Asn | 195 | 200 | 205 |     |
| Leu | Ala | Phe | Ser | Phe | Ser | Gly | Leu | Lys | Asn | Ala | Val | Arg | Leu | Glu | Val | 210 | 215 | 220 |     |
| Glu | Lys | Asn | Ala | His | Asn | Leu | Asn | Asp | Glu | Val | Lys | Gln | Lys | Ile | Gly | 225 | 230 | 235 | 240 |



(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP478

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met Asn Ile Tyr Gln Lys Asn Leu Gln Ala Leu Phe Lys Lys Asp Pro  
1 5 10 15  
Leu Leu Phe Ala Lys Leu Lys Ala Ile Lys Glu Asn Lys Lys Tyr Glu  
20 25 30  
Val Phe Leu Gly Asn Asp Ser Ala Asn Phe Asn Leu Leu Asp Lys Glu  
35 40 45  
Thr Asn Thr Pro Leu Phe Glu Lys Ser Pro Leu Asp Ser Ser Leu Glu  
50 55 60  
Leu Tyr Lys Asn Ser Glu Ile His Met Leu Tyr Pro Tyr Leu Tyr Tyr  
65 70 75 80  
Phe Gly Leu Gly Asn Gly Val Phe Tyr Arg Leu Leu Leu Gly Asn Glu  
85 90 95  
Asn Leu Lys Arg Leu Val Val Ile Glu Pro Glu Ile Glu Val Ile Phe  
100 105 110  
Ile Val Leu Asn Leu Leu Asp Phe Ser Thr Glu Ile Leu Glu Asn Arg  
115 120 125  
Leu Ile Leu Leu His Ala Ser Phe Cys Asn Tyr Asn Met Ile Ala Ser  
130 135 140  
Leu Phe Asp Met Asp Lys Lys Ser Arg Leu Tyr Ala Arg Met Tyr Asp  
145 150 155 160  
Leu Lys Leu Phe Asn Ala Tyr Tyr Glu Arg Tyr Ser His Gln Met Ile  
165 170 175  
Glu Ile Asn Gln His Phe Thr Arg Ala Leu Glu His Gly Ala Ile Ser  
180 185 190  
Val Gly Asn Asp Ala Lys Ala His Ser  
195 200

569

Figure 478A-page 569

- AA

Figure 479A-page 570

(A) LENGTH: 129 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

HPP 479

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION:

[illegible]





(2) INFORMATION FOR SEQ ID NO:4740887\_f3\_10: AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

572

Figure 481A - page 572

(ii) MOLECULE TYPE: protein

HPP 481

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Lys | Ile | Gln | Thr | Ile | Ser | Thr | Leu | Val | Leu | Thr | Ile | Ile | Met | Val |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |  |
| Ile | Gln | Lys | Met | Ile | Val | Gly | Lys | Ile | Ser | Pro | His | Lys | Thr | Ala | Glu |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Glu | Phe | Thr | Asn | Leu | Met | Leu | Asn | Met | Ile | Ala | Val | Leu | Asp | Ser | Gln |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Ser | Trp | Gly | Asp | Ala | Ile | Leu | Asn | Ala | Pro | Phe | Glu | Phe | Thr | Asn | Ser |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Pro | Thr | Asp | Cys | Asp | Asn | Asp | Pro | Ser | Lys | Cys | Val | Asn | Pro | Gly | Thr |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |
| Asn | Gly | Leu | Val | Asn | Ser | Lys | Val | Asp | Gln | Lys | Tyr | Val | Leu | Asn | Lys |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Gln | Asp | Ile | Val | Asn | Lys | Phe | Lys | Asn | Lys | Ala | Asp | Leu | Asp | Val | Ile |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Val | Leu | Lys | Asp | Ser | Gly | Val | Val | Gly | Unk | Unk | Asn | Gly | Tyr | Gly | Asn |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Asp | Gly | Glu | Tyr | Gly | Thr | Leu | Gly | Val | Unk | Ala | Tyr | Ala | Leu | Gly | Ser |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 308 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

573

Figure 482A-page 573

(ii) MOLECULE TYPE: protein

HPP482

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Val | Val | Ile | Arg | Leu | Val | Leu | Asn | Met | Leu | Thr | Cys | Gln | Ile | Ser | Tyr |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Ile | Arg | Ile | Ser | Tyr | Leu | Val | Ser | Val | Ser | Asp | Phe | Val | Ile | Cys | Lys |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Glu | Arg | Phe | Met | Asp | Glu | Ile | Lys | Thr | Leu | Leu | Val | Asp | Phe | Phe | Pro |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Gln | Ala | Lys | His | Phe | Gly | Ile | Ile | Leu | Ile | Lys | Ala | Ile | Val | Val | Phe |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Cys | Ile | Gly | Phe | Tyr | Phe | Ser | Phe | Phe | Leu | Arg | Asn | Lys | Thr | Met | Lys |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |
| Leu | Leu | Ser | Lys | Lys | Asp | Glu | Ile | Leu | Ala | Asn | Phe | Val | Ala | Gln | Val |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Thr | Phe | Ile | Leu | Ile | Leu | Ile | Ile | Thr | Thr | Ile | Ile | Ala | Leu | Ser | Thr |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Leu | Gly | Val | Gln | Thr | Thr | Ser | Ile | Ile | Thr | Val | Leu | Gly | Thr | Val | Gly |  |
|     |     |     | 115 |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Ile | Ala | Val | Ala | Leu | Ala | Leu | Lys | Asp | Tyr | Leu | Ser | Ser | Ile | Ala | Gly |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Gly | Ile | Ile | Leu | Ile | Ile | Leu | His | Pro | Phe | Lys | Lys | Gly | Asp | Ile | Ile |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |
| Glu | Ile | Ser | Gly | Leu | Glu | Gly | Lys | Val | Glu | Ala | Leu | Asn | Phe | Phe | Asn |  |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |  |
| Thr | Ser | Leu | Arg | Leu | His | Asp | Gly | Arg | Leu | Ala | Val | Leu | Pro | Asn | Arg |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |
| Ser | Val | Ala | Asn | Ser | Asn | Ile | Ile | Asn | Ser | Asn | Asn | Thr | Ala | Cys | Arg |  |
|     |     |     | 195 |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |
| Arg | Ile | Glu | Trp | Val | Cys | Gly | Val | Gly | Tyr | Gly | Ser | Asp | Ile | Glu | Leu |  |
|     |     |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |
| Val | His | Lys | Thr | Ile | Lys | Asp | Val | Ile | Asp | Gly | Met | Glu | Lys | Ile | Asp |  |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |  |

Lys Asn Met Pro Thr Phe Ile Gly Ile Thr Asp Phe Gly Gln Ser Ser  
245 250 255

574

Leu Asn Phe Thr Ile Arg Val Trp Ala Lys Ile Glu Asp Gly Ile Phe  
260 265 270

Figure 482A-page 574

Asn Val Arg Ser Glu Leu Ile Glu Arg Ile Lys Asn Ala Leu Asp Ala  
275 280 285

Asn Arg Ile Glu Ile Pro Phe Asn Lys Leu Asp Ile Ser Ile Asn Lys  
290 295 300

Gln Asp Ser Ser Lys  
305

575

Figure 483A-page 575

HPD 483

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(A) ORGANISM: *Helicobacter pylori*

[illegible]

(2) INFORMATION FOR SEQ ID NO:4787562\_c3\_5:- AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

576  
Figure 484 A - page 576

(ii) MOLECULE TYPE: protein

HPP 484

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Cys | Leu | Ala | Ile | Pro | Ser | Lys | Val | Ile | Ala | Ile | Asn | Asp | Asn | Val |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Leu | Leu | Glu | Thr | Leu | Gly | Val | Gln | Arg | Glu | Ala | Ser | Leu | Asp | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Glu | Ser | Val | Lys | Val | Gly | Asp | Tyr | Val | Leu | Leu | His | Ile | Gly |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |

|     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|
| Tyr | Val | Met | Ser | Lys | Asp |
|     | 50  |     |     |     |     |

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 201 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

Figure 485A- page 577

(ii) MOLECULE TYPE: protein

HPP 485

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

## (xi) SEQUENCE DESCRIPTION:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Tyr | Leu | Trp | Leu | Phe | Leu | Ile | Tyr | Ala | Ile | Gly | Leu | Phe | Ala | 1   | 5   | 10  | 15  |
| Thr | Asp | Lys | Thr | Leu | Asp | Ile | Ile | Lys | Thr | Ile | Gln | Lys | Leu | Pro | Lys | 20  | 25  | 30  |     |
| Ile | Glu | Val | Arg | Tyr | Ser | Ile | Asp | Asn | Asp | Ala | Asn | Tyr | Ala | Leu | Lys | 35  | 40  | 45  |     |
| Leu | His | Glu | Val | Leu | Ala | Asn | Asp | Leu | Lys | Thr | Ser | Gln | His | Phe | Asp | 50  | 55  | 60  |     |
| Val | Ser | Gln | Asn | Lys | Glu | Gln | Gly | Ala | Ile | Asn | Tyr | Ala | Glu | Leu | Lys | 65  | 70  | 75  | 80  |
| Asp | Lys | Lys | Val | His | Leu | Val | Ala | Leu | Val | Ser | Val | Ala | Val | Glu | Asn | 85  | 90  | 95  |     |
| Gly | Asn | Lys | Ile | Ser | Arg | Leu | Lys | Leu | Tyr | Asp | Val | Asp | Thr | Gly | Thr | 100 | 105 | 110 |     |
| Leu | Lys | Lys | Thr | Phe | Asp | Tyr | Pro | Ile | Val | Ser | Leu | Asp | Leu | Tyr | Pro | 115 | 120 | 125 |     |
| Phe | Ala | Ala | His | Asn | Met | Ala | Ile | Val | Val | Asn | Asp | Tyr | Leu | Lys | Ala | 130 | 135 | 140 |     |
| Pro | Ser | Ile | Ala | Trp | Met | Lys | Arg | Leu | Ile | Val | Phe | Ser | Lys | Tyr | Ile | 145 | 150 | 155 | 160 |
| Gly | Pro | Gly | Ile | Thr | Asn | Ile | Ala | Leu | Ala | Asn | Tyr | Thr | Met | Arg | Tyr | 165 | 170 | 175 |     |
| Gln | Lys | Glu | Ile | Ile | Lys | Asn | Asn | Arg | Leu | Asn | Ile | Phe | Pro | Lys | Trp | 180 | 185 | 190 |     |
| Ala | Asn | Ala | Glu | Gln | Thr | Glu | Phe | Tyr | Tyr | 195 | 200 |     |     |     |     |     |     |     |     |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 486

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: encodes the serologically diverse protein M in St

Met Leu Ser Ser Asn Asp Leu Phe Met Val Val Leu Gly Ala Ile Leu  
1 5 10 15  
Leu Val Leu Val Cys Leu Val Gly Tyr Leu Tyr Leu Lys Glu Lys Glu  
20 25 30  
Phe Tyr His Lys Met Arg Arg Leu Glu Lys Thr Leu Asp Glu Ser Tyr  
35 40 45  
Gln Glu Asn Tyr Leu Tyr Ser Lys Arg Leu Arg Glu Leu Glu Gly Arg  
50 55 60  
Leu Glu Gly Leu Ser Leu Glu Lys Ser Ala Lys Glu Asp Ser Ser Leu  
65 70 75 80  
Lys Thr Thr Leu Ser His Leu Tyr Asn Gln Leu Gln Glu Ile Gln Lys  
85 90 95  
Ser Met Asp Lys Glu Arg Asp Tyr Leu Glu Glu Lys Ile Ile Unk Unk  
100 105 110  
Lys Gln Unk Unk Arg His Gly Ala Leu Cys Arg  
115 120

578

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(2) INFORMATION FOR SEQ ID NO:4826401\_f2\_2: -AA

579

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP487

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: cation efflux system membrane protein czcA

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Val | Val | Ser | Gly | Val | Val | Ile | Ile | Ile | Val | Phe | Phe | Val | Pro | Ile | Leu |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Thr | Leu | Gln | Gly | Leu | Glu | Gly | Lys | Met | Phe | Arg | Pro | Leu | Ala | Gln | Ser |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Ile | Val | Tyr | Ala | Leu | Leu | Gly | Thr | Leu | Val | Leu | Ser | Ile | Thr | Ile | Ile |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Pro | Val | Val | Ser | Ser | Leu | Val | Leu | Lys | Ala | Thr | Pro | His | Ser | Glu | Thr |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Phe | Leu | Thr | Arg | Phe | Leu | Asn | Arg | Ile | Tyr | Ala | Pro | Leu | Leu | Glu | Phe |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |
| Phe | Val | His | Asn | Pro | Lys | Lys | Val | Ile | Leu | Gly | Ala | Phe | Val | Phe | Leu |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Ile | Ala | Ser | Leu | Ser | Leu | Phe | Pro | Phe | Val | Gly | Lys | Asn | Phe | Met | Pro |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Ala | Leu | Asp | Glu | Gly | Asp | Val | Val | Leu | Ser | Val | Glu | Thr | Thr | Pro | Ser |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Ile | Ser | Leu | Asp | Gln | Ser | Lys | Asp | Leu | Met | Leu | Asn | Ile | Glu | Ser | Ala |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Ile | Lys | Lys | His | Val | Lys | Glu | Val | Lys | Ser | Ile | Val | Ala | Arg | Thr | Gly |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |
| Ser | Asp | Glu | Leu | Gly | Leu | Asp | Leu | Gly | Gly | Leu | Asn | Gln | Thr | Asp | Thr |  |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |  |
| Phe | Ile | Ser | Phe | Ile | Pro | Lys | Lys | Glu | Trp |     |     |     |     |     |     |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     |     |     |     |  |

580

Figure 488A - page 580

HPP 488

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION:

Gly Ala Lys Ala Lys Cys Asp His  
65 70

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP489

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met Leu Gly Lys Thr Glu Ser Lys Asp Asn Leu Asn Trp Met Ile Ala  
1 5 10 15  
Leu Ile Ile Glu Lys Asp Lys Val Tyr Glu Gln Val Gly Ser Val Arg  
20 25 30  
Phe Val Val Val Val Ala Ser Ala Ile Met Val Leu Ala Leu Ile Ile  
35 40 45  
Ala Ile Thr Leu Leu Met Arg Ala Ile Val Ser Asn Arg Leu Glu Val  
50 55 60  
Val Ser Ser Thr Leu Ser His Phe Phe Lys Leu Leu Asn Asn Gln Pro  
65 70 75 80  
Ile Leu Ala Thr Unk Asn Trp Unk Lys Arg Asp Leu Met Thr Asn  
85 90 95

581

Figure 489A-page 581

(2) INFORMATION FOR SEQ ID NO:487750\_c1\_42: - AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP490

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Val Ala Leu Val Phe Asp Ser Leu Ile Glu Asn Lys Lys  
1                      5                      10

582

Figure 490A - page 582





(2) INFORMATION FOR SEQ ID NO:4882763\_f3\_4: -AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 236 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

585

Figure 443A - page 585

(ii) MOLECULE TYPE: protein

HPP493

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Glu | Phe | Tyr | Gln | Val | Tyr | Asp | Pro | Leu | Gly | His | Ile | Trp | Leu | Ser |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Ala | Leu | Val | Ala | Leu | Ser | Pro | Ile | Ala | Leu | Phe | Phe | Ile | Ser | Leu | Ile |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Val | Phe | Lys | Leu | Lys | Gly | Tyr | Ser | Ala | Gly | Phe | Leu | Ser | Leu | Ala | Leu |  |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |  |
| Ser | Ile | Leu | Ile | Ala | Leu | Phe | Val | Tyr | Lys | Met | Pro | Val | Gln | Met | Val |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Ser | Ala | Ser | Phe | Phe | Tyr | Gly | Phe | Leu | Tyr | Gly | Leu | Trp | Pro | Ile | Ala |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |
| Trp | Ile | Val | Ile | Ala | Ala | Ile | Phe | Leu | Tyr | Asn | Leu | Ser | Val | Lys | Ser |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Gly | Tyr | Phe | Glu | Ile | Leu | Lys | Glu | Ser | Ile | Leu | Ser | Leu | Thr | Pro | Asp |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| His | Arg | Ile | Leu | Val | Ile | Leu | Ile | Gly | Phe | Cys | Phe | Gly | Ser | Phe | Leu |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Gly | Arg | Unk | Trp | Phe | Trp | Arg | Pro | Gly | Ser | Unk | His | Ser | Gly | Asp | Phe |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Ser | Gly | Leu | Gly | Leu | Asn | Pro | Leu | Tyr | Ala | Ala | Gly | Leu | Cys | Leu | Ile |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |
| Ala | Asn | Thr | Ala | Pro | Unk | Ala | Phe | Gly | Ala | Val | Gly | Ile | Pro | Ile | Thr |  |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |  |
| Ala | Met | Ala | Ser | Val | Val | Gly | Ile | Pro | Glu | Leu | Glu | Ile | Ser | Gln | Met |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |
| Val | Gly | Arg | Val | Leu | Pro | Ile | Phe | Ser | Ile | Gly | Ile | Pro | Phe | Phe | Ile |  |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |
| Val | Phe | Leu | Met | Asp | Gly | Phe | Arg | Gly | Ile | Arg | Glu | Thr | Phe | Pro | Ala |  |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |
| Val | Ala | Val | Thr | Unk | Phe | Ser | Phe | Ala | Thr | Arg | Asn | Phe |     |     |     |  |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     |     |  |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP494

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Glu | Ile | Ile | Leu | Leu | Ile | Val | Ala | Ala | Val | Val | Leu | Phe | Tyr | Phe |  |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |  |
| Tyr | Asn | Thr | Leu | Lys | Glu | Tyr | Leu | Lys | Asn | Pro | Leu | Asn | Pro | Lys | Thr |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Lys | Thr | Glu | Glu | Tyr | Asp | Leu | Lys | Asn | Asp | Pro | Tyr | Leu | Leu | Val | Gln |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Ser | Ser | Pro | Leu | Asp | Lys | Phe | Lys | Gln | Thr | Gln | Ile | Gly | Ala | Tyr | Met |  |
|     |     |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Arg | Leu | Leu | Lys | Phe | Leu | Asp | Ile | Gln | Lys | Asn | Ala | Leu | Asp | Asn | Ala |  |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |  |
| Leu | Arg | Thr | Leu | Phe | Ile | His | Glu | Leu | Glu | Gln | Pro | Leu | Asn | Ser | Glu |  |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |  |
| Gln | Gln | Asn | Leu | Ala | Lys | Glu | Leu | Leu | Asn | Glu | Pro | Val | Asp | Lys | Lys |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Glu | Asn | Phe | Glu | Ser | Leu | Cys | Gln | Glu | Ile | Ala | Asp | His | Thr | His | Gly |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Glu | Tyr | Thr | Lys | Arg | Leu | Lys | Leu | Val | Glu | Phe | Leu | Met | Leu | Leu | Ala |  |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Tyr | Ala | Asp | Gly | Ile | Leu | Asp | Ser | Lys | Glu | Lys | Glu | Leu | Phe | Leu | Asp |  |
| 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     |     | 160 |  |
| Val | Gly | Ala | Phe | Leu | Gln | Ile | Asp | Asn | Gln | Asp | Phe | Asn | Glu | Leu | Tyr |  |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |  |
| Asp | Asn | Phe | Glu | His | Phe | Asn | Ser | Ile | Glu | Ile | Pro | Met | Ser | Leu | Glu |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |
| Glu | Ala | Lys | Asn | Leu | Phe | Glu | Ile | Gln | Thr | His | Thr | Thr | Met | Gln | Asp |  |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |
| Leu | Glu | Lys | Lys | Ala | Leu | Asp | Leu | Ser | Ala | Pro | Tyr | Tyr | His | Lys | Met |  |
|     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |
| Asn | Asp | Asn | Lys | Arg | Tyr | Ser | Glu | Gln | Asp | Phe | Ile | Ser | Leu | Lys | Lys |  |
| 225 |     |     |     |     | 230 |     |     |     | 235 |     |     |     |     |     | 240 |  |



Ile Ala Leu Ala Ser Gln Leu Leu Glu Asn Asp Leu Lys Asp Ser  
245 250 255

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(2) INFORMATION FOR SEQ ID NO:489057\_c3\_5: - 44

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 495

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: HYPOTHETICAL 23.3 KD PROTEIN-INTEGRAL MEMBRANE

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Val | Glu | His | Gly | Lys | Ile | Glu | Thr | Thr | Leu | Ser | Leu | Gly | Ala |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Ser | His | Leu | Glu | Val | Ile | Lys | Met | Met | Leu | Leu | Glu | Ser | Leu | Pro | Ser |
|     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |     |
| Leu | Val | Asn | Asn | Ile | Thr | Ile | Thr | Leu | Ile | Ser | Leu | Ile | Gly | Tyr | Ser |
|     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |     |
| Ala | Lys | Ala | Gly | Ala | Leu | Gly | Ala | Gly | Gly | Leu | Gly | Asp | Leu | Ala | Ile |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Arg | Ile | Gly | Tyr | Gln | Ser | Tyr | Arg | Gly | Asp | Val | Leu | Phe | Tyr | Ala | Val |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     |     | 80  |
| Val | Val | Ile | Ile | Val | Leu | Val | Gln | Ile | Ile | Gln | Ser | Ala | Gly | Asp | Tyr |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Val | Val | Lys | Arg | Leu | Arg | Lys | Asn | Lys | Tyr |     |     |     |     |     |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     |     |     |

588  
Figure 495A - page 588

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 526 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 496

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: stringent response-like protein

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asn | Glu | Ile | Asp | Lys | Ser | Val | Asp | Ile | Gly | Phe | Leu | Arg | Ile | Leu | 1   | 5   | 10  | 15  |
| Asp | Val | Ile | Lys | Lys | Val | Lys | Thr | Pro | Lys | Gly | Gly | Ile | Glu | Val | Leu | 20  | 25  | 30  |     |
| Arg | Thr | Leu | Ile | Asp | Phe | Thr | Pro | Lys | Ile | Glu | Asn | Ala | Leu | Asn | Leu | 35  | 40  | 45  |     |
| Ala | Thr | Lys | Ser | His | Lys | Gly | Gln | Tyr | Arg | Lys | Ser | Gly | Glu | Pro | Tyr | 50  | 55  | 60  |     |
| Ile | Val | His | Pro | Ile | Cys | Val | Ala | Ser | Val | Val | Ala | Phe | Cys | Gly | Gly | 65  | 70  | 75  | 80  |
| Asp | Glu | Ala | Met | Val | Cys | Ala | Ala | Leu | Leu | His | Asp | Val | Val | Glu | Asp | 85  | 90  | 95  |     |
| Thr | Pro | Cys | Glu | Ile | Glu | Thr | Ile | Glu | Arg | Glu | Phe | Gly | Gln | Asp | Val | 100 | 105 | 110 |     |
| Ala | Asn | Leu | Val | Asp | Ala | Leu | Thr | Lys | Ile | Thr | Glu | Ile | Arg | Lys | Glu | 115 | 120 | 125 |     |
| Glu | Leu | Gly | Val | Ser | Ser | Gln | Asp | Pro | Arg | Met | Val | Val | Ser | Ala | Leu | 130 | 135 | 140 |     |
| Thr | Phe | Arg | Lys | Ile | Leu | Ile | Ser | Ala | Ile | Gln | Asp | Pro | Arg | Ala | Leu | 145 | 150 | 155 | 160 |
| Val | Val | Lys | Ile | Ser | Asp | Arg | Leu | His | Asn | Met | Leu | Thr | Leu | Asp | Ala | 165 | 170 | 175 |     |
| Leu | Pro | His | Asp | Lys | Gln | Val | Arg | Ile | Ser | Lys | Glu | Thr | Leu | Ala | Val | 180 | 185 | 190 |     |
| Tyr | Ala | Pro | Ile | Ala | Ser | Arg | Leu | Gly | Met | Ser | Ser | Ile | Lys | Asn | Glu | 195 | 200 | 205 |     |
| Leu | Glu | Asp | Lys | Ser | Phe | Tyr | Tyr | Ile | Tyr | Pro | Glu | Glu | Tyr | Lys | Asn | 210 | 215 | 220 |     |
| Ile | Lys | Glu | Tyr | Leu | His | Lys | Asn | Lys | Gln | Ser | Leu | Leu | Leu | Lys | Leu | 225 | 230 | 235 | 240 |

|            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |  |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|--|
| Asn        | Ala        | Phe        | Ala        | Ser<br>245 | Lys        | Leu        | Glu        | Lys        | Lys<br>250 | Leu        | Phe        | Asp        | Ser        | Gly<br>255 | Phe        |  |
| Ser        | His        | Ser        | Asp<br>260 | Phe        | Lys        | Leu        | Val        | Thr<br>265 | Arg        | Val        | Lys        | Arg        | Pro<br>270 | Tyr        | Ser        |  |
| Ile        | Tyr        | Leu<br>275 | Lys        | Met        | Gln        | Arg        | Lys<br>280 | Gly        | Ala        | Val        | Asn        | Ile<br>285 | Asp        | Glu        | Ile        |  |
| Leu        | Asp<br>290 | Leu        | Leu        | Ala        | Ile        | Arg<br>295 | Ile        | Leu        | Leu        | Lys        | Asn<br>300 | Pro        | Ile        | Asp        | Cys        |  |
| Tyr<br>305 | Lys        | Val        | Leu        | Gly        | Ile<br>310 | Ile        | His        | Leu        | Asn        | Phe<br>315 | Lys        | Pro        | Ile        | Val        | Ser<br>320 |  |
| Arg        | Phe        | Lys        | Asp        | Tyr<br>325 | Ile        | Ala        | Leu        | Pro        | Lys<br>330 | Glu        | Asn        | Gly        | Tyr        | Lys<br>335 | Thr        |  |
| Ile        | His        | Thr        | Thr<br>340 | Ile        | Phe        | Asp        | Glu        | Ser<br>345 | Ser        | Val        | Tyr        | Glu        | Val<br>350 | Gln        | Ile        |  |
| Arg        | Thr        | Phe<br>355 | Asp        | Met        | His        | Met        | Gly<br>360 | Ala        | Glu        | Tyr        | Gly        | Asn<br>365 | Ser        | Ala        | His        |  |
| Trp        | Lys<br>370 | Tyr        | Lys        | Ala        | Gly        | Gly<br>375 | Val        | Asp        | His        | Glu        | Glu<br>380 | His        | His        | Glu        | Gly        |  |
| Met<br>385 | Arg        | Trp        | Leu        | Gln        | Asn<br>390 | Phe        | Lys        | Tyr        | His        | Asp<br>395 | Ser        | Asp        | Leu        | Lys        | Asn<br>400 |  |
| Asp        | Pro        | Lys        | Glu        | Phe<br>405 | Tyr        | Glu        | Leu        | Ala        | Lys<br>410 | Asn        | Asp        | Leu        | Tyr        | Arg<br>415 | Glu        |  |
| Asp        | Ile        | Val        | Val<br>420 | Phe        | Ser        | Pro        | His        | Gly<br>425 | Asp        | Thr        | Tyr        | Thr        | Leu<br>430 | Pro        | Val        |  |
| Gly        | Ala        | Ile<br>435 | Ala        | Leu        | Asp        | Phe        | Ala<br>440 | Tyr        | Met        | Val        | His        | Ser<br>445 | Asp        | Leu        | Gly        |  |
| Asp        | Lys<br>450 | Ala        | Thr        | Asp        | Ala        | Tyr<br>455 | Ile        | Asn        | Ser        | Lys        | Lys<br>460 | Ala        | Leu        | Leu        | Asn        |  |
| Gln<br>465 | Glu        | Leu        | Arg        | Ser        | Gly<br>470 | Asp        | Val        | Val        | Lys        | Ile<br>475 | Ile        | Lys        | Gly        | Asp        | Lys<br>480 |  |
| Val        | Ile        | Pro        | Arg        | Phe<br>485 | Ile        | Trp        | Met        | Asp        | Gln<br>490 | Leu        | Lys        | Thr        | Ser        | Lys<br>495 | Ala        |  |
| Lys        | Asn        | His<br>500 | Leu        | Arg        | Ile        | Gln        | Arg        | Arg<br>505 | Asn        | Arg        | Leu        | Lys        | Glu<br>510 | Ile        | Asp        |  |
| Thr        | Lys        | Ser<br>515 | Met        | Ile        | Asn        | Ile        | Leu<br>520 | Ala        | Thr        | Phe        | Phe        | Trp<br>525 | Ala        | Leu        |            |  |

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 123 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP497

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

## (xi) SEQUENCE DESCRIPTION:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Val | Val | Val | Glu | Asn | Ile | Lys | Asp | Ala | Val | Pro | Leu | Ala | Gln | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Ile | Unk | Gly | Gly | Ile | Pro | Ile | Ile | Glu | Val | Thr | Leu | Arg | Ser | Asn |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Cys | Ala | Leu | Glu | Ala | Ile | Glu | Leu | Ile | Ala | Lys | Asn | Val | Pro | Lys | Met |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Arg | Val | Gly | Ala | Gly | Thr | Ile | Leu | Asn | Leu | Thr | Gln | Leu | Glu | Gln | Ala |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gln | Asn | Arg | Gly | Ala | Glu | Phe | Leu | Ile | Ser | Pro | Gly | Leu | Thr | Ile | Lys |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Leu | Leu | Glu | His | Ala | Lys | Lys | Lys | Asp | Met | Pro | Leu | Ile | Pro | Gly | Val |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ser | Ser | Ser | Ser | Glu | Val | Met | Gln | Ala | Leu | Glu | Leu | Gly | Tyr | Asn | Ala |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Leu | Lys | Phe | Phe | Pro | Ala | Glu | Tyr | Cys | Gly | Gly | Arg |     |     |     |     |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:495312\_c2\_4: -AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 498

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: UDP-N-ACETYLMURAMOYLALANYL-D-GLUTAMATE--2 & 6-DIA

Val Glu Lys Ile Lys Pro Tyr Ala Pro Lys Asp Ser Pro Leu Ile Asp  
1 5 10 15  
Tyr Ser Ser Leu Val Arg Asn Val Gln Ser Thr Leu Lys Gly Thr Ser  
20 25 30  
Phe Glu Thr Leu Ile Asn Gly Val Trp Glu Ser Phe Glu Thr Lys Val  
35 40 45  
Leu Gly Glu Phe Asn Ala Tyr Asn Ile Ala Ser Ala Ile Leu Thr Ala  
50 55 60  
Lys His Leu Gly Leu Glu Thr Glu Arg Ile Lys Arg Leu Val Phe Glu  
65 70 75 80  
Leu Lys Pro Ile Asn His Arg Leu Gln Leu Leu Glu Ala Asn Gln Lys  
85 90 95  
Ile Ile Ile Asp Asp Asn Phe Asn Gly Asn Leu Lys Gly Met  
100 105 110

592

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## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP499

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: iron dicitrate transport protein

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Arg | Ile | Leu | Val | Ser | Leu | Ala | Val | Leu | Ser | His | Ser | Ala | His | 1   | 5   | 10  | 15  |
| Ala | Val | Lys | Thr | His | Asn | Leu | Glu | Arg | Val | Glu | Ala | Ser | Gly | Val | Ala | 20  | 25  | 30  |     |
| Asn | Asp | Lys | Glu | Ala | Pro | Leu | Ser | Trp | Arg | Ser | Lys | Glu | Val | Arg | Asn | 35  | 40  | 45  |     |
| Tyr | Met | Gly | Ser | Arg | Thr | Val | Ile | Ser | Asn | Lys | Gln | Leu | Thr | Lys | Ser | 50  | 55  | 60  |     |
| Ala | Asn | Gln | Ser | Ile | Glu | Glu | Ala | Leu | Gln | Asn | Val | Pro | Gly | Val | His | 65  | 70  | 75  | 80  |
| Ile | Arg | Asn | Ser | Thr | Gly | Ile | Gly | Ala | Val | Pro | Ser | Ile | Ser | Ile | Arg | 85  | 90  | 95  |     |
| Gly | Phe | Gly | Ala | Gly | Gly | Pro | Gly | His | Ser | Asn | Thr | Gly | Met | Ile | Leu | 100 | 105 | 110 |     |
| Val | Asn | Gly | Ile | Pro | Ile | Tyr | Val | Ala | Pro | Tyr | Val | Glu | Ile | Gly | Thr | 115 | 120 | 125 |     |
| Val | Ile | Phe | Pro | Val | Thr | Phe | Gln | Ser | Val | Asp | Arg | Ile | Ser | Val | Thr | 130 | 135 | 140 |     |
| Lys | Gly | Gly | Glu | Ser | Val | Arg | Tyr | Gly | Pro | Asn | Ala | Phe | Gly | Gly | Val | 145 | 150 | 155 | 160 |
| Ile | Asn | Ile | Ile | Thr | Lys | Gly | Ile | Pro | Thr | Asn | Trp | Glu | Ser | Gln | Val | 165 | 170 | 175 |     |
| Ser | Glu | Arg | Thr | Thr | Phe | Trp | Gly | Lys | Ser | Glu | Asn | Gly | Gly | Phe | Phe | 180 | 185 | 190 |     |
| Asn | Gln | Asn | Ser | Lys | Asn | Ile | Asp | Lys | Ser | Leu | Val | Asn | Asn | Met | Leu | 195 | 200 | 205 |     |
| Phe | Asn | Thr | Tyr | Leu | Arg | Thr | Gly | Gly | Met | Met | Asn | Lys | His | Phe | Gly | 210 | 215 | 220 |     |
| Ile | Gln | Ala | Gln | Val | Asn | Trp | Leu | Lys | Gly | Gln | Gly | Phe | Arg | Tyr | Asn | 225 | 230 | 235 | 240 |

[illegible]



## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 188 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 500

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

## (xi) SEQUENCE DESCRIPTION:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Ser | Val | Tyr | Glu | Lys | Gly | Asn | Ala | Leu | Asp | Lys | Arg | Val | Leu | 1   | 5   | 10  | 15  |
| Glu | Glu | Trp | Leu | Leu | Ser | Glu | Asp | Ile | Leu | Met | Glu | Asn | Ala | Ala | Met | 20  | 25  | 30  |     |
| Ala | Leu | Glu | Arg | Ala | Val | Leu | Gln | Asn | Ala | Ser | Leu | Gly | Ala | Lys | Val | 35  | 40  | 45  |     |
| Ile | Ile | Leu | Cys | Gly | Ser | Gly | Asp | Asn | Gly | Gly | Asp | Gly | Tyr | Thr | Leu | 50  | 55  | 60  |     |
| Ala | Arg | Arg | Leu | Val | Gly | Arg | Phe | Lys | Thr | Leu | Val | Phe | Glu | Met | Lys | 65  | 70  | 75  | 80  |
| Leu | Ala | Lys | Ser | Pro | Met | Cys | Gln | Leu | Gln | Lys | Glu | Arg | Ala | Lys | Lys | 85  | 90  | 95  |     |
| Val | Gly | Val | Val | Ile | Lys | Ala | Trp | Glu | Glu | Lys | Asn | Glu | Asp | Leu | Glu | 100 | 105 | 110 |     |
| Cys | Asp | Val | Leu | Val | Asp | Cys | Val | Val | Gly | Ser | Ala | Phe | Lys | Gly | Gly | 115 | 120 | 125 |     |
| Leu | Glu | Pro | Phe | Leu | Asp | Phe | Glu | Ser | Leu | Ser | Gln | Lys | Ala | Arg | Phe | 130 | 135 | 140 |     |
| Lys | Ile | Ala | Cys | Asp | Ile | Pro | Ser | Gly | Ile | Asp | Ser | Lys | Gly | Arg | Val | 145 | 150 | 155 | 160 |
| Asp | Lys | Arg | Ala | Phe | Unk | Unk | Gly | Tyr | Arg | Leu | Ser | Ala | Trp | Ala | Leu | 165 | 170 | 175 |     |
| Phe | Lys | Ser | Cys | Leu | Leu | Ser | Unk | Unk | Unk | Lys | Unk | Tyr |     |     |     | 180 | 185 |     |     |

(2) INFORMATION FOR SEQ ID NO:50253\_c1\_13: - AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 596 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

596  
Figure 501A- page 596

(ii) MOLECULE TYPE: protein

HPP501

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: heat shock protein C62.5 - chaperone-ATPase activ

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Ser | Asn | Gln | Glu | Tyr | Thr | Phe | Gln | Thr | Glu | Ile | Asn | Gln | Leu | Leu |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Asp | Leu | Met | Ile | His | Ser | Leu | Tyr | Ser | Asn | Lys | Glu | Ile | Phe | Leu | Arg |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Glu | Leu | Ile | Ser | Asn | Ala | Ser | Asp | Ala | Leu | Asp | Lys | Leu | Asn | Tyr | Leu |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Met | Leu | Thr | Asp | Glu | Lys | Leu | Lys | Gly | Leu | Asn | Thr | Thr | Pro | Ser | Ile |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| His | Leu | Ser | Phe | Asp | Ser | Gln | Lys | Lys | Thr | Leu | Thr | Ile | Lys | Asp | Asn |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |
| Gly | Ile | Gly | Met | Asp | Lys | Ser | Asp | Leu | Ile | Glu | His | Leu | Gly | Thr | Ile |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Ala | Lys | Ser | Gly | Thr | Lys | Ser | Phe | Leu | Ser | Ala | Leu | Ser | Gly | Asp | Lys |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Lys | Lys | Asp | Ser | Ala | Leu | Ile | Gly | Gln | Phe | Gly | Val | Gly | Phe | Tyr | Ser |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Ala | Phe | Met | Val | Ala | Ser | Lys | Ile | Val | Val | Gln | Thr | Lys | Lys | Val | Thr |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Ser | His | Gln | Ala | Tyr | Ala | Trp | Val | Ser | Asp | Gly | Lys | Gly | Lys | Phe | Glu |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |
| Ile | Ser | Glu | Cys | Val | Lys | Glu | Glu | Gln | Gly | Thr | Glu | Ile | Thr | Leu | Phe |  |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |  |
| Leu | Lys | Glu | Glu | Asp | Ser | His | Phe | Ala | Ser | Arg | Trp | Glu | Ile | Asp | Ser |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |
| Val | Val | Lys | Lys | Tyr | Ser | Glu | His | Ile | Pro | Phe | Pro | Ile | Phe | Leu | Thr |  |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |
| Tyr | Thr | Asp | Thr | Lys | Phe | Glu | Gly | Glu | Gly | Asp | Asn | Lys | Lys | Glu | Val |  |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |
| Lys | Glu | Glu | Lys | Cys | Asp | Gln | Ile | Asn | Gln | Ala | Ser | Ala | Leu | Trp | Lys |  |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |  |

|            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Met        | Asn        | Lys        | Ser        | Glu<br>245 | Leu        | Lys        | Glu        | Lys        | Asp<br>250 | Tyr        | Lys        | Asp        | Phe        | Tyr<br>255 | Gln        |
| Ser        | Phe        | Ala        | His<br>260 | Asp        | Asn        | Ser        | Glu        | Pro<br>265 | Leu        | Ser        | Tyr        | Ile        | His<br>270 | Asn        | Lys        |
| Val        | Glu        | Gly<br>275 | Ser        | Leu        | Glu        | Tyr        | Thr<br>280 | Thr        | Leu        | Phe        | Tyr        | Ile<br>285 | Pro        | Ser        | Lys        |
| Ala        | Pro<br>290 | Phe        | Asp        | Leu        | Phe        | Arg<br>295 | Val        | Asp        | Tyr        | Lys        | Ser<br>300 | Gly        | Val        | Lys        | Leu        |
| Tyr<br>305 | Val        | Lys        | Arg        | Val        | Phe<br>310 | Ile        | Thr        | Asp        | Asp<br>315 | Lys        | Glu        | Leu        | Leu        | Pro<br>320 |            |
| Ser        | Tyr        | Leu        | Arg        | Phe<br>325 | Val        | Lys        | Gly        | Val        | Ile<br>330 | Asp        | Ser        | Glu        | Asp        | Leu<br>335 | Pro        |
| Leu        | Asn        | Val        | Ser<br>340 | Arg        | Glu        | Ile        | Leu        | Gln<br>345 | Gln        | Asn        | Lys        | Ile        | Leu<br>350 | Ala        | Asn        |
| Ile        | Arg        | Ser<br>355 | Ala        | Ser        | Val        | Lys        | Lys<br>360 | Ile        | Leu        | Ser        | Glu        | Ile<br>365 | Glu        | Arg        | Leu        |
| Ser        | Lys<br>370 | Asp        | Asn        | Lys        | Asn        | Tyr<br>375 | His        | Lys        | Phe        | Tyr        | Glu<br>380 | Pro        | Phe        | Gly        | Lys        |
| Val<br>385 | Leu        | Lys        | Glu        | Gly        | Leu<br>390 | Tyr        | Gly        | Asp        | Phe        | Glu<br>395 | Asn        | Lys        | Glu        | Lys        | Leu<br>400 |
| Leu        | Glu        | Leu        | Leu        | Arg<br>405 | Phe        | Tyr        | Ser        | Lys        | Asp<br>410 | Lys        | Gly        | Glu        | Trp        | Ile<br>415 | Ser        |
| Leu        | Lys        | Glu        | Tyr<br>420 | Lys        | Glu        | Asn        | Leu        | Lys<br>425 | Glu        | Asn        | Gln        | Lys        | Ser<br>430 | Ile        | Tyr        |
| Tyr        | Leu        | Leu<br>435 | Gly        | Glu        | Asn        | Leu        | Asp<br>440 | Leu        | Leu        | Lys        | Ala        | Ser<br>445 | Pro        | Leu        | Leu        |
| Glu        | Lys<br>450 | Tyr        | Ala        | Gln        | Lys        | Gly<br>455 | Tyr        | Asp        | Val        | Leu        | Leu<br>460 | Leu        | Ser        | Asp        | Glu        |
| Ile<br>465 | Asp        | Ala        | Phe        | Val        | Met<br>470 | Pro        | Gly        | Val        | Asn        | Glu<br>475 | Tyr        | Asp        | Lys        | Thr        | Pro<br>480 |
| Phe        | Arg        | Asp        | Ala        | Ser<br>485 | His        | Ser        | Glu        | Ser        | Leu<br>490 | Lys        | Glu        | Leu        | Gly        | Leu<br>495 | Ala        |
| Glu        | Ile        | His<br>500 | Asp        | Glu        | Val        | Lys        | Asp        | Gln<br>505 | Phe        | Lys        | Asp        | Leu        | Ile<br>510 | Lys        | Ala        |
| Phe        | Glu        | Glu<br>515 | Asn        | Leu        | Lys        | Asp        | Glu        | Ile<br>520 | Lys        | Gly        | Val        | Glu<br>525 | Leu        | Ser        | Gly        |
| His<br>530 | Leu        | Thr        | Ser        | Ala        | Val        | Ala<br>535 | Leu        | Ile        | Gly        | Asp        | Glu<br>540 | Pro        | Asn        | Ala        | Met        |
| Met<br>545 | Ala        | Asn        | Trp        | Met        | Arg<br>550 | Gln        | Met        | Gly        | Gln        | Ser<br>555 | Val        | Pro        | Glu        | Ser        | Lys<br>560 |

Lys Thr Leu Glu Leu Asn Pro Asn His Ala Ile Leu Gln Lys Leu Leu  
565 570 575

Lys Cys Glu Asp Lys Glu Gln Leu Ser Ala Phe Ile Trp Leu Leu Tyr  
580 585 590

Asp Gly Arg Ser Phe  
595

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 155 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 502

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

## (xi) SEQUENCE DESCRIPTION:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Asn | Leu | Gly | Ala | Tyr | Tyr | Thr | Pro | Pro | Tyr | Leu | Val | Asp | Cys | Ala |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Tyr | Lys | Leu | Leu | Lys | Lys | His | Val | Gly | Ile | Glu | Asn | Tyr | Thr | Leu | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asp | Thr | Ala | Cys | Gly | Asn | Lys | Glu | Phe | Leu | Lys | Leu | His | His | Pro | Lys |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Lys | Ile | Gly | Ala | Asp | Ile | Asp | Pro | Lys | Cys | Asp | Ala | Leu | Ile | Ile | Asn |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ala | Leu | Ala | Asn | Pro | Lys | Arg | Glu | Asn | Tyr | Gly | Ile | Ser | Gln | Asp | Glu |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     |     | 80  |
| Pro | Leu | Ile | Ile | Val | Gly | Asn | Pro | Pro | Tyr | Asn | Asp | Arg | Thr | Ser | Phe |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ile | Lys | Gln | Asp | Ile | Lys | Asn | Lys | Asp | Phe | Ile | Phe | Glu | Ile | Asp | Asn |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Asp | Leu | Lys | Ser | Arg | Asp | Leu | Gly | Ile | Ser | Phe | Leu | Lys | Ser | Phe | Ala |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ile | Leu | Lys | Pro | Ala | Phe | Ile | Cys | Val | Leu | His | Pro | Leu | Ser | Tyr | Leu |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Ile | Lys | Glu | Ala | Asn | Phe | Lys | Gln | Phe | Lys | Ala | Ile |     |     |     |     |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     |     |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: protein

HPP 503

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: PHOSPHOLIPASE A1

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Lys | Ser | Ile | Leu | Leu | Phe | Ile | Ile | Phe | Val | Val | Cys | Gln | Leu | Glu |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Gly | Lys | Lys | Phe | Ser | Gln | Asp | Asn | Phe | Lys | Val | Asp | Tyr | Asn | Tyr | Tyr |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Leu | Arg | Lys | Gln | Asp | Leu | His | Ile | Ile | Lys | Thr | Gln | Asn | Asp | Leu | Ser |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Asn | Ala | Trp | Tyr | Leu | Pro | Pro | Gln | Lys | Ala | Pro | Lys | Glu | His | Ser | Trp |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Val | Asp | Phe | Ala | Lys | Lys | Tyr | Leu | Asn | Met | Met | Asp | Tyr | Leu | Gly | Thr |  |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |  |
| Tyr | Phe | Leu | Pro | Phe | Tyr | His | Ser | Phe | Thr | Pro | Ile | Phe | Gln | Trp | Tyr |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| His | Pro | Asn | Ile | Asn | Pro | Tyr | Lys | Arg | Asn | Glu | Phe | Lys | Phe | Gln | Ile |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |  |
| Ser | Phe | Arg | Val | Pro | Val | Phe | Arg | His | Ile | Leu | Trp | Thr | Lys | Gly | Thr |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Leu | Tyr | Leu | Asp | Tyr | Thr | Gln | Thr | Asn | Trp | Phe | Gln | Ile | Tyr | Asn | Asp |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Pro | Gln | Ser | Ala | Pro | Met | Arg | Met | Ile | Lys | Phe | His | Ala |     |     |     |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     |     |  |

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 190 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 504

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

## (xi) SEQUENCE DESCRIPTION:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Leu | Met | Gly | Val | Ser | Gln | Gly | Leu | Pro | Asn | Thr | Thr | Ser | Lys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Phe | Gly | Ile | Glu | Phe | Asp | Ser | Leu | Ala | Asp | Val | Val | Ala | Phe | Gly | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Pro | Ser | Leu | Ile | Thr | Tyr | Phe | Tyr | Val | Gly | Tyr | Asn | Phe | Gly | Arg |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ile | Gly | Met | Ala | Val | Ser | Ala | Leu | Phe | Val | Ile | Phe | Gly | Ala | Ile | Arg |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Leu | Ala | Arg | Phe | Asn | Ile | Ser | Thr | Asn | Thr | Ser | Asp | Pro | Tyr | Ser | Phe |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Ile | Gly | Ile | Pro | Ile | Pro | Ala | Ala | Ala | Val | Leu | Val | Val | Leu | Cys | Val |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Leu | Leu | Asp | Asn | Lys | Tyr | His | Phe | Leu | Glu | Gly | Asn | Thr | Glu | Lys | Leu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Phe | Leu | Gly | Phe | Ile | Val | Leu | Leu | Gly | Val | Leu | Met | Val | Ser | Asn | Ile |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Arg | Tyr | Pro | Asn | Phe | Lys | Lys | Val | Lys | Trp | Asn | Leu | Lys | Leu | Phe | Ile |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Leu | Val | Leu | Ile | Phe | Leu | Ser | Leu | Val | Phe | Val | Arg | Pro | Leu | Glu | Ala |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Leu | Ser | Val | Phe | Met | Gly | Leu | Tyr | Leu | Ile | Tyr | Gly | Ile | Ile | Arg | Trp |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ile | Phe | Leu | Met | Val | Lys | Ile | Thr | Phe | Asn | Lys | Asn | Lys | Ser | Ala |     |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP505

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ile | Gly | Val | Tyr | Pro | Asn | Tyr | Ser | Lys | Lys | Gln | Leu | Lys | Arg | Pro |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Val | Ile | Phe | Val | Ser | Arg | Glu | Leu | Ala | Leu | Ala | Asn | Gly | Ile | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Thr | Asp | Ala | Tyr | Asp | Ile | Glu | Ala | Asn | Leu | Tyr | Met | Asn | Ala | Arg | Ile |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Val | Met | Unk | Asn | Asn | Lys | Arg | Lys | His | Tyr | Glu | Gln | Arg | Val | Asn | Leu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| His | Phe | Unk | Arg | Ser | Leu | Gly | Unk | Val | Phe | Asp | His | Arg | Ser | Asn | His |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |
| Val | Leu | Cys | Asp | Glu | Lys | Asp | Leu | Leu | Arg |     |     |     |     |     |     |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     |     |



(2) INFORMATION FOR SEQ ID NO:5138\_f2\_6:-4A

603

Figure 5D6A - page 603

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 506

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Val | Lys | Ile | Thr | Ile | Met | Ile | Lys | Asp | Phe | Asn | His | Tyr | Cys | Arg | Lys |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Ile | Thr | Arg | Gly | Phe | Val | Lys | Ile | Pro | Thr | Lys | Lys | Gln | Gly | Ala | Lys |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Lys | Met | Lys | Lys | Ala | Gly | Phe | Leu | Phe | Leu | Ala | Ala | Met | Ala | Ile | Ile |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Val | Val | Ser | Leu | Asn | Ala | Lys | Asp | Pro | Asn | Val | Leu | Arg | Lys | Ile | Val |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Phe | Glu | Lys | Cys | Leu | Pro | Asn | Tyr | Glu | Lys | Asn | Gln | Asn | Pro | Ser | Pro |  |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |  |
| Cys | Ile | Glu | Val | Lys | Pro | Asp | Ala | Gly | Tyr | Val | Val | Leu | Lys | Asp | Ile |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Asn | Gly | Pro | Leu | Gln | Tyr | Leu | Leu | Met | Pro | Thr | Thr | His | Ile | Ser | Gly |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Ile | Glu | Asn | Pro | Leu | Leu | Leu | Asp | Pro | Ser | Thr | Pro | Asn | Phe | Phe | Tyr |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Leu | Ser | Trp | Gln | Ala | Arg | Asp | Phe | Met | Ser | Unk | Lys | Tyr | Gly | Lys | Pro |  |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Ile | Pro | Asp | Tyr | Ala | Ile | Ser | Leu | Thr | Ile | Asn | Ser | Lys | Lys | Gly | Arg |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |
| Ser | Gln | Asn | His | Phe | His | Ile | His | Ile | Ser | Cys | Ile | Ser | Leu | Asp | Val |  |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |  |
| Arg | Lys | Gln | Leu | Asp | Asn | Asn | Leu | Lys | Asn | Ile | Asn | Ser | Arg | Trp | Ser |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |
| Pro | Leu | Ser | Gly | Gly | Leu | Asn | Gly | His | Lys | Tyr | Leu | Ala | Arg | Arg | Val |  |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |
| Thr | Glu | Ser | Glu | Leu | Ala | Gln | Lys | Ser | Pro | Phe | Val | Met | Leu | Ala | Lys |  |
|     |     |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |
| Glu | Val | Pro | Asn | Ala | His | Lys | Arg | Met | Gly | Asp | Tyr | Gly | Leu | Ala | Val |  |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |  |



(2) INFORMATION FOR SEQ ID NO:5194840\_f3\_4: - AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: hypothetical 38.1 kd protein in bcr 5' region

Met Ala Ala Ser Asn Phe His Phe Ser Ala Leu Unk Unk Leu Gly Phe  
1 5 10 15

Gly Met Pro Ile Gly Ser Ala Ser Leu Gly Glu Leu Val Asn Gln Gly  
20 25 30

Lys Asp Asn Leu Thr Thr Pro His Leu Ala Val Val Ala Phe Val Ala  
35 40 45

Ile Ser Leu Leu Leu Ser Val Leu Val Phe Ile Gly Glu Gly Val Arg  
50 55 60

Asp Ala Phe Asn Ala Asn Met Leu Lys  
65 70

605

Figure 507A - page 605

HPP 507

(2) INFORMATION FOR SEQ ID NO:5265957\_c2\_5: -AA

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: surface antigen

Val Leu Thr Ser Gly Asp Met Ile Thr Cys Pro Tyr Cys Gly Arg Ile  
1 5 10 15

Leu Tyr Ala Glu Ser Thr His Glu Ser Asn Ala Gln Pro Pro Lys Glu  
20 25 30

Ser Gln Pro Lys Glu Ser Gln Glu Glu Ser Gln Glu Glu Ser Gln Glu  
35 40 45

Glu Ser Gln Glu Ala Val Arg Leu Ile Val  
50 55

606  
Figure 5D8A - page 606

HPP 508

(2) INFORMATION FOR SEQ ID NO:5267037\_c2\_20: - AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: ROD SHAPE-DETERMINING PROTEIN

Met Ala Leu Asp Lys Arg Ile Trp Met Gln Phe Asp Leu Leu Pro Phe  
1 5 10 15  
Val Phe Ile Ile Pro Leu Leu Val Val Ser Phe Leu Leu Ile Phe Glu  
20 25 30  
Ser Ser Ala Val Leu Ser Leu Lys Gln Gly Val Tyr Tyr Ala Ile Gly  
35 40 45  
Phe Leu Leu Phe Trp Val Val Phe Phe Ile Pro Phe Arg Lys Leu Asp  
50 55 60  
Arg Trp Leu Phe Ala Leu Tyr Trp Ala Cys Val Ile Leu Leu Ala Leu  
65 70 75 80  
Val Asp Phe Met Gly Ser Ser Lys Leu Gly  
85 90

607  
Figure 509A - page 607

HPP 509

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 278 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met Lys Leu Asn Asp Pro Phe Thr Ser Pro Asn Lys Ala Lys Lys Glu  
1 5 10 15  
Leu Ser Pro Lys Gly Phe Arg Gly Gly Leu Glu Ser Glu Ile Leu Leu  
20 25 30  
Gly Phe Val Leu Gln Lys Glu Arg Val Phe Leu His Thr His Glu His  
35 40 45  
Leu Glu Leu Ser His Glu Glu Glu Thr Arg Phe Phe Glu Leu Val Gly  
50 55 60  
Lys Arg Leu Asn Asp Cys Pro Ile Glu Tyr Leu Leu Gly Ser Cys Asp  
65 70 75 80  
Phe Tyr Gly Arg Ser Phe Phe Val Asn Glu His Val Leu Ile Pro Arg  
85 90 95  
Pro Glu Thr Glu Ile Leu Val Gln Lys Ala Leu Asn Ile Ile Ser Gln  
100 105 110  
Tyr His Leu Lys Glu Ile Gly Glu Ile Gly Ile Gly Ser Gly Cys Val  
115 120 125  
Ser Val Ser Leu Ala Leu Glu Asn Pro Asn Leu Ser Ile Tyr Ala Ser  
130 135 140  
Asp Ile Ser Pro Lys Ala Leu Glu Val Ala Leu Lys Asn Ile Glu Arg  
145 150 155 160  
Phe Cys Leu Lys Glu Arg Val Phe Leu Lys Gln Thr Arg Leu Trp Asp  
165 170 175  
His Met Pro Thr Ile Glu Met Leu Val Ser Asn Pro Pro Tyr Ile Ala  
180 185 190  
Arg Asn Tyr Pro Leu Glu Lys Ser Val Leu Lys Glu Pro His Glu Ala  
195 200 205  
Leu Phe Gly Gly Val Lys Gly Asp Glu Ile Leu Lys Glu Ile Val Phe  
210 215 220  
Leu Ala Ala Lys Leu Lys Ile Pro Phe Leu Val Cys Glu Met Gly Tyr  
225 230 235 240

608

Figure 510A-page 608

HPP 510

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Gln | Leu | Lys | Ser | Leu | Lys | Glu | Cys | Leu | Glu | Phe | Cys | Gly | Tyr | Asp |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Ala | Glu | Phe | Tyr | Lys | Asp | Leu | Ser | Gly | Phe | Asp | Arg | Gly | Phe | Val | Gly |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Val | Leu | Lys | Ser | Phe | Leu | Arg |     |     |     |     |     |     |     |     |     |
|     |     | 275 |     |     |     |     |     |     |     |     |     |     |     |     |     |

609

Figure 510A-page 609

(2) INFORMATION FOR SEQ ID NO:5325005\_f1\_2: -AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

610  
Figure 511A - page 610

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP511

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ile | Ser | Phe | Ile | Gly | Phe | Glu | Cys | Ser | Ala | Leu | Lys | Val | Phe | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Phe | Gly | Tyr | Ile | Val | Phe | Lys | Unk | Trp | His | Tyr | Ser | Ala | Ile | Arg |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

|     |     |     |     |
|-----|-----|-----|-----|
| Leu | Ile | Val | Ile |
|     |     |     | 35  |



(2) INFORMATION FOR SEQ ID NO:5440436\_c2\_5: - A A

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: OUTER MEMBRANE PROTEIN P6 PRECURSOR (OMP P6) (15 K

Val Gln Lys Ala Lys Glu Asn His Met Lys Val Leu Leu Glu Gly Asn  
1 5 10 15  
Thr Asp Glu Phe Gly Ser Ser Glu Tyr Asn Gln Ala Leu Gly Val Lys  
20 25 30  
Arg Thr Leu Ser Val Lys Thr Leu Leu Val Ile Lys Gly Val Glu Lys  
35 40 45  
Asp Met Ile Lys Thr Ile Ser Phe Gly Glu Ser Lys Pro Lys Cys Val  
50 55 60  
Gln Lys Thr Arg Glu Cys Tyr Arg Glu Asn Arg Arg Val Asp Val Lys  
65 70 75 80  
Leu Val Lys

611

Figure 512A - page 611

HPP512

(2) INFORMATION FOR SEQ ID NO:55843\_c1\_3: - AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Val Ile Gln Ser His Pro Lys Gln Thr Leu Ile Glu Asp Glu Asn Tyr  
1 5 10 15  
Phe Tyr Ala Asn Lys Gly Leu Tyr Lys Thr Asn Lys Glu Ala Phe Leu  
20 25 30  
Arg Val Tyr Lys Ile Pro Glu Ser Met Pro Ile Glu Lys Arg Glu Ser  
35 40 45  
Leu Ser Lys Val Ser Lys Ile Phe Leu Ala Leu Leu Phe Phe Ile Ser  
50 55 60  
Ser Met Leu Phe Gly Ile Phe Trp Arg Leu Pro Lys Arg Leu Asp Thr  
65 70 75 80  
Lys Met Ser Leu Glu Ser Ala His Lys Asn Glu Leu Glu Asn Ala Phe  
85 90 95  
Gln Arg Tyr Asp Ala Leu Gly Val Arg Phe Glu Asp Ile Ala Gly Val  
100 105 110  
Asn Glu Val Lys Glu Glu Leu Leu Glu Val Ile Asp Tyr Leu Lys Lys  
115 120 125  
Pro

612

Figure 513A-page 612

HPP 513

(2) INFORMATION FOR SEQ ID NO:5869090\_f2\_4: - A A

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met Phe Val Val Lys Met Val Leu Gly Phe Leu Ile Leu Leu Ser Pro  
1 5 10 15  
Leu Cys Ala Thr Gly Leu Asp Ile Ser Gln Thr Asp Ile Ile Glu Arg  
20 25 30  
Ser Leu Asn Phe Leu Leu Phe Val Gly Ile Leu Trp Tyr Phe Leu Ala  
35 40 45  
Lys Arg Leu Arg Ser Phe Leu His Ser Lys Ser Leu Glu Ile Ser Lys  
50 55 60  
Arg Leu Glu Glu Ile Gln Ala Gln Leu Lys Val Ser Lys Glu His Lys  
65 70 75 80  
Lys Lys Leu Leu Lys Glu Leu Glu Gln Ala Lys Glu Lys Ala Glu Leu  
85 90 95  
Ile Ile Ser Asp Ala Asn Lys Glu Ala Leu His Asp His Ala Lys Ile  
100 105 110  
Arg Ile Thr Asn Gln Asn Gly Cys Gly Lys Phe Asp Gln Lys Phe  
115 120 125

613

Figure 514A-page 613

HPP514

(2) INFORMATION FOR SEQ ID NO:5875152\_f1\_2: -A A

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 275 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: molybdate-binding periplasmic protein precursor

Met Arg Val Leu Glu Trp Lys Tyr Trp Leu Asn Thr Asp Lys Trp Asp  
1 5 10 15  
Thr Pro Thr Asn Lys Pro Pro Gln Thr Phe Lys Ile Gln Ile Phe Lys  
20 25 30  
Ile Gln Ile Gly Ile Ile Asn Asn Phe Asn His Leu Ile Lys Gly Ser  
35 40 45  
Ser Met Lys Asn Ala Phe Lys Ala Phe Ala Leu Leu Ile Val Phe Phe  
50 55 60  
Ser Asn Ala Leu Leu Ala Gln Asp Leu Lys Ile Ala Ala Ala Ala Asn  
65 70 75 80  
Leu Thr Arg Ala Leu Lys Ala Leu Val Lys Glu Phe Gln Lys Glu His  
85 90 95  
Pro Lys Asp Ala Ile Asn Ile Ser Phe Asn Ser Ser Gly Lys Leu Tyr  
100 105 110  
Ala Gln Ile Ala Gln Asn Ala Pro Phe Asp Leu Phe Ile Ser Ala Asp  
115 120 125  
Ile Ala Arg Pro Lys Lys Leu Tyr Asp Glu Lys Ile Thr Pro Phe Lys  
130 135 140  
Glu Glu Val Tyr Ala Lys Gly Val Leu Val Leu Trp Ser Glu Asn Leu  
145 150 155 160  
Lys Met Asp Ser Leu Glu Ile Leu Lys Asp Pro Lys Ile Lys Arg Ile  
165 170 175  
Ala Met Ala Asn Pro Lys Leu Ala Pro Tyr Gly Lys Ala Ser Met Glu  
180 185 190  
Val Leu Asp Arg Leu Lys Leu Thr Pro Ser Leu Lys Ser Lys Ile Ile  
195 200 205  
Tyr Gly Ala Ser Ile Ser Gln Ala His Gln Phe Ile Ala Thr Lys Asn  
210 215 220  
Ala Gln Ile Gly Phe Gly Ala Leu Ser Leu Ile Asp Lys Lys Asp Lys  
225 230 235 240

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Figure 515A - page 614

HPP 515

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Leu | Ser | Tyr | Phe | Ile | Ile | Asp | Lys | Thr | Leu | Tyr | Asn | Pro | Ile | Glu |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Gln | Ala | Leu | Ile | Ile | Thr | Lys | Asn | Gly | Ala | Asn | Asn | Pro | Leu | Ala | Lys |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Val | Phe | Lys | Asp |     |     |     |     |     |     |     |     |     |     |     |     |
|     |     | 275 |     |     |     |     |     |     |     |     |     |     |     |     |     |

Figure 515A - page 615

(2) INFORMATION FOR SEQ ID NO:5878208\_f2\_7: -AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Val Ala Leu Leu Glu Pro Ser Val Met Tyr Leu Thr Glu Lys Tyr Gln  
1 5 10 15  
Tyr Ser Arg Phe Lys Val Thr Trp Gly Leu Val Ala Leu Ile Phe Val  
20 25 30  
Val Gly Val Val Leu Ile Phe Ser Leu His Lys Asp Tyr Lys Asp Tyr  
35 40 45  
Leu Thr Phe Phe Glu Lys Ser Leu Phe Asp Trp Leu Asp Phe Ala Ser  
50 55 60  
Ser Thr Ile Ile Unk Pro Leu Gly Gly Met Unk Thr Phe Ile Phe Met  
65 70 75 80  
Gly Trp Val Leu Lys Lys Glu Lys Leu Arg Leu Leu Ser Ala His Phe  
85 90 95  
Leu Gly Pro Lys Leu Phe Ala Thr Trp Tyr Phe Leu Leu Lys Tyr Ile  
100 105 110  
Thr Pro Leu Ile Val Phe Ser Ile Trp Leu Ser Lys Ile Tyr  
115 120 125

616  
Figure 516A - page 616

HPP 516

(2) INFORMATION FOR SEQ ID NO:5879160\_c3\_26: - AA

617

Figure 517A - page 617

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 517

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Val | Gly | Leu | Met | Lys | Ile | Arg | Phe | Met | Gly | Arg | Ser | Val | Phe | Val | Gly |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Asp | Leu | Glu | Arg | Ile | Glu | Glu | Val | Ala | Arg | Phe | Glu | Glu | Phe | Trp | Leu |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Leu | Gly | Gly | Gln | Lys | Ala | Ile | Lys | Glu | Pro | Arg | Arg | Leu | Val | Leu | Glu |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Ile | Ala | Leu | Lys | His | Gln | Leu | Asn | Lys | Leu | Leu | Lys | Arg | Val | Gln | Lys |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| His | Phe | Lys | Glu | Asp | Glu | Leu | Gly | Ile | Phe | Lys | Gln | Met | His | Asp | Lys |  |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |  |
| Lys | Ile | Gln | Ser | Val | Ala | Thr | Asn | Ser | Ile | Gly | Arg | Leu | Phe | Asp | Ile |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Val | Ala | Phe | Ser | Leu | Gly | Val | Val | Gly | Thr | Ile | Ser | Phe | Glu | Ala | Glu |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Ser | Gly | Gln | Val | Leu | Glu | Asn | Leu | Ala | Leu | Gln | Ser | Asp | Glu | Ile | Ala |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Phe | Tyr | Pro | Phe | Glu | Ile | Lys | Asn | Ser | Val | Val | Arg | Leu | Lys | Glu | Phe |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Tyr | Gln | Ala | Phe | Glu | Lys | Asp | Leu | Gly | Val | Leu | Glu | Pro | Lys | Arg | Ile |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |
| Ala | Lys | Lys | Phe | Phe | Asn | Ser | Leu | Val | Glu | Ile | Ile | Thr | Ala | Leu | Ile |  |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |  |
| Ala | Pro | Phe | Lys | Gly | His | Val | Val | Val | Cys | Ser | Gly | Gly | Val | Phe | Cys |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |
| Asn | Gln | Leu | Leu | Cys | Glu | Gln | Leu | Ala | Lys | Arg | Leu | Lys | Lys | Leu | Gln |  |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |
| Arg | Glu | Tyr | Phe | Phe | His | Lys | His | Phe | Pro | Pro | Asn | Asp | Arg | Ser | Ile |  |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |
| Pro | Val | Gly | Gln | Ala | Leu | Met | Ala | Tyr | Phe | Asn | Pro | Thr | Ile | Ile | Lys |  |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |  |

Lys Gly

618  
Figure 517A - page 618



(2) INFORMATION FOR SEQ ID NO:5891412\_c3\_10: -AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP518

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: 3-deoxy-D-manno-octulosonic acid transferase

Met Gly Lys Lys Leu Lys Thr Leu Glu Thr Leu Val Val Thr Glu Ala  
1 5 10 15  
Glu Leu Trp Phe Asn Val Phe Asp Thr Ala Gln Lys Leu Gly Ala Lys  
20 25 30  
Thr Met Leu Ile Asn Ala Arg Ile Ser Val Arg Ser Tyr Pro Lys Tyr  
35 40 45  
Gln Arg Phe Ser Phe Phe Tyr Ala Leu Leu Phe Lys Arg Ile Asp Leu  
50 55 60  
Ile Leu Ala Gln Ser Lys Ala Asp Gln Lys Arg Leu Leu Asn Leu Gly  
65 70 75 80  
Ala Lys Lys Val Val Asp Phe Leu Asn Ile Lys Arg Phe Ser Lys Pro  
85 90 95  
Val Ile Thr Ser Phe Tyr Pro Lys Asn Pro Ser Ala Leu Asn Ile Val  
100 105 110  
Leu Ala Ser Thr His Glu Gly Glu Glu Glu Leu Gly Leu Lys Ala Phe  
115 120 125  
Leu Glu Leu Lys Lys Thr Phe Lys Asn Ala Arg Leu Phe Val Val Pro  
130 135 140  
Arg His Pro Glu Arg Phe Lys Ser Val Arg Asn Leu Leu Gln Asp Ile  
145 150 155 160  
Leu Lys Arg Ala Phe  
165

619  
Figure 518A-page 619



- 44

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 153 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP520

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Val Ile Val Ala Trp Leu Phe Arg Phe Lys Ser Ile Ala Phe Ser Ile  
1 5 10 15

Leu Ile Thr Leu Leu Val Ile Leu Val Asp Ile Trp Val Tyr Ser Asp  
20 25 30

Val Arg Gln Phe Leu Leu Asp Thr Ser Ser Ser Phe Ile Trp Leu Leu  
35 40 45

Ile Ala Leu Leu Ile Lys Trp Gly Val Ile Val Ile Ser Ala Arg Lys  
50 55 60

Cys Tyr Gln Phe Ser Gln Lys Met Phe Ala Leu Ile Gln Arg Lys Arg  
65 70 75 80

Gln Ile Arg Glu Asn Leu Lys Asn Arg Ser Asn Arg Lys Asp Ala Lys  
85 90 95

Asn Phe Glu Lys Leu Ser Asn Ile Ala Glu Glu Ile Ile Ser Lys Lys  
100 105 110

Gln Glu Glu Ser His His Lys Glu Asp Ser Asn Asp Glu Asn His Lys  
115 120 125

Asp Lys Leu Ser Asn Ile Thr Glu Glu Met Ile Leu Lys Lys Gln Glu  
130 135 140

Glu Leu Lys Ala Arg Lys Asp Lys Gly Asp  
145 150

(2) INFORMATION FOR SEQ ID NO:6093906\_c2\_8: -AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 296 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Val Leu Met Ala Leu Asn Asp Lys Arg Tyr Gly Leu Glu Ala Gly Ile  
1 5 10 15  
Lys Tyr Phe Thr Met Gly Ala Met Ala Ser Ala Phe Phe Ala Met Gly  
20 25 30  
Ala Met Ala Phe Tyr Leu Leu Thr Gly Ser Leu Asn Leu Glu Val Ile  
35 40 45  
Thr Leu Tyr Leu His Thr Glu Gly Ile Thr Asn Pro Met Leu Phe Ala  
50 55 60  
Met Gly Thr Ile Phe Leu Ile Gly Ala Ile Gly Phe Lys Val Ser Leu  
65 70 75 80  
Val Pro Phe His Thr Trp Met Pro Asp Val Tyr Glu Gly Asn Asn Pro  
85 90 95  
Val Phe Ala Ser Tyr Ile Ser Ile Val Pro Lys Ile Ala Gly Phe Val  
100 105 110  
Val Ala Thr Arg Leu Phe Gly Ala Phe Ile Asp Thr His Thr Ala Trp  
115 120 125  
Val Glu Asp Ile Phe Tyr Val Leu Ile Leu Met Thr Ile Thr Ile Pro  
130 135 140  
Asn Phe Ile Ala Leu Trp Gln Glu Asp Val Lys Arg Met Leu Ala Tyr  
145 150 155 160  
Ser Ser Ile Ser His Ser Gly Phe Ala Leu Ala Cys Val Phe Ile His  
165 170 175  
Thr Glu Asp Ser Gln Gln Ala Met Phe Val Tyr Trp Phe Met Phe Ala  
180 185 190  
Phe Thr Tyr Ile Gly Ala Phe Gly Leu Leu Trp Leu Leu Lys Ser Arg  
195 200 205  
Glu Lys Thr Trp Asp Glu Arg Tyr Asp His Pro Tyr Ser Lys Phe Asn  
210 215 220  
Gly Leu Ile Lys Thr His Pro Leu Val Ala Ile Leu Gly Ala Ile Phe  
225 230 235 240

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Figure 521A-page 622

HPP521

Val Phe Gly Leu Ala Gly Ile Pro Pro Phe Ser Val Phe Trp Gly Lys  
245 250 255

Phe Leu Ala Val Glu Ser Ala Leu Glu Ser Asn His Ile Leu Leu Ala  
260 265 270

Val Val Met Leu Val Asn Ser Ala Val Ala Ala Phe Tyr Tyr Phe Arg  
275 280 285

Trp Leu Val Ala Met Phe Phe Asn Lys  
290 295

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP522

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

## (xi) SEQUENCE DESCRIPTION:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asn | Tyr | Pro | Asn | Leu | Pro | Asn | Ser | Ala | Leu | Unk | Ile | Ser | Glu | Gln | 1   | 5   | 10  | 15  |
| Pro | Glu | Val | Lys | Glu | Ile | Thr | Asn | Glu | Leu | Leu | Lys | Gln | Leu | Gln | Asn | 20  | 25  | 30  |     |
| Ala | Leu | Arg | Ser | Asn | Ala | His | Phe | Ser | Glu | Gln | Val | Glu | Leu | Ser | Leu | 35  | 40  | 45  |     |
| Lys | Cys | Ile | Val | Arg | Ile | Leu | Glu | Val | Leu | Leu | Ser | Leu | Asp | Phe | Phe | 50  | 55  | 60  |     |
| Lys | Asn | Ala | Asn | Glu | Ile | Asp | Ser | Ser | Leu | Arg | Asn | Ser | Ile | Glu | Trp | 65  | 70  | 75  | 80  |
| Leu | Thr | Asn | Ala | Gly | Glu | Ser | Leu | Lys | Leu | Lys | Met | Lys | Glu | Tyr | Glu | 85  | 90  | 95  |     |
| Arg | Phe | Phe | Ser | Glu | Phe | Asn | Thr | Ser | Met | His | Ala | Asn | Glu | Gln | Glu | 100 | 105 | 110 |     |
| Val | Thr | Asn | Thr | Leu | Asn | Ala | Asn | Ala | Glu | Asn | Ile | Lys | Ser | Unk | Ile | 115 | 120 | 125 |     |
| Lys | Unk | Leu | Glu | Asn | Gln | Leu | Ile | Glu | Thr | Thr | Thr | Arg | Leu | Leu | Thr | 130 | 135 | 140 |     |
| Ser | Tyr | Gln | Ile | Phe | Leu | Asn | Gln | Ala | Arg | Asp | Asn | Ala | Asn | Asn | Gln | 145 | 150 | 155 | 160 |
| Ile | Thr | Lys | Asn | Lys | Thr | Unk | Ser | Leu | Glu | Ala | Ile | Thr | Gln | Ala | Lys | 165 | 170 | 175 |     |
| Asn | Asn | Ser |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 189 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP523

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

## (xi) SEQUENCE DESCRIPTION: lipopolysaccharide epitope

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ile | Asn | Ser | Lys | Lys | Ser | Leu | Lys | Lys | Gly | Leu | Arg | Gly | Phe | Phe | 1   | 5   | 10  | 15  |
| Lys | Ile | Leu | Lys | Asp | Arg | Asn | Gly | Ala | His | Phe | Ser | Cys | Gly | Ala | Thr | 20  | 25  | 30  |     |
| Ser | Gly | Phe | Gly | Leu | Glu | Ile | Ala | Lys | Ala | Phe | Leu | Gln | Lys | Asn | His | 35  | 40  | 45  |     |
| Val | Val | Phe | Gly | Thr | Gly | Arg | Arg | Gln | Glu | Asn | Leu | Gln | Lys | Leu | Gln | 50  | 55  | 60  |     |
| Leu | Ala | Tyr | Pro | Lys | Arg | Phe | Ile | Pro | Leu | Cys | Phe | Asp | Leu | Gln | Asn | 65  | 70  | 75  | 80  |
| Lys | Pro | Glu | Thr | Lys | Arg | Ala | Ile | Glu | Thr | Ile | Phe | Ser | Met | Thr | Asp | 85  | 90  | 95  |     |
| Arg | Ile | Asp | Ala | Leu | Ile | Asn | Asn | Ala | Gly | Leu | Ala | Leu | Gly | Leu | Asn | 100 | 105 | 110 |     |
| Lys | Ala | Tyr | Glu | Cys | Glu | Leu | Asp | Asp | Trp | Glu | Val | Met | Ile | Asp | Thr | 115 | 120 | 125 |     |
| Asn | Ile | Lys | Gly | Leu | Leu | His | Leu | Thr | Arg | Leu | Ile | Leu | Pro | Ser | Met | 130 | 135 | 140 |     |
| Ile | Glu | His | Asp | Gln | Gly | Thr | Ile | Ile | Asn | Leu | Gly | Ser | Ile | Ala | Gly | 145 | 150 | 155 | 160 |
| Thr | Tyr | Ala | Tyr | Pro | Gly | Gly | Lys | Ser | Met | Glu | Arg | Ala | Arg | Arg | Cys | 165 | 170 | 175 |     |
| Glu | Thr | Unk | Unk | Unk | Lys | Phe | Ala | Ser | Gly | Arg | Gly | Trp | His | 180 | 185 | 190 |     |     |     |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Val Glu Val Gln Tyr Tyr Gly Trp Arg Ile Asn Leu Phe Asn Met Phe  
1 5 10 15  
Pro Asn Val Ile Phe Leu Lys Pro Leu Lys Glu Ser Asp Glu Met Ser  
20 25 30  
Lys Pro Val Phe Ser Trp Ile Leu Tyr Ala Leu Leu Leu Val Gly Phe  
35 40 45  
Phe Ile Ser Ala Arg Ser Val Cys Thr Leu Phe Lys Gly Lys Ala His  
50 55 60

626

Figure 524A - page 626

HPP 524



(2) INFORMATION FOR SEQ ID NO:6288949\_c1\_2:-AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP525

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: flagellar biosynthetic protein

Val Phe Ala Thr Asp Ser Ser Ser Phe Ser Met Gly Leu Thr Met Ala  
1 5 10 15  
Ser Ala Tyr Glu Pro Ile Ser Gly Ser Gln Lys Pro Ile Val Gly Gln  
20 25 30  
Ala Leu Leu Leu Leu Ala Ile Leu Ile Leu Leu Asp Leu Ser Phe His  
35 40 45  
His Gln Ile Ile Leu Phe Val Asp His Ser Leu Lys Ala Val Pro Leu  
50 55 60  
Gly Arg Phe Val Phe Glu Pro Glu Leu Ala Lys Asn Ile Val Lys Ala  
65 70 75 80  
Phe Ser His Leu Phe Val Ile Gly Phe Ser Met Ala Phe Pro Ile Leu  
85 90 95  
Cys Leu Val Leu Leu Ser Asp Ile Ile Phe Gly Met Ile Met Lys Thr  
100 105 110  
His Pro Gln Phe Asn Leu Leu Ala Ile Gly Phe Pro Val Lys Ile Ala  
115 120 125  
Ile Gly Phe Val Gly Ile Ile Leu Ile Ala Ser Ala Ile Met Gly Arg  
130 135 140  
Phe Lys Glu Glu Ile Ser Leu Ala Phe Ser Val Ile Ser Lys Ile Phe  
145 150 155 160

627

Figure 525A - page 627

(2) INFORMATION FOR SEQ ID NO:630\_f1\_1: -AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 526

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Asp | Leu | Phe | Met | Ser | Leu | Leu | Gly | Trp | Phe | Ile | Ile | Leu | Ile |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gly | Gly | Ser | Val | His | Val | Gly | Asp | Arg | Val | Arg | Ile | Ala | Lys | Gly | Thr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asp | Ile | Phe | Ile | Gly | Asp | Val | Leu | Asp | Thr | Ser | Asn | Val | Val | His |     |
|     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |     |     |     |

628

Figure 526A - page 628

(2) INFORMATION FOR SEQ ID NO:6495137\_f1\_1: -AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met Tyr Gly Val Lys Glu Ile Lys Asp Lys Ile Asp Lys Gln Leu His  
1 5 10 15  
Asn Asn Asp His Leu Phe Glu Gly Leu Phe Gly Glu Lys Glu Asp Leu  
20 25 30  
Lys Lys Leu Val Ser Met Phe Gly Gln Leu Arg Phe Gln Lys Arg Trp  
35 40 45  
Ser Gln Thr Pro Arg Val Pro Gln Thr Ser Val Leu Gly His Thr Leu  
50 55 60  
Cys Val Ala Ile Met Gly Tyr Leu Leu Ser Phe Asp Leu Lys Ala Cys  
65 70 75 80  
Lys Ser Met Arg Ile Asn His Phe Leu Gly Gly Leu Phe Pro  
85 90

629

Figure 527A-page 629

HPP 527

-44

Figure 528A - pag 630A

HPP528

(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: YES

(A) ORGANISM: *Helicobacter pylori*

Ile Ala  
145

-44

631

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 214 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 529

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: signal recognition particle protein

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ser | Gly | Val | Val | Leu | Ser | Lys | Phe | Asp | Ser | Asp | Ser | Lys | Gly | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

Ile Ala Leu Gly Ile Thr Tyr Gln Leu Gly Leu Pro Leu Arg Phe Ile  
20 25 30

Gly Ser Gly Glu Lys Ile Pro Asp Leu Asp Val Phe Met Pro Glu Arg  
35 40 45

Ile Val Gly Arg Leu Met Gly Ala Gly Asp Ile Ile Ser Leu Ala Glu  
50 55 60

Lys Thr Ala Ser Val Leu Asn Pro Asn Glu Ala Lys Asp Leu Ser Lys  
65 70 75 80

Lys Leu Lys Lys Gly Gln Phe Thr Phe Asn Asp Phe Leu Asn Gln Ile  
85 90 95

Glu Lys Val Lys Lys Leu Gly Ser Met Ser Ser Leu Ile Ser Met Ile  
100 105 110

Pro Gly Leu Gly Asn Met Ala Ser Ala Leu Lys Asp Thr Asp Leu Glu  
115 120 125

Ser Ser Leu Glu Val Lys Lys Ile Lys Ala Met Val Asn Ser Met Thr  
130 135 140

Lys Lys Glu Arg Glu Asn Pro Glu Ile Leu Asn Gly Ser Arg Arg Lys  
145 150 155 160

Arg Ile Ala Leu Gly Asn Gly Leu Glu Glu Thr Glu Ile Asn Arg Ile  
165 170 175

Ile Lys Arg Phe Asp Gln Ala Ser Lys Met Ala Lys Arg Leu Thr Asn  
180 185 190

Lys Lys Gly Ile Ser Asp Met Met Asn Leu Thr Thr Arg Leu Lys Ile  
195 200 205

Lys His Ile Pro Lys Met Arg  
210 215

- AA

632

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 530

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Val Gly Ser Glu Ile Gln Gly Gly Leu Lys Gly Asp Val Lys Asp Val  
1 5 10 15

Leu Leu Leu Asp Val Thr Pro Leu Ser Leu Gly Ile Glu Thr Leu Gly  
20 25 30

Gly Val Met Thr Lys Val Ile Asp Arg Gly Thr Thr Ile Pro Ala Lys  
35 40 45

Lys Ser Gln Val Phe Asn Pro Glu Asp Asn Gln Pro Ala Val Ser Ile  
50 55 60

Met Val Leu Gln Gly Glu Gly Asn Trp Gln Gly Ile Ile Asn Leu Trp  
65 70 75 80

Val Asn Leu Ile Cys Lys Ala  
85

633

Figure 531A - page 633

- HPP 531

[illegible]

(2) INFORMATION FOR SEQ ID NO:663530\_f1\_2:- AA

634  
Figure 532A - page 634

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 532

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Gly | Val | Leu | Gly | Met | Phe | Ala | Phe | Phe | Ser | Trp | Val | Phe | Leu | Phe |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Lys | His | Asn | Leu | Ser | His | Lys | Ile | Arg | Leu | Tyr | His | Glu | Lys | Lys | Asp |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Phe | Asp | Lys | Leu | Leu | Lys | Gln | Ile | Leu | Ser | Gln | Asp | Thr | Gln | Lys | Thr |  |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Phe | Leu | Lys | Thr | Lys | Phe | Lys | Ser | Asp | Leu | Ala | Lys | Asn | Leu | Ser | Gln |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Ile | Leu | Ala | Arg | Tyr | Asp | Leu | Lys | Ala | Asp | Leu | Asn | Thr | Pro | Asn | Ser |  |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |  |
| Gly | Cys | Glu | Lys | Val | Asp | Asn | Leu | Phe | Lys | His | Tyr | His | Asn | Ile | Glu |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Asn | Asn | Thr | Leu | Glu | Pro | Lys | Asp | His | Ala | Lys | His | Ser | Leu | Ala | Tyr |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Glu | His | Ala | Tyr | Phe | Ser | Lys | Arg | Leu | Lys | Ala | Phe | Ile | His | Asn | Asp |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Leu | Lys | Asn | Ala | Phe | Glu | Val | Leu | Thr | Asn | Ala | Gln | Ile | Pro | Leu | Glu |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Leu | Arg | Arg | Tyr | Ala | Tyr | Arg | Asn | Arg | Pro | Lys | Arg | Gln | Gln | Lys | Arg |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |
| Gly | Phe | Lys | Gly | Cys | Glu | Cys | Asp | Ala | Arg | Gly | Phe | Gly |     |     |     |  |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     |     |  |



635

HPP 533

(D) TOPOLOGY: linear

(A) ORGANISM: *Helicobacter pylori*

Val

-AA

634

Figure 534A - page 636

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 103 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 534

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION:

Val Ala Lys Asn Leu Val Ala Ser Gly Val Cys Asp Lys Ala Thr Val  
1 5 10 15

Gln Leu Ala Tyr Ala Ile Gly Val Ile Glu Pro Val Ser Ile Tyr Val  
20 25 30

Asn Thr His Asn Thr Ser Lys His Ser Ser Ala Glu Leu Glu Lys Cys  
35 40 45

Val Lys Ser Val Phe Lys Leu Thr Pro Lys Gly Ile Ile Glu Ser Leu  
50 55 60

Asp Leu Leu Arg Pro Ile Tyr Ser Leu Thr Ser Ala Tyr Gly His Phe  
65 70 75 80

Gly Arg Glu Leu Glu Glu Phe Thr Trp Glu Lys Thr Asn Lys Val Glu  
85 90 95

Glu Ile Lys Ala Phe Phe Lys Arg  
100

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 535

(iii) HYPOTHETICAL: YES

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

## (xi) SEQUENCE DESCRIPTION:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Arg | Leu | Phe | Arg | Phe | Val | Gly | Trp | Tyr | Tyr | Phe | Lys | Tyr | Phe | Leu | 1   | 5   | 10  | 15  |
| Ile | Val | Leu | Leu | Ala | Leu | Glu | Leu | Phe | Phe | Val | Gly | Ile | Asp | Ser | Leu | 20  | 25  | 30  |     |
| Lys | Tyr | Ala | Asp | Lys | Met | Pro | Asp | Ser | Ala | Asn | Met | Ile | Ile | Leu | Phe | 35  | 40  | 45  |     |
| Phe | Thr | Tyr | Asp | Ile | Leu | Phe | Ala | Leu | Asn | Tyr | Thr | Leu | Pro | Ile | Ser | 50  | 55  | 60  |     |
| Leu | Leu | Leu | Ala | Met | Val | Leu | Phe | Tyr | Ile | Thr | Phe | Ile | Lys | Ser | Asn | 65  | 70  | 75  | 80  |
| Gln | Tyr | Thr | Ala | Leu | Leu | Ser | Ile | Gly | Phe | Ser | Lys | Cys | Gln | Ile | Leu | 85  | 90  | 95  |     |
| Ser | Pro | Ile | Phe | Leu | Ile | Ser | Leu | Phe | Phe | Thr | Ala | Val | Tyr | Val | Gly | 100 | 105 | 110 |     |
| Leu | Asn | Ala | Thr | Pro | Phe | Val | Tyr | Met | Glu | Glu | Lys | Thr | Gln | Asn | Leu | 115 | 120 | 125 |     |
| Ile | Tyr | Lys | Asp | Asn | Ser | Leu | Ser | Val | Ser | Glu | His | Leu | Leu | Val | Lys | 130 | 135 | 140 |     |
| Tyr | Asn | Asp | Asp | Tyr | Val | Tyr | Phe | Asp | Lys | Ile | Asn | Pro | Leu | Leu | Gln | 145 | 150 | 155 | 160 |
| Lys | Ala | Gln | Asn | Ile | Lys | Val | Phe | Arg | Leu | Lys | Asp | Lys | Thr | Leu | Glu | 165 | 170 | 175 |     |
| Ser | Tyr | Ala | Glu | Ala | Lys | Glu | Ala | Phe | Phe | Glu | Asp | Lys | Tyr | Trp | Ile | 180 | 185 | 190 |     |
| Leu | His | Asp | Thr | Thr | Ile | Tyr | Glu | Met | Pro | Leu | Ser | Phe | Glu | Leu | Gly | 195 | 200 | 205 |     |
| Ala | Asn | Ala | Leu | Asn | Thr | Thr | His | Leu | Glu | Thr | Phe | Lys | Thr | Leu | Lys | 210 | 215 | 220 |     |
| Asn | Phe | Arg | Pro | Lys | Val | Leu | Asp | Thr | Ile | Tyr | Gln | Asn | Lys | Pro | Ala | 225 | 230 | 235 | 240 |



(2) INFORMATION FOR SEQ ID NO:6845425\_f3\_2: -AA

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Figure 536A - page 639

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 536

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: reacts with antibodies to chloroplast envelope pr

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Glu | Lys | Ala | His | Pro | Asp | Val | Phe | Asn | Leu | Leu | Leu | Gln | Val | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Asp | Glu | Gly | His | Leu | Thr | Asp | Ser | Lys | Gly | Val | Arg | Val | Asp | Phe | Lys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asn | Thr | Ile | Leu | Ile | Leu | Thr | Ser | Asn | Val | Ala | Ser | Gly | Ala | Leu | Leu |
|     |     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Glu | Glu | Asp | Leu | Ser | Glu | Ala | Asp | Lys | Gln | Lys | Ala | Ile | Lys | Glu | Ser |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Arg | Gln | Phe | Phe | Lys | Pro | Glu | Phe | Leu | Asn | Arg | Leu | Asp | Glu | Ile |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Ile | Ser | Phe | Asn | Ala | Leu | Asp | Ser | His | Ala | Ile | Ile |     |     |     |     |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     |     |

640

Figure 537 A- page 640

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP537

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: putrescine transport atp-binding

Val Leu Arg Leu Met Arg Leu Glu Asn Leu Ser Gln Gln Lys Ile Pro  
1 5 10 15

Lys Leu Ser Gly Gly Gln Ala Gln Arg Val Ala Leu Ala Arg Ala Leu  
20 25 30

Ile Ala Ala Lys Asn Leu Leu Leu Leu Asp Glu Pro Leu Asn Ala Leu  
35 40 45

Asp Asn Ala Leu Lys Asn Glu Val Gln Gln Gly Leu Leu Asp Phe Ile  
50 55 60

Lys Arg Glu Asn Leu Ser Val Leu Leu Val Ser His Asp Pro Asn Glu  
65 70 75 80

Ile Thr Lys Leu Ala Arg Thr Phe Leu Phe Leu Asn Asn Gly Val Ile  
85 90 95

Asp Pro Asn Gln Glu Asn Arg Leu Phe Ser Asn Arg Leu Leu Val Lys  
100 105 110

Pro Leu Phe Glu Asp Glu Asn Tyr Cys His Tyr Glu Val Ile Pro Gln  
115 120 125

Thr Ile Ser Leu Pro Lys Asp Cys Leu Asn Pro Thr Phe Lys Leu Asp  
130 135 140

Phe Ile Gln Asn Lys Lys Phe  
145 150

(2) INFORMATION FOR SEQ ID NO:6933202\_f2\_1: - AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

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Figure 538A-page 641

(ii) MOLECULE TYPE: protein

HPP 538

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Trp | Gly | Val | Glu | Ile | Unk | Glu | Phe | Ser | Gln | Ile | Ile | Ala | Cys | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Glu | Ile | Thr | Leu | Gln | Ile | Ala | Leu | Asn | Ala | Gln | Glu | Asn | Ala | Leu | Ile |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ile | Thr | His | His | Pro | Leu | Ile | Phe | Lys | Pro | Leu | Lys | Thr | Leu | Asn | Asp |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Glu | Ala | Tyr | Pro | Gly | Asn | Ile | Leu | Lys | Ile | Leu | Ile | Gln | Lys | Thr | Phe |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gln | Ser | Ser | Ala | Cys | Thr | Arg | Ile | Leu | Thr | Lys | Arg | Ile |     |     |     |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:7031343\_c2\_17: AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP539

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Phe | Leu | Asp | Arg | Arg | Leu | Ile | Val | Met | Val | Thr | Asp | Ser | Lys | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Arg | Tyr | Ile | Asn | Val | His | Ile | Leu | Phe | Arg | Gln | Ile | Ser | Leu | Tyr |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Leu | Leu | Ser | Val | Val | Gly | Ser | Leu | Leu | Phe | Leu | Gly | Val | Ser |     |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |

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Figure 539A - page 642



643

Figure 540A - page 643

(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: YES

HPP 540

(A) ORGANISM: *Helicobacter pylori*

Met Asn Val Leu Asn Ala Lys Glu Cys Val Thr Pro Ile Thr Arg Ser  
1 5 10 15

Val Lys Tyr His Gln Gln Ser Ala Glu Ile Arg Ala Leu Gln Leu Gln  
20 25 30

Ser Tyr Lys Met Ala Lys Met Ala Leu Asp Asn Asn Leu Lys Leu Val  
35 40 45

Lys Asp Lys Lys Pro Ala Val Ile Leu Asp Leu Asp Glu Thr Val Leu  
50 55 60

Asn Thr Phe Asp Tyr Ala Gly Tyr Leu Val Lys Asn Cys Ile Lys Tyr  
65 70 75 80

Thr Pro Glu Thr Trp Asp Lys Phe Glu Lys Glu Gly Ser Leu Thr Leu  
85 90 95

Ile Pro Gly Ala Leu Asp Phe Leu Glu Tyr Ala Asn Ser Lys Gly Val  
100 105 110

Lys Ile Phe Tyr Ile Ser Asn Arg Thr Gln Lys Asn Lys Ala Phe Thr  
115 120 125

Leu Lys Thr Leu Lys Ser Phe Lys Leu Pro Gln Val Ser Glu Glu Ser  
130 135 140

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Leu | Leu | Lys | Glu | Lys | Gly | Lys | Pro | Lys | Ala | Val | Arg | Arg | Glu | Leu |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |

Val Ala Lys Asp Tyr Ala Ile Val Leu Gln Val Gly Asp Thr Leu His  
165 170 175

Asp Phe Asp Ala Ile Phe Ala Lys Asp Ala Lys Asn Ser Gln Glu Gln  
180 185 190

Gln Ala Lys Val Leu Gln Asn Ala Gln Lys Phe Gly Thr Glu Trp Ile  
195 200 205

Ile Leu Pro Asn Ser Leu Tyr Gly Thr Trp Glu Asp Gly Pro Ile Lys  
210 215 220

Ala Trp Gln Asn Lys Lys  
225 230

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 238 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP541

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met Ile Tyr Gly Val Leu Asp Gly Leu Phe Leu Ala Ile Leu Gln Ala  
 1 5 10 15

Gln Asn Tyr Arg Phe His Ser Leu Tyr Leu Phe Glu Glu Asn Leu Asp  
 20 25 30

Leu Phe Lys Ile Ser Cys Tyr Phe Ala Arg Tyr Glu Asp Leu Ile Lys  
 35 40 45

Lys Gly Ala Lys Leu Phe Ile Gln Gly Phe Phe Asn Pro Asn Glu Leu  
 50 55 60

Lys Met Asp Phe Leu Lys Arg Pro Ile Thr His Ser Phe Leu Lys Leu  
 65 70 75 80

Glu Ile Met Pro Tyr Lys Ser Ala Phe Asn Leu Arg Met Arg Glu Asn  
 85 90 95

Ile Gln Ser Tyr Tyr Lys Gln Ala Leu Arg Gly Trp Gly Ser Phe Glu  
 100 105 110

Asp Glu Leu Leu Gly Leu Lys Asn Thr Leu Lys Asn Leu Pro Leu Tyr  
 115 120 125

Gln Thr Leu Lys Thr Lys Pro Lys Lys Ile Asn Ala Pro Ile Cys Val  
 130 135 140

Val Gly Asn Gly Pro Ser Leu Asp Leu Leu Leu Asp Phe Leu Lys Glu  
 145 150 155 160

Asn Glu Glu Lys Phe Ile Ile Phe Ser Cys Gly Thr Ala Leu Lys Pro  
 165 170 175

Leu Lys Ala His Gly Val Lys Val Asp Phe Gln Ile Glu Val Glu Arg  
 180 185 190

Ile Asp Tyr Leu Lys Glu Val Leu Glu Arg Ala Pro Leu Glu Asp Thr  
 195 200 205

Pro Leu Met Gly Ala Asn Met Leu Asn Pro Asn Ala Phe Asp Leu Ala  
 210 215 220

Lys Glu Ala Leu Met Phe Met Arg Gly Gly Ser Ala Cys Ala Val  
 225 230 235

644

Figure 541A- page 644

- AA

645

Figure 542A - page 645

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 542

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Helicobacter pylori*

(xi) SEQUENCE DESCRIPTION: influenzae type B lipooligosaccharide

Met Leu Ala Ala Gly Leu Thr Leu Pro Glu Phe Gly Cys Tyr Leu Ser  
1 5 10 15

His Tyr Leu Leu Trp Lys Glu Cys Val Lys Leu Asp Gln Pro Val Val  
20 25 30

Ile Leu Glu Asp Asp Val Thr Leu Unk Ser His Phe Met Gln Ala Leu  
35 40 45

Glu Asp Cys Leu Lys Ser Pro Phe Asp Phe Val Arg Leu Tyr Gly Cys  
50 55 60

Tyr Trp Tyr Tyr Gln Arg Asp Lys Ile Pro Cys Phe Ala Gln Arg Ile  
65 70 75 80

Cys Ile Ser Ser Leu  
85

(2) INFORMATION FOR SEQ ID NO:783432\_c2\_9: - AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 288 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

Hpp 543

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Ala | Phe | Leu | Lys | Thr | Pro | Arg | Asn | Ser | Ala | Phe | Ala | Leu | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ile | Phe | Val | Gly | Ala | Leu | Leu | Phe | Tyr | Trp | Cys | Ala | Leu | Arg | Leu | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| His | Ser | Asp | Phe | Thr | Tyr | Leu | Leu | Pro | Leu | Ile | Ile | Val | Leu | Val | Ala |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Leu | Val | Tyr | Gly | Val | Leu | Phe | Tyr | Leu | Leu | Leu | Tyr | Phe | Glu | Asn | Pro |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Tyr | Phe | Arg | Leu | Leu | Ser | Phe | Leu | Gly | Ser | Ser | Phe | Ile | His | Pro | Phe |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Gly | Phe | Asp | Trp | Leu | Val | Pro | Asp | Ser | Phe | Phe | Ser | Tyr | Ser | Val | Phe |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Arg | Val | Asp | Lys | Leu | Ser | Leu | Gly | Leu | Ile | Phe | Leu | Ala | Cys | Ile | Phe |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Leu | Ser | Ala | Gln | Asn | Leu | Lys | Lys | Tyr | Arg | Met | Ile | Gly | Val | Leu | Leu |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Leu | Leu | Gly | Ala | Leu | Asp | Phe | His | Phe | Phe | Lys | Ile | Ser | Asp | Leu | Lys |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Glu | Val | Gly | Asn | Ile | Glu | Leu | Val | Ser | Thr | Arg | Thr | Pro | Gln | Asp | Leu |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Lys | Phe | Asp | Ser | Asn | Tyr | Leu | Asn | Asn | Ile | Glu | Asn | Asn | Ile | Leu | Lys |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Glu | Ile | Lys | Leu | Ala | Gln | Ser | Lys | Gln | Lys | Thr | Leu | Ile | Val | Phe | Pro |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Glu | Thr | Ala | Tyr | Pro | Ile | Ala | Leu | Glu | Asn | Ser | Pro | Phe | Lys | Thr | Gln |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Leu | Glu | Asp | Leu | Ser | Asp | Lys | Ile | Ala | Ile | Leu | Ile | Gly | Thr | Leu | Arg |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Ala | Gln | Gly | Tyr | Ser | Leu | Tyr | Asn | Ser | Ser | Phe | Leu | Phe | Ser | Lys | Lys |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |

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Figure 543A - page 646

Ser Val Gln Ile Ala Asp Lys Val Ile Leu Ala Pro Phe Gly Glu Ile  
245 250 255

6A7

Met Pro Leu Pro Glu Phe Leu Gln Lys Pro Leu Glu Lys Leu Phe Phe  
260 265 270

Figure 543A-page 6A7

Ala Arg Ala Leu Ile Tyr Thr Ala Thr Leu Pro Ile Ser Ala Ile Leu  
275 280 285

His

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 435 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 544

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met Asn Asp Pro Lys His Val Val Tyr Val Trp Leu Asp Ala Leu Leu  
1 5 10 15  
Asn Tyr Ala Ser Ala Leu Gly Tyr Leu Asn Gly Leu Asp Asn Lys Met  
20 25 30  
Ala His Phe Glu Arg Ala Arg His Ile Val Gly Lys Asp Ile Leu Arg  
35 40 45  
Phe His Ala Ile Tyr Trp Pro Ala Phe Leu Met Ser Leu Asn Leu Pro  
50 55 60  
Leu Phe Lys Gln Leu Cys Val His Gly Trp Trp Thr Ile Glu Gly Val  
65 70 75 80  
Lys Met Ser Lys Ser Leu Gly Asn Val Leu Asp Ala Gln Lys Leu Ala  
85 90 95  
Met Glu Tyr Gly Ile Glu Glu Leu Arg Tyr Phe Leu Leu Arg Glu Val  
100 105 110  
Pro Phe Gly Gln Asp Gly Asp Phe Ser Lys Lys Ala Leu Val Glu Arg  
115 120 125  
Ile Asn Ala Asn Leu Asn Asn Asp Leu Gly Asn Leu Leu Asn Arg Leu  
130 135 140  
Leu Gly Met Ala Lys Lys Tyr Phe Asn Tyr Ser Leu Lys Ser Thr Lys  
145 150 155 160  
Ile Thr Ala Tyr Tyr Pro Lys Glu Leu Glu Lys Ala His Gln Ile Leu  
165 170 175  
Asp Asn Ala Asn Ser Phe Val Pro Lys Met Gln Leu His Lys Ala Leu  
180 185 190  
Glu Glu Leu Phe Asn Ile Tyr Asp Phe Leu Asn Lys Leu Ile Ala Lys  
195 200 205  
Glu Glu Pro Trp Val Leu His Lys Asn Asn Glu Ser Glu Lys Leu Glu  
210 215 220  
Ala Leu Leu Ser Leu Ile Ala Asn Thr Leu Leu Gln Ser Ser Phe Leu  
225 230 235 240

CAS

Figure 544A - page 648

Figure 544A - page 649

[illegible]

(2) INFORMATION FOR SEQ ID NO:80257\_c1\_23: -AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 545

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met Lys Arg Pro Ile Ser Lys Leu Lys Gln Asn Phe Leu Gln Phe Lys  
1 5 10 15  
His Ser Phe Asn Lys His Leu Asp Lys Tyr Ser Leu Tyr Tyr Arg Leu  
20 25 30  
Phe Asn Ile Ser Ser Ile Val Ile Gly Phe Leu Ile Ala Leu Phe Ser  
35 40 45  
Tyr Gly Ala Gly Val Ile Leu Val Tyr Pro Ile Leu Phe Leu Phe Ala  
50 55 60  
Leu Ile Ile Lys Pro Ser Phe Phe Tyr Tyr Thr Thr Tyr Leu Leu Leu  
65 70 75 80  
Leu Val Ser Leu Ser Ile Ile Ser Lys Tyr Tyr Leu Leu Ser His Ala  
85 90 95  
Asn Phe Thr Met Lys Leu Ile Met Leu Met Thr Gln Trp Gln Asn Trp  
100 105 110  
Phe Leu

650

Figure 545A - page 650



(2) INFORMATION FOR SEQ ID NO:84691\_f2\_2:-AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP546

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ile | Gly | His | Ala | Ile | Gly | Gly | Leu | Val | Leu | Met | Gln | His | Phe | Trp |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Arg | Lys | Lys | Gly | Glu | Leu | Tyr | Phe | Ile | Lys | Leu | Ile | Phe | Phe | Ile | Phe |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | His | Phe | Phe | Ser |     |     |     |     |     |     |     |     |     |     |     |
|     |     |     | 35  |     |     |     |     |     |     |     |     |     |     |     |     |

651

Figure 546A - page 651

(2) INFORMATION FOR SEQ ID NO:85786\_c1\_10: -AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 547

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Gly | Phe | Glu | Lys | Ser | Ile | Leu | Asp | Asn | Leu | Asn | Gly | Ala | Gln | Lys |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Ile | Val | Ala | Cys | His | Ile | Gln | Gly | Pro | Leu | Leu | Ile | Leu | Ala | Gly | Ala |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Gly | Ser | Gly | Lys | Thr | Lys | Thr | Leu | Thr | Ser | Arg | Leu | Ala | Tyr | Leu | Ile |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Gly | Ala | Cys | Gly | Val | Pro | Ser | Glu | Asn | Thr | Leu | Thr | Leu | Thr | Phe | Thr |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Asn | Lys | Ala | Ser | Lys | Glu | Met | Gln | Glu | Arg | Ala | Leu | Lys | Leu | Leu | Lys |  |
| 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     | 80  |  |
| Asn | Gln | Ala | Leu | Ile | Pro | Pro | Leu | Leu | Cys | Thr | Phe | His | Arg | Phe | Gly |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Leu | Leu | Phe | Leu | Arg | Gln | His | Met | Asn | Leu | Leu | Lys | Arg | Ala | Cys | Asp |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Phe | Ser | Val | Leu | Asp | Ser | Asp | Glu | Val | Lys | Thr | Leu | Cys | Lys | Gln | Leu |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Lys | Ile | Ser | Asn | Phe | Arg | Ala | Ser | Ile | Ser | Gln | Ile | Lys | Asn | Gly | Met |  |
|     |     |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Met | Asp | Leu | Ser | Val | Gln | Asp | Ser | Glu | Cys | Tyr | Lys | Ala | Tyr | Glu | Leu |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |
| Tyr | Gln | Asn | Ala | Leu | Lys | Lys | Asp | Asn | Leu | Val | Glu | Phe |     |     |     |  |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     |     |  |

652  
Figure 547A - page 652

(2) INFORMATION FOR SEQ ID NO:867183\_f1\_1: -AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 548

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Val Unk Ala Met Lys Arg Leu His Leu Ser Val Lys Asp Ala Glu Asn  
1 5 10 15  
Phe Asp Ala Ile Leu Arg Glu Arg Pro Phe Phe Lys Asp Leu Ile Glu  
20 25 30  
Phe Met Val Ser Gly Pro Val Val Val Met Val Leu Glu Gly Lys Asp  
35 40 45  
Ala Val Ala Lys Asn Arg Glu Leu Met Gly Ala Thr Asp Pro Lys Leu  
50 55 60  
Ala Gln Lys Gly Thr Ile Arg Ala Asp Phe Ala Glu Ser Ile Asp Ala  
65 70 75 80  
Asn Ala Val His Gly Ser Asp Ser Leu Glu Asn Ala His Asn Glu Ile  
85 90 95  
Ala Phe Phe Phe Ala Ala Arg Glu Phe  
100 105

653

Figure 548A-pg 653

(2) INFORMATION FOR SEQ ID NO:875042\_f1\_2: -AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 549

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: SODIUM-DEPENDENT PROLINE TRANSPORTER

Val Phe Thr Tyr Ser Leu Gly Gln Val Phe Phe Ser Leu Ser Ile Gly  
1 5 10 15  
Leu Gly Ile Asn Ile Thr Tyr Ala Ala Val Thr Asp Lys Thr Gln Asn  
20 25 30  
Leu Leu Lys Ser Thr Ile Trp Val Val Leu Ser Gly Ile Leu Ile Ser  
35 40 45  
Leu Val Unk Gly Leu Met Ile Phe Thr Phe Val Phe Glu Tyr Gly Ala  
50 55 60  
Asn Val Ser Gln Gly Thr Gly Leu Ile Phe Thr Ser Leu Pro Val Val  
65 70 75 80  
Phe Gly Gln Met Gly Ala Ile Gly Val Pro Cys Phe Asn Ser Phe Leu  
85 90 95  
Ala Arg Ala Arg Phe Cys Trp His His Phe Tyr Gly Gly Phe Ile Arg  
100 105 110  
Ala Lys Arg Asp Val Ser Tyr Arg Lys Val Ser Ile Leu Ser Phe  
115 120 125

654

Figure 549A - page 654

655

$$\vdots - AA$$

HPP 550

(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: YES

(A) ORGANISM: *Helicobacter pylori*

Met Lys Pro Leu His Phe Ser His Leu Asp Arg Glu Gln Ser Gly Asp  
1 5 10 15

Val Gly Phe Ile Ile Lys Asn Leu Ile Phe Leu Gly Val Phe Ser Leu  
20 25 30

Leu Gly Trp Leu Asn Thr Glu Tyr Phe Leu Trp Pro Ser Met Leu Glu  
35 40 45

Leu Lys Lys Ile Leu Leu Glu Glu Asn Arg Lys Lys Ser Val Leu Glu  
50 55 60

Tyr Ala Gln Arg His Phe Glu Thr Ala Leu Ala Asn Tyr Arg Asn Gln  
65 70 75 80

Lys Glu Thr Ser Glu Ser Leu Leu Lys Ile Phe Asn Asp Glu Glu Ser  
85 90 95

Arg Arg Ile Leu Glu Lys Ile Leu Lys Lys Cys Phe Asp Ala Tyr Lys  
100 105 110

Ile Lys Pro Leu Leu Ser Gln Asn Pro Ser Gln Lys Thr Gln Phe Phe  
115 120 125

Ile Met Ala Arg Ala Ser Glu Leu Glu Lys Thr Tyr Leu Phe Phe Thr  
130 135 140

```

Leu Ile Asn Lys Tyr Leu
145 150

```



Figure 552 A- page 657

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- |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Met<br>1   | Leu        | Ser        | Ala        | His<br>5   | Gln        | Pro        | Phe        | Lys        | Asn<br>10  | Tyr        | Pro        | Asp        | Leu        | Ile<br>15  | Lys        |
| Lys        | Glu        | Leu        | Gln<br>20  | Glu        | His        | Asn        | Ala        | Tyr<br>25  | Ala        | Ser        | Val        | Ala        | Ser<br>30  | Gly        | Val        |
| Pro        | Ala        | Met<br>35  | Cys        | Asp        | Gly        | Ile        | Thr<br>40  | Gln        | Gly        | Tyr        | Glu        | Gly<br>45  | Met        | Glu        | Leu        |
| Ser        | Leu<br>50  | Phe        | Ser        | Arg        | Asp        | Val<br>55  | Ile        | Ala        | Leu        | Ser        | Thr<br>60  | Unk        | Val        | Gly        | Leu        |
| Ser<br>65  | His        | Asn        | Val        | Phe        | Asp<br>70  | Gly        | Ala        | Phe        | Phe        | Leu<br>75  | Gly        | Val        | Cys        | Asp        | Lys<br>80  |
| Ile        | Val        | Pro        | Gly        | Leu<br>85  | Leu        | Ile        | Gly        | Ala        | Leu<br>90  | Ser        | Phe        | Gly        | Asn        | Leu<br>95  | Ala        |
| Ser        | Val        | Phe        | Val<br>100 | Pro        | Ser        | Gly        | Pro        | Met<br>105 | Val        | Ser        | Gly        | Ile        | Glu<br>110 | Asn        | Tyr        |
| Lys        | Lys        | Ala<br>115 | Lys        | Ala        | Arg        | Gln        | Asp<br>120 | Phe        | Ala        | Met        | Gly        | Lys<br>125 | Ile        | Asn        | Arg        |
| Glu        | Glu<br>130 | Leu        | Leu        | Lys        | Val        | Glu<br>135 | Met        | Gln        | Ser        | Tyr        | His<br>140 | Asp        | Val        | Gly        | Thr        |
| Cys<br>145 | Thr        | Phe        | Tyr        | Gly        | Thr<br>150 | Ala        | Asn        | Ser        | Asn        | Gln<br>155 | Met        | Met        | Met        | Glu        | Phe<br>160 |
| Met        | Gly        | Leu        | His        | Val<br>165 | Ala        | Asn        | Ser        | Ser        | Phe<br>170 | Ile        | Asn        | Pro        | Asn        | Asn<br>175 | Pro        |
| Leu        | Arg        | Lys        | Val<br>180 | Leu        | Val        | Glu        | Glu        | Ser<br>185 | Ala        | Lys        | Arg        | Leu        | Ala<br>190 | Ser        | Gly        |
| Lys        | Val        | Leu<br>195 | Pro        | Leu        | Ala        | Lys        | Leu<br>200 | Ile        | Asp        | Glu        | Lys        | Ser<br>205 | Ile        | Leu        | Asn        |
| Ala        | Leu<br>210 | Ile        | Gly        | Leu        | Met        | Ala<br>215 | Thr        | Gly        | Gly        | Ser        | Thr<br>220 | Asn        | His        | Thr        | Leu        |
| His<br>225 | Leu        | Ile        | Ala        | Ile        | Ala<br>230 | Asp        | Leu        | Val        | Gly        |            |            |            |            |            |            |

(2) INFORMATION FOR SEQ ID NO:917152\_f1\_3: -AA

658

Figure 553A - page 658

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

HPP 553

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: minor flagellin flaB precursor-H.pylori

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Trp | Leu | Lys | Thr | Leu | Thr | Leu | Gln | Thr | Leu | Asn | Thr | Asp | Lys | Ala |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Leu | Gln | Glu | Phe | Ser | Lys | Thr | Met | Glu | Ala | Phe | Lys | Thr | Lys | Leu | Ile |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gln | Ser | Ala | Asn | Asp | Val | His | Ser | Glu | Thr | Ser | Arg | Ala | Ala | Ile | Ala |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Asn | Asp | Leu | Glu | Arg | Leu | Lys | Glu | His | Met | Ile | Asn | Val | Ala | Asn | Thr |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Ser | Ile | Gly | Gly | Glu | Phe | Leu | Phe | Gly | Gly | Ser | Lys | Val | Asp | Arg | Pro |
| 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     |     | 80  |
| Pro | Ile | Asp | Ser | Asn | Gly | Lys | Tyr | His | Gly | Asn | Gly | Glu | Asp | Leu | Asn |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ala | Leu | Ile | Ser | Ser | Asp | Asn | Leu | Val | Pro | Tyr | Asn | Ile | Ser | Gly | Gln |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Asp | Leu | Phe | Leu | Gly | Thr | Asp | Lys | Asp | Lys | His | Lys | Leu | Ile | Thr | Thr |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Asn | Ile | Lys | Leu | Leu | Asn | Gln | Asn | Lys | Leu | His | Leu | Met |     |     |     |
|     |     | 130 |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |



(2) INFORMATION FOR SEQ ID NO:917200\_c2\_8:-AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 554

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met Val Phe Phe His Lys Lys Ile Ile Leu Asn Phe Ile Tyr Ser Leu  
1 5 10 15  
Met Val Ala Phe Leu Phe His Leu Ser Tyr Gly Val Leu Leu Lys Ala  
20 25 30  
Asp Gly Met Ala Lys Lys Gln Thr Leu Leu Val Gly Glu Arg Leu Val  
35 40 45  
Trp Asp Lys Leu Thr Leu Leu Gly Phe Leu Glu Lys Asn His Ile Pro  
50 55 60  
Gln Lys Leu Tyr Tyr Asn Leu Ser Ser Gln Asp Lys Glu Leu Ser Ala  
65 70 75 80  
Glu Ile Gln Ser Asn Val Thr Tyr Tyr Thr Leu Arg Asp Ala Asn Asn  
85 90 95  
Thr Leu Ile Gln Ala Leu Ile Pro Tyr  
100 105

659

Figure 554A-page 659

(2) INFORMATION FOR SEQ ID NO:9776562\_c3\_13: -AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

HPP 555

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met Lys Phe Leu Lys Phe Phe Ala Ser Ser Val Thr Leu Asp Glu Lys  
1 5 10 15  
Phe Leu Met Phe Leu Leu Cys Asn Ala Leu Ser Asn Ala Tyr Lys Asn  
20 25 30  
Ser Asp Leu Phe Ser Phe Ser Lys Gly Phe Leu Gly Ala Phe Leu Ile  
35 40 45  
Gly Phe Val Val Tyr Tyr Gly Cys Ala Leu Ile Pro Lys Lys Arg Leu  
50 55 60  
Lys Tyr Ser Leu Glu Trp Leu Phe Ile Gly Ser Gly Ile Ile Phe Ser  
65 70 75 80  
Val Ala Glu Ile Phe Thr Leu Phe Met Phe Lys Met Pro Phe Ser Lys  
85 90 95  
Gly Leu Ile Asp Thr Leu Leu Ala Thr Asn Ser Ser Glu Thr Met Ala  
100 105 110  
Phe Ile Lys Ser Tyr Lys Asn Tyr Leu Leu Tyr Tyr Ala Leu Ile Leu  
115 120 125  
Ile Ala Leu Leu Ile Ala Ile Lys Ile Ile Arg Phe Arg Ala Leu Val  
130 135 140  
Pro Gly Val Ile Ala Ser Val Leu Gly Leu Ser Ile Leu Thr Ile Gly  
145 150 155 160  
Ser Val Arg Asn Ile Lys His Leu Thr Lys Asn Asp Ala Ile Leu Lys  
165 170 175  
Arg Ser Leu Phe Ser Leu Ser Leu Ala Arg Gly Phe Tyr Ser Ala Tyr  
180 185 190  
Leu Ser Leu Phe Asp Arg Gln Gln Ala Ile Lys Phe Tyr Ser Phe Leu  
195 200 205  
Asn Asn Leu Tyr Leu Pro Ser Asp Tyr Leu Ser Ser Thr Gly Asp Ile  
210 215 220  
Ser Asn Val Val Leu Val Ile Ala Lys Ala Arg Ala Glu Ile Ser Cys  
225 230 235 240

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Figure 555A-page 660

Asn Ser Met Ala Ile Ala Phe Leu Ile Ile Pro Tyr Thr Ser Glu Leu  
245 250 255

661

Ala Asn Glu Arg Glu Arg Glu Arg Glu  
260 265

Figure 555A-page 661

(2) INFORMATION FOR SEQ ID NO:978477\_f2\_1: -AA

662  
Figure 556A-page 662

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 378 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

H PP 556

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: fibronectin/fibrinogen-binding protein (FBP54 may

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Phe | Phe | Leu | Leu | Lys | Lys | Phe | Ser | Unk | Phe | Leu | Asn | Thr | Gln |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Thr | His | Phe | Asn | Leu | Lys | Arg | Leu | Asn | Ala | Ser | Ser | Phe | Leu | Leu | Glu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Thr | Phe | Ser | Lys | Glu | Lys | His | Ala | Phe | Val | Val | Asp | Leu | Ser | Ala | Pro |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Tyr | Ile | Gly | Leu | Ser | Lys | Lys | Pro | Pro | Glu | Ser | Val | Leu | Lys | Asn | Thr |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Ala | Leu | Asp | Phe | Cys | Leu | Asn | Lys | Phe | Thr | Lys | Asn | Ala | Lys | Ile |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Leu | Gln | Ala | Asn | Val | Ile | Asp | Asn | Asp | Arg | Ile | Leu | Glu | Ile | Lys | Gly |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ala | Lys | Asp | Leu | Ala | Tyr | Lys | Ser | Glu | Thr | Phe | Ile | Leu | Arg | Leu | Glu |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Met | Ile | Pro | Lys | Lys | Ala | Asn | Leu | Met | Ile | Leu | Asp | Gln | Glu | Lys | Cys |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Val | Ile | Glu | Ala | Phe | Arg | Phe | Asn | Asp | Arg | Val | Ala | Lys | Asn | Asp | Ile |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Leu | Gly | Ala | Leu | Pro | Pro | Asn | Ile | Tyr | Glu | His | Gln | Glu | Glu | Asp | Leu |
| 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     |     | 160 |
| Asp | Phe | Lys | Gly | Leu | Leu | Asp | Ile | Leu | Glu | Lys | Asp | Phe | Leu | Ser | Tyr |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Gln | His | Lys | Glu | Leu | Glu | His | Lys | Lys | Asn | Gln | Ile | Ile | Lys | Arg | Leu |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Asn | Ala | Gln | Lys | Glu | Arg | Leu | Lys | Glu | Lys | Leu | Glu | Lys | Leu | Glu | Asp |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Pro | Lys | Thr | Leu | Gln | Leu | Glu | Ala | Lys | Glu | Leu | Gln | Thr | Gln | Ala | Ser |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Leu | Leu | Leu | Thr | Tyr | Gln | His | Leu | Ile | Asn | Arg | Arg | Glu | Asn | Arg | Val |
| 225 |     |     |     |     | 230 |     |     |     | 235 |     |     |     |     |     | 240 |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Ile | Leu | Lys | Asp | Phe | Glu | Asp | Lys | Glu | Cys | Met | Ile | Glu | Ile | Asp | Lys |  |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |  |
| Ser | Met | Pro | Leu | Asn | Ala | Phe | Ile | Asn | Lys | Lys | Phe | Thr | Leu | Ser | Lys |  |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |  |
| Lys | Lys | Lys | Gln | Lys | Ser | Gln | Phe | Leu | Tyr | Leu | Glu | Glu | Glu | Asn | Leu |  |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |  |
| Lys | Glu | Lys | Ile | Ala | Phe | Lys | Glu | Asn | Gln | Ile | Asn | Tyr | Val | Arg | Asp |  |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |  |
| Ala | Ala | Glu | Glu | Ser | Val | Leu | Glu | Met | Phe | Met | Pro | Val | Lys | Asn | Ser |  |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |  |
| Lys | Ile | Lys | Arg | Pro | Met | Asn | Gly | Tyr | Glu | Val | Leu | Tyr | Tyr | Lys | Asp |  |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |  |
| Unk | Lys | Unk | Gly | Unk | Gly | Lys | Thr | Lys | Lys | Arg | Ile | Ser | Ser | Phe | Tyr |  |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |  |
| Lys | Thr | Gln | Unk | Arg | Met | Ile | Leu | Asp | Ala | Unk | Arg | Asp | Ile | Pro | Gly |  |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |  |
| Unk | His | Leu | Ile | Val | Phe | Ser | Lys | Unk | Ile | Ala |     |     |     |     |     |  |
|     | 370 |     |     |     |     | 375 |     |     |     |     |     |     |     |     |     |  |

643  
Figure 556A -  
page 663

(2) INFORMATION FOR SEQ ID NO:98191\_f2\_2: - AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION:

Met Unk Phe Unk Arg Unk Val Gly Unk Unk Lys Ser Unk Leu Leu Val  
1 5 10 15

Glu Gly Leu Val Unk Leu Gly Phe Unk Gly Phe Leu Lys Ser Leu Arg  
20 25 30

Leu Unk Gly Gly Gly Unk Phe Asn Ser Asn Ser Ile Lys Trp Unk Gly  
35 40 45

Tyr Lys Lys Ile Lys Lys Leu  
50 55

664  
Figure 557A-page 664

HPP 557

(2) INFORMATION FOR SEQ ID NO:9954743\_c2\_14:-AA

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Helicobacter pylori

(xi) SEQUENCE DESCRIPTION: weak similarity to vacA (duplication?)

Met Trp Leu Ser Glu His Phe Ala Ala Lys Gly Gly Asn Pro Leu Phe  
1 5 10 15  
Ala Pro Tyr Tyr Leu Gln Asp Asn Pro Thr Glu His Ile Val Thr Leu  
20 25 30  
Met Lys Asp Ile Thr Ser Ala Leu Gly Met Leu Ser Asn Ser Asn Leu  
35 40 45  
Lys Asn Asn Ser Thr Asp Val Leu Gln Leu Asn Thr Tyr Thr Gln Gln  
50 55 60  
Met Ser Arg Leu Ala Lys Leu Ser Asn Phe Ala Ser Phe Asp Ser Thr  
65 70 75 80  
Asp Phe Ser Glu Arg Leu Ser Ser Leu Lys Asn Gln Arg Phe Ala Asp  
85 90 95  
Ala Val Pro Asn Ala Met Asp Val Ile Leu Lys Tyr Ser Gln Arg Asp  
100 105 110  
Lys Leu Lys Asn Asn Leu Trp Ala Thr Gly Val Gly Gly Val Ser Phe  
115 120 125  
Val Glu Asn Gly Thr Gly Thr Leu Tyr Gly Val Asn Val Gly Tyr Asp  
130 135 140  
Arg Phe Val Arg Gly Val Ile Val Gly Gly Tyr Ala Ala Tyr Gly Tyr  
145 150 155 160  
Ser Gly Phe Tyr Glu Arg Ile Thr Ser Ser Lys Ser Asp Asn Val Asp  
165 170 175  
Val Gly Met Tyr Ala Arg Ala Phe Ile Lys Lys Ser Glu Leu Thr Phe  
180 185 190  
Arg Arg

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